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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN

🔘 (57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human brain is described. Also described are single exon nucleic acid probes expressed in the brain and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN

CROSS REFERENCE TO RELATED APPLICATIONS

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The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S.provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY REFERENCE THEREOF

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The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto_BRAIN.txt, created 24 January 2001, having 25,840,972 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

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The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genomederived single exon nucleic acid probes expressed in human

brain and single exon nucleic acid microarrays that include such probes.

Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., Proc. Natl. Acad. Sci. USA 70(4):1209-13 (1973); Gilbert et al., Proc. Natl. Acad. Sci. USA 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins — known or suspected — about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., Nature 308(5955):153-8 (1984).

More recently, however, the development of high
throughput sequencing methods and devices, in concert with
large public and private undertakings to sequence the human
and other genomes, has altered this investigational
paradigm: today, sequence information often precedes
understanding of the basic biology of the encoded protein
product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences — that is, those accessible through isolation of mRNA — are of greatest initial interest. This "expressed sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,

Science 252:1651 (1991); Williamson, Drug Discov. Today

4:115 (1999)). For nucleic acids sequenced by this

approach, often the only biological information that is

known a priori with any certainty is the likelihood of

biologic expression itself. By virtue of the species and

tissue from which the mRNA had originally been obtained,

most such sequences are also annotated with the identity of

the species and at least one tissue in which expression

appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot be presumed; often the only a priori biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing approaches — and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species — there is an increasing need for methods that rapidly and effectively permit the functions of nucleic sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, Science 280:995 (1998); Pennisi, Science 283: 1822-1823 (1999), there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the C. elegans genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. C. elegans Sequencing Consortium, 10 Science 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of Arabidopsis predicts over 4000 genes, Lin et al., Nature, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the 15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many 20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence — and most importantly, but not exclusively, regions that

25 function to encode genes — to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., Proc. Natl. Acad. Sci. USA 88(24):11261-5 (1991); Xu et al., Genet. Eng. 16:241-53 (1994); Uberbacher et al., Methods Enzymol. 266:259-81 (1996); GENEFINDER, Solovyev et al., Nucl. Acids. Res. 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., J. Mol.
Biol. 268:78-94 (1997), predict many putative genes without
known homology or function. Such programs are known,
however, to give high false positive rates. Burset et al.,
Genomics 34:353-367 (1996). Using a consensus obtained by
a plurality of such programs is known to increase the
reliability of calling exons from genomic sequence.
Ansari-Lari et al., Genome Res. 8(1):29-40 (1998)

Identification of functional genes from genomic
data remains, however, an imperfect art. For example, in
reporting the full sequence of human chromosome 21, the
Chromosome 21 Mapping and Sequencing Consortium reports
that prior bioinformatic estimates of human gene number may
need to be revised substantially downwards. Nature
405:311-199 (2000); Reeves, Nature 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically — and specifically, that permit the expression of regions predicted to encode protein — readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays: A Practical Approach

25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., Genomics 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., Cancer Res. (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast Saccharomyces cerevisiae. De Risi et al., Science 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single exon genes, i.e., lack introns, Lopez et al., RNA 5:1135-1137 (1999); Goffeau et al., Science 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the brain and nervous system are a significant cause of human morbidity and mortality.

Increasingly, genetic factors are being found that

contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.

There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the brain and nervous system particularly those diseases with polygenic etiology.

30 Summary of the Invention

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional

information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel

genome-derived single exon nucleic acid microarrays useful
for verifying the expression of putative genes identified
within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids

10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single

15 exon nucleic acid probes for measuring gene expression in a sample derived from human brain, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality
of probes is amplifiable using at least one common primer.
Preferably, each of said plurality of probes is amplifiable
using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,434 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

25 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is is addressably disposed upon a substrate.

Suitable substrates include a filter membrane
30 which may, preferably, be nitrocellulose or nylon. The
13 nylon may preferably, be positively-charged. Other suitable
14 substrates include glass, amorphous silicon, crystalline
15 silicon, and plastic. Further suitable materials include
16 polymethylacrylic, polyethylene, polypropylene,

35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

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polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is 5 provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of 10 amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

15 In another aspect, the invention provides genomederived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon 20 probes that include specifically-hybridizable fragments of SEQ ID Nos. 12,822 - 25,434, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 12,821.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 -30 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

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In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a 35 nucleotide sequence as set out in any of SEQ ID NOs.:

12,822 - 25,434 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,435 - 37,811or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon
nucleic acid probe in accordance with the third or fourth
aspects of the invention is between 3kb and 25kb in length.
It is preferred that said probe is no more than 3kb,
suitably no more than 5kb, more suitably no more than 10kb,
preferably 15kb, more preferably 20kb or, most preferably,
no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3

and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human brain, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human brain; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic 30 genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are

derived from mRNA from the brain of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon 5 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,

10 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in

15 a plurality of tissues and/or cell types using

hybridization to single exon microarrays having a probe

with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types 20 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1-25,434 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 12,822 - 25,434, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,821.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 25,435 - 37,811.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,435 - 37,811, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

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Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

"nucleic acid microarray" include all the devices so called
in Schena (ed.), DNA Microarrays: A Practical Approach
(Practical Approach Series), Oxford University Press (1999)
(ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60
(1999); and Schena (ed.), Microarray Biochip: Tools and
Technology, Eaton Publishing Company/BioTechniques Books
Division (2000) (ISBN: 1881299376). As so defined, the
term "microarray" and phrase "nucleic acid microarray"
further include substrate-bound collections of plural
nucleic acids in which the nucleic acids are distributably
disposed on a plurality of beads, rather than on a unitary
planar substrate, as is described, inter alia, in Brenner

et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

- As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick
- 10 complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a 5 portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a 10 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF 15 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another 20 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit 25 specific binding when they exhibit avidity of at least 10^7 , preferably at least 108, more preferably at least 109 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual 35 object of the display.

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As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

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Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;
FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described,

30 of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (1 x 10⁻³⁰) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 (1 x 10⁻³⁰) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

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Methods and Apparatus for Predicting, Confirming,

Annotating, and Displaying Functional Regions From Genomic

Sequence Data

outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original

sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting inter alia of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100
in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI).

Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. brigsii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into 15 mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

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25 FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and 30 facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of 5 functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 10 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified inter alia using gene prediction approaches, comparative sequence analysis 15 approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, 20 corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic 30 sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

25

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in 35 addition, such operative criteria can be enforced in

subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a

required minimal individual genomic sequence fragment
length, such as 10 kb, more typically 20 kb, 30 kb, 40kb,
and preferably 50 kb or more, as well as an optional
further or alternative requirement that sequence from any
given clone, such as a bacterial artificial chromosome

("BAC"), be presented in no more than a finite maximal
number of fragments, such as no more than 20 separate
pieces, more typically no more than 15 fragments, even more
typically no more than about 10 - 12 fragments.

Results using the present invention have shown
that genomic sequence from bacterial artificial chromosomes
(BACs) is sufficient for gene prediction analysis according
to the present invention if the sequence is at least 50 kb
in length, and if additionally the sequence from any given
BAC is presented in fewer than 15, and preferably fewer
than 10, fragments. Accordingly, query 20 can incorporate
a requirement that data accessioned from BAC sequencing be
in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of

30 sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus,

35 as further described in Examples 1 and 2, infra, it is

possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query 35 criteria, the returned sequence is then passed to optional

preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable,
including artifactual, sequence can be identified
algorithmically without comparison to external databases
and thereafter removed. For example, synthetic polylinker
sequence can be identified by an algorithm that identifies
a significantly higher than average density of known
restriction sites. As another example, vector sequence can
be identified by algorithms that identify nucleotide or
codon usage at variance with that of the bulk of the
genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the

undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".

Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.

Such formatting can and typically will include, inter alia, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating

35 transcription, regulating message transport after

transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene
30 finding software programs yield a range of results. For
the newly accessioned human genomic sequence input in
Example 1, for example, GRAIL identified the greatest
percentage of genomic sequence as putative coding region,
2% of the data analyzed; GENEFINDER was second, calling 1%;
35 and DICTION yielded the least putative coding region, with

0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further

20 described in Example 1, infra, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process

can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the
10 multiple analyses required to achieve consensus can be done
in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to 20 identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based inter alia upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the genespecific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify

and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving

5 hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

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Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the 5 polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with 10 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer 20 amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

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Therefore, amplification schemes can alternatively, and preferably, be designed to amplify 25 regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it 35 has been discovered that the percentage success at

amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at http://www-genome.wi.mit.edu/cgi-bin/primer/), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from

which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning: A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

15 Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, 20 the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes 25 not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, 5 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, 10 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination 20 thereof.

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Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, http://cmgm.stanford.edu/pbrown/mguide/index.html), or 25 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of E. coli genes can 35 readily be used. As further described in Example 1, 16 or

32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.

If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
high density microarrays constructed on planar substrates,
the methods of the present invention for confirming the
expression of ORFs predicted from genomic sequence can use
any of the known types of microarrays, as herein defined,
including lower density planar arrays, and microarrays on
nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.

25 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For

example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will 5 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one 10 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created 20 by in situ synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

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Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or 25 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the de novo construction of "problem specific" 30 libraries targeted at a particular biological question, R.S. Thomas et al., Cancer Res. (in press). Such microarrays are herein collectively denominated "EST, microarrays".

Such EST microarrays by definition can measure 35 expression only of those genes found in EST libraries,

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shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective 5 genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be 10 determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, infra, the remaining population of genes identified from genomic sequence by the methods of the 15 present invention — that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA 20 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

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In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present 30 invention depends upon a successful amplification from genomic material, a priori knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse 35 transcription and cloning of unknown message in EST

approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genomederived single exon microarrays of the present invention
lack homopolymeric stretches derived from message
polyadenylation, and thus can provide more specific signal.
Typically, at least about 50, 60 or 75% of the probes on
the genome-derived single exon microarrays of the present
invention lack homopolymeric regions consisting of A or T,
where a homopolymeric region is defined for purposes herein
as stretches of 25 or more, typically 30 or more, identical
nucleotides.

A further distinction, which also affects the

25 specificity of hybridization, is occasioned by the typical
derivation of EST microarray probes from cloned material.

Because much of the probe material disposed as probes on
EST microarrays is excised or amplified from plasmid,
phage, or phagemid vectors, EST microarrays typically

30 include a fair amount of vector sequence, more so when the
probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from

genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-15 hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker

20 multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include

25 artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even

smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such

5 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual

15 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be

20 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partiallyspliced message, probes disposed upon EST arrays will often
include multiple exons. The percentage of such exonspanning probes in an EST microarray can be calculated, on
average, based upon the predicted number of exons/gene for
the given species and the average length of the immobilized
probes. For human genes, the near-complete sequence of
human chromosome 22, Dunham et al., Nature 402(6761):489-95
(1999), predicts that human genes average 5.5 exons/gene.
Even with probes of 200 - 500 bp, the vast majority of
human EST microarray probes include more than one exon.

35 In contrast, by virtue of their origin from

algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genomederived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genomederived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA.

Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from in situ synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic 5 synthesis process.

Typically, probes arrayed on in situ synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to 10 achieve unambiguous sequence-specific hybridization results, the in situ synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present 20 invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved 25 for in situ synthesis microarrays.

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A further distinction is that the probes in in situ synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention 30 typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on in situ microarrays causes large percentage differences in the melting temperature of probes hybridized to their 35 complementary target sequence, and thus causes large

percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over in situ synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the in situ synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., Proc. Natl. Acad. Sci. USA 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear

genes in Saccharomyces cerevisiae - that is, only about 4
- 5% - have standard, spliceosomal, introns, Lopez et al.,
Nucl. Acids Res. 28:85-86 (2000); Spingola et al., RNA
5(2):221-34 (1999). Furthermore, the entire yeast genome
has already been sequenced. These two facts permit the
ready amplification and disposition of single-ORF amplicons
on such microarray without the requirement for antecedent
use of gene prediction and/or comparative sequence
analyses.

Thus, a significant aspect of the present

invention is the ability to identify and to confirm

expression of predicted coding regions in genomic sequence

drawn from eukaryotic organisms that have a higher

percentage of genes having introns than do yeast such as

Saccharomyces cerevisiae, particularly in genomic sequence

drawn from eukaryotes in which at least about 10, 20 or 50%

of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

. After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the

20 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, infra.

mRNA can be prepared by standard techniques, see

30 Ausubel et al. and Maniatis et al., or purchased
commercially. The mRNA is then typically reversetranscribed in the presence of labeled nucleotides: the
index source (that in which expression is desired to be
measured) is reverse transcribed in the presence of

35 nucleotides labeled with a first label, typically a

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fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As 5 further described in Example 2, infra, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are 15 related to the original sequence.

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Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain 20 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for 25 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived 30 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate 35 can be used, greater efficiency is obtained using higher

density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome10 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'
15 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation

information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

10

Although the use of high density genome-derived microarrays on solid planar substrates is presently a

15 preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide") polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query —

including information on identical sequences and
information on nonidentical sequences that have diffuse or
focal regions of sequence homology to the query sequence can then be passed directly to process 500, or used to
inform analyses subsequently undertaken in process 200,
process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an

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annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left 5 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

10

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides 15 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other 20 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. 25 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or 30 fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity 35 or identity to an input query sequence. When visual

display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection 5 tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional 10 sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method 20 and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

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25 Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c 30 represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. 35 For example, rectangles 83a can represent the results from

GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83

5 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue,

density, or texture of rectangles 83 can be used further to
report a measure of the bioinformatic reliability of the
prediction. For example, many gene prediction programs
will report a measure of the reliability of prediction.
Thus, increasing degrees of such reliability can be

indicated, e.g., by increasing density of shading. Where
display 80 is used as a graphical user interface, such
measures of reliability, and indeed all other results
output by the program, can additionally or alternatively be
made accessible through linkage from individual rectangles
83, as by time-delayed window ("tool tip" window), or by
pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, 5 such function can usefully be indicated and userselectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the 10 portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional 15 inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an 20 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

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Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 30 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted supra, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the 35 probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of 5 expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting 10 thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be 20 predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified 25 in existing expression data bases.

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Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and 30 displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity 35 has a user-selectable lower threshold). Alternatively, as

many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links

5 directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of

25 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to

30 depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed infra, such

relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user

interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented infra.

BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

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The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is

protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon

15 microarrays of the present invention, we have for example
readily identified a large number of unique ORFs from human
genomic sequence. Using single exon probes that encompass
these ORFs, we have demonstrated, through microarray
hybridization analysis, the expression of 12,821 of these

20 ORFs in brain.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in brain is currently available for use in measuring the level of its ORF's expression in brain.

Diseases of the brain and nervous system are a significant cause of human morbidity and mortality.

Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.

For example, over the past few decades

35 Alzheimer's disease (AD), once considered a rare disorder,

has become recognized as a major public health problem; over 4,000,000 people in the United States are now estimated to suffer with various stages of this progressive, degenerative brain disorder.

Although there is no agreement on the exact incidence or prevalence of Alzheimer's disease, in part due to varying diagnostic criteria and difficulties of differential diagnosis among dementias, the studies are consistent in pointing to an exponential rise in prevalence of this disease with age. After age 65, the percentage of affected people approximately doubles with every decade of life, regardless of definition. Among people age 85 or older, studies suggest that 25 to 35 percent have dementia, including Alzheimer's disease; one study reports that 47.2 percent of people over age 85 have Alzheimer's disease, exclusive of other dementias.

Alzheimer's disease progressively destroys memory, reason, judgment, language, and, eventually, the ability to carry out even the simplest of tasks. Anatomic changes associated with Alzheimer's disease begin in the entorhinal cortex, proceed to the hippocampus, and then gradually spread to other regions, particularly the cerebral cortex. Chief among such anatomic changes are the presence of characteristic extracellular plaques and internal neurofibrillary tangles.

Alzheimer's disease has been suspected to have a multifactorial genetic etiological component for almost half a century. Sjogren et al., Acta Psychiat. Neurol. Scand. 82(suppl.): 1-152 (1952).

At least four genes have been identified to date that contribute to development of Alzheimer's disease: AD1 is caused by mutations in the amyloid precursor gene (APP); AD2 is associated with the APOE4 allele on chromosome 19; AD3 is caused by mutation in a chromosome 14 gene encoding a 7-transmembrane domain protein, presentilin-1 (PSEN1), and

AD4 is caused by mutation in a gene on chromosome 1 that encodes a similar 7-transmembrane domain protein, presenilin-2 (PSEN2).

There is strong evidence, however, for additional, as yet uncharacterized, AD loci on other chromosomes.

For example, Daw et al., Am. J. Hum. Genet. 66: 196-204 (2000), estimated the number of additional quantitative trait loci (QTLs) and their contribution to the variance in age at onset of AD, and reported that 4 loci make a contribution to the variance in age at onset of late-onset AD similar to or greater in magnitude than that made by apoE, with one locus making a contribution several times greater than that of apoE. These results suggest that several genes not yet localized may play a larger role than does apoE in late-onset AD.

In accord, three groups recently announced the possible existence of an AD susceptibility gene on chromosome 10. Bertram et al., Science 290(5500):2302-2303 (2000); Ertekin-Taner et al., Science 290(5500):2303-2304 (2000); and Myers et al., Science 290(5500):2304-23055 (2000).

As another example, multiple sclerosis (MS)

25 affects about 350,000 Americans, with approximately 200 new cases diagnosed each week, with an estimated annual monetary cost in the U.S. alone of \$2.5 billion.

Clinically, MS is an unpredictable disorder, with symptoms, presentation and course falling broadly into one of several clinical patterns. In relapsing-remitting (RR) MS, the disease first manifests as a series of attacks followed by complete or partial remissions, with symptoms returning later after a period of stability. In primary-progressive (PP) MS, there is a gradual clinical decline with no distinct remissions, although there may be

temporary plateaus or minor relief from symptoms.

Secondary-progressive (SP) MS begins with a relapsingremitting course followed by a later primary-progressive
course. Rarely, patients may have a progressive-relapsing

(PR) course in which the disease takes a progressive
path punctuated by acute attacks. PP, SP, and PR MS are
sometimes lumped together and called chronic progressive
MS. The waxing and waning course characteristic of RR, SP
and PR MS makes differential diagnosis difficult.

Anatomically, MS attacks are associated with focal inflammation in areas of the white matter of the central nervous system (CNS), accompanied or followed by demyelination in these areas, termed plaques. Destruction of the myelin sheath slows or blocks neurological transmission, leading to diminished or lost function. Clinical manifestations depend upon the location of the plaques and severity of demyelination, and range from fatigue, the most common symptom of MS, to visual impairment, due to inflammation of the optic nerve, termed optic neuritis, to numbness and paresthesias, to focal muscular weakness, ataxia, and bladder incontinence.

Increasing evidence suggests that genotype contributes to susceptibility to MS.

As early as 1965, McAlpine, in Multiple

25 Sclerosis: A Reappraisal (McAlpine, ed.), Williams and
Wilkins Co. pp. 61-74 (1965), concluded that the risk to a
first-degree relative of a patient with multiple sclerosis
is at least 15 times that for a member of the general
population, but could discern no definite genetic pattern

30 of inheritance.

Subsequently, many studies associated MS with HLA (MHC) haplotype. Haines et al., Hum. Molec. Genet. 7:1229-1234 (1998), studying a data set of 98 multiplex MS families, confirmed earlier reports that genetic linkage to the MHC can be explained by association with the HLA-DR2

allele, but suggested that MHC association explains only between 17% and 62% of the genetic etiology of MS.

From a review of genomic screens, Dyment et al.,
Hum. Molec. Genet. 6: 1693-1698 (1997), concluded that a

5 number of genes with interacting effects are likely and
that no single region has a major influence on familial
risk. Chataway et al., Brain 121: 1869-1887 (1998),
reporting a follow-up on U.K. studies using a systematic
genome screen to determine the genetic basis of MS, stated

10 that a gene of major effect had been excluded from 95% of
the genome and one with a moderate role from 65%, results
thus suggesting that multiple sclerosis depends on
independent or epistatic effects of several genes, each
with small individual effects, rather than a very few genes

15 of major biologic importance.

As a yet further example, schizophrenia has long been recognized to have complex, likely polygenic, genetic contributions.

Schizophrenia is a common psychiatric disorder, 20 occurring in 1 to 1.5 percent of the population worldwide, and is characterized by variable constellations of symptoms drawn from a universe of behavioral abnormalities. Although there are accepted alternative diagnostic criteria, primary criteria for diagnosis require two or 25 more of the following, each present for a significant portion of time during a 1-month period (or less if successfully treated): (1) delusions; (2) hallucinations ; (3) disorganized speech (e.g., frequent derailment or incoherence); (4) grossly disorganized or catatonic 30 behavior; (5) negative symptoms, i.e., affective flattening, alogia, or avolition. (Diagnostic and Statistic Manual of Mental Disorders DSM-IV-TR, American Psychiatric Association (2000)). Only one such symptom is required if delusions are bizarre or hallucinations 35 consist of a voice keeping up a running commentary on the

person's behavior or thoughts, or consist of two or more voices conversing with each other.

Three-quarters of persons with schizophrenia develop the disease between 16 and 25 years of age: onset is uncommon after age 30, rare after age 40. In the 16 to 25 year old age group, schizophrenia affects more men than women; in the 25-30 year old group, the incidence is higher in women than in men. Studies have shown that some persons with schizophrenia recover completely, and many others improve to the point where they can live independently, often with the maintenance of drug therapy. However, approximately 15 percent of people with schizophrenia respond only moderately to medication and require extensive support throughout their lives, while another 15 percent simply do not respond to existing treatment.

Schizophrenia has long been known to have a significant genetic component. Studies have consistently demonstrated that the risk to relatives of a proband with schizophrenia is higher than the risk to relatives of 20 controls. Moldin, in Genetics and Mental Disorders: Report. of the NIMH Genetics Workgroup (NIH publication 98-4268, (1998), reviewed family and twin studies published between 1920 and 1987 and found the recurrence risk ratios to be 48 for monozygotic twins, 11 for first-degree relatives, 4.25 25 for second-degree relatives, and 2 for third-degree relatives. He also found that concordance rates for monozygotic twins averaged 46%, even when reared in different families, whereas the concordance rates for dizygotic twins averaged only 14%. The prevalence of 30 schizophrenia is known to be higher in biologic than in adoptive relatives of schizophrenic adoptees.

The mode of inheritance is unclear, however.

Susceptibility has been mapped to many loci, including chromosomes 1q21-q22, 5, 6p23, 8p22-p21, 11q, 13q14-q21, 13q32, 15q15, 15q14, 18p, and 22q11. Chromosome

19 has also been implicated in schizophrenia, at 2 different sites, as have sites on the X chromosome. al., Nature Genet. 25:376-377 (2000) report more specifically that the NOTCH4 locus is associated with 5 susceptibility to schizophrenia.

In general, however, it is believed that development of schizophrenia involves multiple loci.

For example, Williams et al., Hum. Molec. Genet. 8:1729-1739 (1999) undertook a systematic search for 10 linkage in 196 affected sib pairs (ASPs) with schizophrenia. Using 229 microsatellite markers at an average intermarker distance of 17.26 cM, followed in a second stage by a further 54 markers allowing the regions identified in stage 1 to be typed at an average spacing of 15 5.15 cM, Williams et al. considered results on chromosomes 4p, 18q, and Xcen as suggestive; however, given the scores, Williams et al. interpreted their results as suggesting that common genes of major effect (susceptibility ratio more than 3) are unlikely to exist for schizophrenia.

Similarly, Shaw et al., Am. J. Med. Genet. 81(5):364-76 (1998), in a genome-wide search for schizophrenia susceptibility genes, found that twelve chromosomes (1, 2, 4, 5, 8, 10, 11, 12, 13, 14, 16, and 22) had at least one region with a nominal P value < 0.05, 25 that two of these chromosomes had a nominal P value <0.01 (chromosomes 13 and 16), and that five chromosomes (1, 2, 4, 11, and 13) had at least one marker with a lod score >2.0, suggesting the existence of multiple loci that contribute to schizophrenia susceptibility.

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As yet another example, multiple genes are thought to predispose to epilepsy.

Epilepsy is characterized by recurrent, paroxysmal disorders of cerebral function (seizures); that is, by sudden, brief attacks of altered consciousness, 35 motor activity, sensory phenomena, or inappropriate

behavior. The risk of developing epilepsy is 1% in the period from birth to age 20, and 3% at age 75.

Epilepsy is caused by excessive discharge of cerebral neurons. Clinical manifestations depend on the type and location of discharge. In partial seizures, for example, the excess neuronal discharge is contained within one region of the cerebral cortex. Simple partial seizures consist of motor, sensory, or psychomotor phenomena without loss of consciousness; the specific phenomenon reflects the affected area of the brain. In generalized seizures, the discharge bilaterally and diffusely involves the entire cortex. Sometimes a focal lesion of one part of a hemisphere activates the entire cerebrum bilaterally so rapidly that it produces a generalized tonic-clonic seizure before a focal sign appears.

Epilepsy is a family of disorders. Those that are idiopathic are believed to have multiple genetic contributions. For example, idiopathic generalized epilepsy (IGE) is characterized by recurring generalized seizures in the absence of detectable brain lesions and/or metabolic abnormalities. Twin and family studies suggest that genetic factors play a key part in its etiology. Although a mutation in the CACNB4 gene can cause the disorder, linkage to 8q24, Zara et al., Hum. Molec. Genet. 4: 1201-1207(1995), 3q26 and 14q23, Sander et al., Hum. Molec. Genet. 9:1465-1472 (2000), and 2q36 has been also demonstrated, with a multilocus model appearing to fit best the observed familial patterns.

Polygenic contributions to the etiology of various neurologic cancers have similarly been described.

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For example, gliomas account for 45% of intracranial tumors, and multiple loci have been implicated in its development, with losses of chromosome 17p, increase in copy number of chromosome 7, structural abnormalities of

chromosomes 9p and 19q, and genes on chromosome 10 among the suspects.

Other significant diseases of brain and nervous tissue are also believed to have a genetic, typically 5 polygenic, etiologic component. These diseases include, for example, Parkinson's disease, dementia with Lewy bodies, frontotemporal dementia, corticobasal ganglionic degeneration, progressive supranuclear palsy, prion diseases (Creutzfeld-Jakob, Gerstmann-Strausller-Shenker, 10 familial fatal insomnia), Tourette's Syndrome, corticobasal degeneration, multiple system atrophy, striatonigral degeneration, Shy-Drager syndrome, olivopontocerebellar atrophy, spinocerebellar ataxia, Friedreich ataxia, ataxiatelangiectasia, amyotrophic lateral sclerosis, bulbospinal 15 atrophy (Kennedy's syndrome), spinal muscular atrophy, neuronal storage diseases (sphingolipid, mucopolysaccharide, mucolipid), leukodystrophy, Krabbe disease, metachromic leukodystrophy, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Canavan disease, 20 mitochondrial encephalomyopathy, Leigh disease, neurofibromatosis (Type 1 and Type II), tuberous sclerosis, paraneoplastic syndrome, subacute cerebellar degeneration, subacute sensory neuropathy, opsoclonus/myoclonus, retinal degeneration, stiff-man syndrome and Von Hippel-Lindau 25 disease.

Many neurologic cancers other than gliomas have also been shown or suspected to have genetic bases or contributions. Among these cancers are astrocytoma, fibrillary astrocytoma, pilocytic astrocytoma, pleomorphic xanthoastrocytoma, oligodendroglioma, ependymoma, gangliocytoma, ganglioglioma, medulloblastoma, primary brain germ cell tumor, pineocytoma, pineoblastoma, and meningioma.

Other disorders of brain and central nervous system that likely have genetic components include the

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various forms of neural deafness, catatonia, depression, bipolar (manic-depressive) disorder, Wilson's Disease, Pick disease, neuromyelitis optica (Devic disease), central pontine myelinolysis, Marchiafava-Bignami disease, 5 Guillain-Barre syndrome, sleep disorders (insomnia, myoclonus, narcolepsy, cataplexy, sleep apnea), amnesia, aphasias (including Broca's aphasia and Wernicke's aphasia), cortical blindness, visual agnosia, auditory agnosia, and Kluver-Bucy syndrome.

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The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human brain, particularly those diseases with polygenic etiology. With each of the single 15 exon probes described herein shown to be expressed at detectable levels in human brain, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known 25 to be characteristic of a given neurologic disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the 30 patient's brain (or other CNS tissues, including cultured tissues) to the genome-derived single exon microarray of the present invention. Reference profiles are be obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating 35 gene expression profiles, without regard to the function of

the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of neurologic disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human brain. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at

15 sufficiently high hybridization stringency, which

stringencies are well known in the art — see Ausubel et al.

and Maniatis et al. — each probe reports the level of

expression of message specifically containing that ORF.

It should be appreciated, however, that the
20 probes of the present invention, for which expression in
the brain has been demonstrated are useful for both
measurement in the brain and for survey of expression in
other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was

measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

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The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays — conventionally using microarrays having probes derived from expressed message — is well-established as useful in the biological research arts (see Lockhart et al. Nature 405, 827-836).

Microarrays have been used to determine gene 20 expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," Proc. 25 Natl. Acad. Sci. USA 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," Arch. Biochem. Biophys. 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell 30 Gene Expression During HIV-1 Infection Using cDNA Microarrays," Virology 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence, " Curr. Biol. 9(17):939-45 (1999);

35 Voehringer et al., "Gene Microarray Identification of Redox

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and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," Proc. Natl. Acad. Sci. USA 97(6):2680-5 (2000)).

Microarrays have also been used to determine 5 abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays, " Proc. Natl. Acad. Sci. USA 96(12):6745-50 (1999); Perou et al., 10 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, Proc. Natl. Acad. Sci. USA 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and 15 Microarray Analysis," Oncogene 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," Ann. Neurol. 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the 20 Molecular Pharmacology of Cancer, " Nat. Genet. 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression, " Cancer Res. 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, 30 serving, in essence, as negative controls.

25

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway 35 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter 5 a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile 10 and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., Trends Biochem. Sci. 24(5):168-173 (1999) and Zweiger, Trends Biotechnol. 17(11):429-436 (1999); Schena et al.

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The invention particularly provides genome-20 derived single-exon probes known to be expressed in brain.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules 30 so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates,

35 morpholino analogs, and peptide nucleic acids (PNA), as are

described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression.

Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, inter alia, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be
20 sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be

25 packaged with amplification primers, either in a single
composition that comprises probe template and primers, or
in a kit that comprises such primers separately packaged
therefrom. As earlier mentioned, the ORF-specific
5' primers used for genomic amplification can have a first
30 common sequence added thereto, and the ORF-specific 3'
primers used for genomic amplification can have a second,
different, common sequence added thereto, thus permitting,
in this embodiment, the use of a single set of 5' and 3'
primers to amplify any one of the probes. The probe

35 composition and/or kit can also include buffers, enzyme,

1

etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however — that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) — length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that
dictates the minimum size of such probe is that each such
probe must be capable of specifically identifying in a
hybridization reaction the exon from which it is drawn. In
theory, a probe of as little as 17 nucleotides is capable
of uniquely identifying its cognate sequence in the human
genome. For hybridization to expressed message — a subset
of target sequence that is much reduced in complexity as
compared to genomic sequence — even fewer nucleotides are
required for specificity.

Therefore, the probes of the present invention

30 can include as few as 20, 25 or 50 bp or ORF, or more. In
particular embodiments, the ORF sequences are given in SEQ

ID NOS. 12,822 - 25,434, respectively, for probe SEQ ID

NOS. 1 - 12,821. The minimum amount of ORF required to be
included in the probe of the present invention in order to

35 provide specific signal in either solution phase or

microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,822 - 25,434 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, inter alia, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 μ g/ μ l human cot1 DNA, and 0.5 % SDS, in a 10 humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization 15 at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room 20 temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, inter alia, radioactive labels, such as ³H, ³²P, ³³P, ³⁵S, ¹²⁵I, ¹³¹I; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

Green and other labels described in Haugland,

Handbook of Fluorescent Probes and Research Chemicals, 7th
ed., Molecular Probes Inc., Eugene, OR (2000), or
fluorescence resonance energy transfer tandem conjugates
thereof; labels suitable for chemiluminescent and/or
enhanced chemiluminescent detection; labels suitable for

ESR and NMR detection; and labels that include one member

of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural
individual probes, the probes are typically made available
in amplifiable form in a spatially-addressable ordered set,
typically one per well of a microtiter dish. Although a 96
well microtiter plate can be used, greater efficiency is
obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific
5' primers used for genomic amplification had a first
common sequence added thereto, and the ORF-specific 3'
primers used for genomic amplification had a second,
different, common sequence added thereto, a single set of
5' and 3' primers can be used to amplify all of the probes
from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human brain.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

25

The single exon probes of the present invention,

30 as well as fragments of the single exon probes comprising
selectively hybridizable portions of the probe ORF, can be
used to obtain the full length cDNA that includes the ORF
by (i) screening of cDNA libraries; (ii) rapid
amplification of cDNA ends ("RACE"); or (iii) other

35 conventional means, as are described, inter alia, in

Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term

5 "microarray" has the meaning given in the definitional section of this description, supra.

The invention particularly provides genomederived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human brain. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 12,821.

When used for gene expression analysis, the 15 genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray 20 surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a 25 fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means 30 can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon

35 microarray, each of the nucleic acids having SEQ ID NOS.: 1

12,821 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,822 - 25,434, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 12,821 can be used, or that portion thereof in SEQ ID NOS. 12,822 - 25,434 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL Protein, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, inter alia, in Chan et al. (eds.), Fmoc Solid Phase Peptide

20 Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7), Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,822 - 25,434. Such amino acid sequences are set out in SEQ ID NOS: 25,435 - 37,811. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that

have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

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Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from 15 GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs.

The three programs predict genes using independent algorithmic methods developed on independent training sets:

GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different

25 heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and 60.7% of genomic sequence, GRAIL and

DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding 5 region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

15 PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the aminomodified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3

30 (available online for use at

http://www-genome.wi.mit.edu/cgi-bin/primer/). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single

set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant 5 further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

10

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of 15 agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest 20 directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range 25 of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, 30 with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process 35 was adjusted to amplify 1000, 1500 or 2000 bp fragments

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from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and 10 standard protocols.

- 5

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Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some 15 submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression 20 ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not 25 shown).

The 350 MB of genomic DNA was, by the abovedescribed process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII 30 Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 E. coli genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against

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the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less

5 than 1 e⁻¹⁰⁰) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1 e⁻⁵ to 1 e⁻⁹⁹). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., Nature Genet. 3:266
15 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function	of Predic	ted ORFs As	Deduced From Comparative
Sequence	Analysis		
			•
Total	V6 chip	V7 chip	Function Predicted from
			Comparative Sequence
			Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal

45	19	26	Transport	
21	17	14	Growth Factor	
17	12	5	Cytochrome	
50	33	17	Channel	

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

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The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1)

15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia

Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA[†] mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT,

100μM dATP, 100 μM dGTP, 100 μM dTTP, 50 μM dCTP, 50 μM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 5 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured 10 for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 ug/ul human cot1 DNA, and 0.5 % SDS.

15

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1% SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in 20 water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing 25 Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, 30 since every highly expressed gene in the tissue/cell typespecific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were 35 normalized using the average ratio or average signal,

respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the E. coli control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression

10 across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

25

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 30 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the

matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic 5 expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the 15 following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

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It was further observed that there were many more "novel" genes among those that were up-regulated in only 20 one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was 25 measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher 30 likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have 35 high homology to genes present in the GenBank human EST

database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than 1e-30 ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

30

25

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR)

and northern blot analysis.

10

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray 5 experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300 1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734 1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as 15 measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay 20 methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the 25 power of our methodology — which combines bioinformatic prediction with expression confirmation using genomederived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides 30 correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very 35 low (normalized) signal (less than 0.5, determined to be

biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray

5 hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

r.		of the Mos	st Highly	
Expressed G				2
Expressed G	енез вхр.	ressed on	га ти ргат	1
Microarray	Normal	Expressi	Homology	Gene Function
Sequence	ized	on Ratio	to EST	as described by
Name	Signal		present	GenBank
	-		in	
			GenBank	
AP000217-1	5.2	+7.7	High	S-100 protein,
:				b-chain, Ca ²⁺
				binding protein
				expressed in
				central nervous
				system
AP000047-1	2.3		High	Unknown
				Function
AC006548-9	1.7		High	Similar to
				mouse membrane
				glyco-protein
				M6, expressed
				in central
				nervous system

AC007245-5 1.5 High Similar to amphiphysin synaptic vesicle-associated	ı, a
synaptic vesicle-associated	· 1
vesicle- associated	
	i
protein. Re	ef 21
L44140-4 1.2 +2.0 High Endothelial	-
actin-bindi	ng
protein for	ınd
in nonmuscl	_e
filamin	
AC004689-9 1.2 '+3.5 High Protein	
Phosphatase)
PP2A, neuro	nal/
downregulat	es
activated	
protein kir	ıases
AL031657-1 1.2 +3.0 High Unknown	
function/	
Contains th	ıe
anhyrin mot	if,
a common	
protein	
sequence mo	tif
AC009266-2 1.1 +3.7 Low Low homolog	y to
the	
Synaptotagm	nin I
protein in	
rat/present	: at
low levels	
throughout	rat
brain	
AP000086-1 1.0 +2.7 Low Unknown, ve	ry
poor homolo) gy
to collager	ı

AC004689-3	1.0	High	Protein
			Phosphatase
			PP2A, neuronal/
			downregulates
	:	;	activated
			protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca²⁺ binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, Neurochem. Res. 9:1097 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., Trends Biochem. Sci. 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to

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tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, 5 AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in 10 the literature to be found in brain and liver (Joshi et al., J. Neurol. Sci. 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 10 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-15 chromosome RNA-binding motif (Chai et al., Genomics 49(2):283-89 (1998)) (AC007320-3). A low homology analog (APO0123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., Mol. Genet. 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. 25 The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average 30 expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

20

tissue, of GAPDH	son of Expression Ra	atio, for each
	AC006064 (n = 4)	Control $(n = 5)$
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ±0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again

5 demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray

10 experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe

sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

10 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression
25 measured across 10 tissues. As is readily seen in the
Mondrian, the five chip sequences on the array show
identical expression patterns, elegantly demonstrating the
reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure,

it is clear that our ability to find known genes is very
good. A novel gene is also found from 86.6 kb to 88.6 kb,
upon which all the exon finding programs agree. We are
confident we have two exons from a single gene since they
show the same expression patterns and the exons are
proximal to each other. Backgrounds in the following
colors indicate a known gene (top to bottom):
red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = al anti-chymotrypsin (P01011); mauve = 40S
ribosomal protein (P08865). Note that chip sequence 8 and
12 did not sequence verify.

15 EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2,

supra, were applied to additional human genomic sequence as
it became newly available in GenBank to identify unique
exons in the human genome that could be shown to be
expressed at significant levels in brain tissue.

These unique exons are within longer probe

sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 12,821 single exon probes, each

fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 12,821 unique single exon probes are clearly presented in the Sequence Listing as SEQ 5 ID Nos.: 1 - 12,821. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID NOs.: 12,822 - 25,434, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is
25 determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more that a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than $35 \mod + 2.4$ (the value 2.4 is roughly 12 times the

observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified 5 control spot populations are calculated.

The mean + 3x the standard deviation (mean +(3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

10

20

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. 15 Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human brain tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 12,822 - 25,434 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because 25 the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the 30 three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were 35 found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO:. of the exon contained within the probe: "EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe,

the accession number of the database sequence that yielded
the "Most Similar (top) Hit BLAST E Value", along with the
name of the database in which the database sequence is
found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

15 corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS .: . The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn 20 from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts 25 with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging 30 ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried

35 databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of 1e-05 (i.e., 1 x 10^{-5}) and 1e-100 (i.e., 1 x 10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, supra, a BLAST E value of 1e-30 was used as the boundary when only two classes were to be defined for analysis (unknown, >1e-30; known <1e-30) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about 1e-100 — which is probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not
20 have the intronic and/or intergenic sequence present within
the single exon probes listed in the Table. Second, even
the ORF itself is unlikely in such cases to be present
identically in the databases, since most of the EST and
mRNA clones in existing databases include multiple exons,
25 without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 12,821) and probe exon (SEQ ID NOs.: 12,822 - 25,434, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

- (c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and
 - (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

10

EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Brain

15

<u>Table 4</u> (536 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human brain.

20

CLAIMS

A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
 from human brain comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.

- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 4. A spatially-addressable set of single exon nucleic acid 20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,822 - 25,434.
- 5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 6. A spatially-addressable set of single exon nucleic acid 30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
- 7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

- 8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.
- 9. A spatially-addressable set of single exon nucleic acid 10 probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.
- 10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 9 characterised in that said set of probes is addressably disposed upon a substrate.
- 11. A spatially-addressable set of single exon nucleic acid 20 probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.
- 12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1-11.
- 13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain
 30 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human brain.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,822 - 25,434 or a complementary sequence or a fragment thereof.

5

- 15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,435 37,811, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.
- 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
- 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 25 kb in length.
 - 18. A single exon nucleic acid probe as claimed in any one of claims 13 17, wherein said probe is DNA, RNA or PNA.

25

- 19. A single exon nucleic acid probe as claimed in any one of claims 13 18, wherein said probe is detectably labeled.
- 30 20. A single exon nucleic acid probe as claimed in any one of claims 13 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 21. A single exon nucleic acid probe as claimed in any one 35 of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human brain, comprising:

contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human brain; and then

measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the brain of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

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24. A method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence according to the method of claim 23; and

30 then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

35 wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

- 25. A nucleic acid sequence as set out in any of SEQ ID $\frac{1}{2}$ NOs: $\frac{1}{2}$, 434 which encodes a peptide.
 - 26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 25,434.
- 10 27. A peptide comprising a sequence as set out in any of SEQ ID NOs: 25,435 37,811.

Page 1 of 536 Table 4 Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain	Top Hit Descriptor																																		
jie Exon Probe	Top Hit Database Source																																		
בוצ	Top Hit Acession No.																																		
	Most Similar (Top) Hit BLAST E Value																	1.																	
	Expression Signal	6.47	15.92	2.15	10.88	1.22	1.22	3.19	6.1	3.31	1.44	6.78	1.44	2.14	2.7	2.91	1	1	2.83	1.42	12.04	1	1.67	1.03	1.62	6.4	0.97	0.97	1.07	0.76	0.99	5.38	1.3	1.57	1.57
	ORF SEQ ID NO:	25868								27160					27627						28915		29042								ı			30500	
	Exon SEQ ID NO:	13223	13638	13782	14029	14235		14355		14461	14485	14492	14621	14707	14892)	i I	15292		16198	16261		16402	16678	16913	16971	16989	ı		17099	17518				17985
	Probe SEQ ID NO:	437	869	1022	1279	1488	1488	1609	1633	1718	1743	1750	1884	1971	2162	2277	2578	2578	3181	3442	3505	3549	3649	3928	4173	4230	4248	4248	4303	4361	4784	4983	4995	5176	6176

Page 2 of 536
Table 4

			_	 _	Д,						, ,							٠.,	_,		_		ٽ	-,		بحا	*	4	.11	# -0-1	۲,	77	#7		- 47
Single Exon Probes Expressed in Brain	Top Hit Descriptor																																		Homo seplens LSS gene, partial, exons 15, 16, 17 and 18
jle Exon Pro	Top Hit Database Source																																		NT
Sing	Top Hit Acession No.																																		9.9E+00 AJ239028.1
	Most Similar (Top) Hit BLAST E Value																																		9.9E+00
	Expression Signal	4.3	6.14	3.97	9.0	3.28	1.62	1.75	1.27	7.7	1.1	-	1		1.78		1.4	1.49	0.59	0.59	2.67	0.77	1.24	0.94				1.34	2.2			2.47	1.52		17.79
	ORF SEQ ID NO:				31356	31362	31673	31699		•		32774	32775	33071	33072		33780	34214	34598			35515				36195		36879			37328				31703
	SEQ ID	18139	18308		1			1 :	1	ł	1					ı	ı	1				22318		}					1	l	24023	1	ļ	ı	1
	Probe SEQ ID NO:	5336	5510	5593	5648	5854	5932	5958	6322	8434	6454	7025	7025	7311	7311	7712	7860	8384	8759	8759	9434	9996	9782	9922	10328	10328	10582	10749	10952	11030	11332	11485	12313	12609	5961

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Table 4
Single Exon Probes Expressed in Brain

Top Hit Descriptor	Haemophilus influenzae Rd section 31 of 163 of the complete genome	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1	Gallus gallus ornithine transcarbernylase (OTC) gene, exon 1	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gif2h2) genes, complete cds	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gif2h2) genes, complete cds	Dengue virus type 3 membrane protein (prM/M)/senvelope glycoprotein (E) polyprotein mRN/A, partial ods	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds	Mus musculus AT3 gene for antithrombin, complete cds	Homo saplens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial	product	601651038R1 NIH MGC 81 Hamo sapiens cDNA clone IMAGE:3934592 3'	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA	Zea mays mRNA for legumain-like protease (see2a)	BREFELDIN A RESISTANCE PROTEIN	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit	Thermoplasma acidophilum complete genome; segment 3/5	THROMBOSPONDIN 1 PRECURSOR	THROMBOSPONDIN 1 PRECURSOR	602128876F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4285506 6'	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
Top Hit Database Source	NT	LN L	Ę	Ę	N	FN	F	r L	FZ	Ľ	닐	SWISSPROT	. TN	į	TOGGG!/KG	FST HIMAN	LN	F	NT	N	SWISSPROT	TN	TN	SWISSPROT	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT
Top Hit Acession No.	J32716.1	Y18930.1	Y18930.1	4F065630.1	9.6E+00 AF065630.1	9.6E+00 AF242432.1	9.6E+00 AF242432.1	.11433.1	-11433.1	9.4E+00 AB043785.1	4F130990.1	9.3E+00 P11210	9.1E+00 AF095609.1		9.1E+00 AF085609.1	8.0E+00 RE971806 1	8.7E+00 AB019788.1	8.7E+00 AB019788.1	5031804 NT	8.1E+00 AJ131719.1	941820	221489.1	7.5E+00 AL445065.1	935441	-35441	7.4E+00 BF700517.1	-04929	-04929
Most Similar (Top) Hit BLAST E Value	9.8E+00 U32716.1	9.8E+00 Y18930.1	9.8E+00 Y18930.1	9.6E+00	9.6E+00		9.6E+00	9.4E+00 L11433.1	9.4E+00 L11433.1	9.4E+00/	9.3E+00	9.3E+00	9.1E+00 /	i,	9.1E+00 AF0956	8 9F+00	8.75+00	8.7E+00/	8.4E+00	8.1E+00/	8.0E+00 P41820	7.6E+00 Z21489.1	7.5E+00	7.5E+00 P35441	7.5E+00 P35441	7.4E+00	7.4E+00	7.4E+00
Expression Signal	1.74	0.44	0.44	0.73	0.73	1.17	1.17	-	-	2.87	0.91	3.06	2.46		2.45	55.55	2.28	2.28	2.3	3.58	2	0.89	1.9	1.61	1.61	2.66	2.7	2.7
ORF SEQ ID NO:	33730	35489	35490		32685	36187	36188	28119		28334		34733	30645		30040	31685	32041	32042		33545								34488
SEQ ID NO:	20600	22295		19639	19639	22968	22968	15381		15690		ı	18022		18022		1	l	13216	20426		20745						21343
Probe SEQ ID NO:	7905	9643	9643	6901	6901	10321	10321	2671	2671	2924	7997	8901	5214	, , , ,	5214	5945	6287	6287	430	9322	11122	8051	7246	8259	8229	5711	8651	8651

Page 4 of 536 Table 4 Single Exon Probes Expressed In Brain

		Γ	Γ	Γ	Γ	Γ	Π	Г	Γ	Γ	Γ	Γ	Т	Г	Γ	٦		Γ	Г	Γ	Γ	Γ		Г	Г	Γ	Γ	Γ				\neg		П
Top Hit Descriptor	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds	RC0-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOWAIN PROTEIN 1)	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION	ARGININE KINASE (AK)	WD-40 REPEAT PROTEIN MSI3	60S RIBOSOMAL PROTEIN L4 (L2)	DNA MISMATCH REPAIR PROTEIN MUTS	SKT5 PROTEIN	za07o11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291860 5'	za07c11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291860 5'	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS:	OUTER CAPSID PROTEINS VP5 AND VP8]	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)	602152573F1 NIH_MGC_81 Homo saplens cDNA clone IMAGE:4293427 5'	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]	601678435F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3960969 5'	Schizophyllum commune unknown mRNA	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA	601468031F1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:3871303 5'	Pyrococcus harlkoshli OT3 genomic DNA, 1166001-1485000 nt. position (6/7)	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2	Delnococcus radiodurans R1 section 1 of 2 of the complete chromosome 2	Mus musculus mixed lineage kinase 3 (Mik3) and two pore domain K+ channel subunit (Kcnk6) genes,	complete cds	Homo sapiens DESC1 protein (DESC1), mRNA	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
Top Hit Database Source	LN	N.	EST_HUMAN	SWISSPROT	SWISSPROT	NT	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN		SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	TN	LΝ	EST_HUMAN	L	LN	LN		L	Į.	L
Top Hit Acession No.	+00 L12051.1	+00 L12051.1	+00 BE179090.1	+00 P28166	+00 P28166	+00 AL161595.2	+00 P05850	+00 P48610	100 022469	+00 P35679	+00 P44834	+00 P34226	+00 W03412.1	+00 W03412.1		+00 P36307			21.1	+00 Q9ZE07	100 Q9ZE07	+00 Q10309	+00 P03374	HO0 BE866001.1	+00 AY010901.1	6754621 NT	:+00 BE780163.1		100 AE001862.1	HO0 AE001862.1		HO0 AF155142.1	7661557 NT	HOD AF302046.1
Most Similar (Top) Hit BLAST E Value	7.2E+00	7.2E+00	7.2E+00	7.1E+00	7.1E+00	7.1E+00	7.1E+00	7.0E+00	7.0E+00	6.9E+00	6.9E+00	9€.9	6.8E	6.8E		6.8E+00		6.6E+00	6.6E+00	6.6E+00	6.6E-	6.6E	6.5E	6.5E+00	8.2E+00	6.2E+00	6.0E+00	6.0E+00		6.0E+00		5.9E+00 /	5.8E+00	5.7E+00/
Expression Signal	3.58	3.58	0.71	1.28	1.28	8.63	3.28	3.37	1.51	1.92	1.38	0.47	1.53	1.53		1.29	3.24	0.72	0.61	2.36	2.36	1.97	7	0.49	1.55	9.0	1.46	0.46	0.67	0.67		7.32	0.99	0.85
ORF SEQ ID NO:	28390	28391			32801		37350					36125		33624			35969		32216	35827	35828		34931	36067	35488	36337	32717	35565	36274	36275		32193		32816
Exon SEQ ID NÖ:	15743	15743		19740	19740		24047					Ĺ		20503						22622					22294			L	23057	23057				19752
Probe SEQ ID NO:	2977	2977	6931	7049	7049	9498	11359	9882	11215	8181	10249	10267	7808	7808		9031	10109	5202	6450	9974	9974	11073	9079	10203	9642	10460	6936	9716	10411	10411		6428	3514	7061

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)	LYCOPENE BETA CYCLASE	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)	Chicken alpha-cardiac actin gene	Chicken alpha-cardiac actin gene	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]	REP1 PROTEIN	REP1 PROTEIN	RHODOPSIN	RHODOPSIN	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR	QV4-HT0691-270400-186-f09 HT0691 Homo saplens cDNA	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I	RHODOPSIN	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'	Canis familiaris skeletal muscie chloride channel CIC-1 (CLCN1) mRNA, complete cds	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis	(HLA+I) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds	Eunice australis histone H3 (H3) gene, partal cds	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA	PM0-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
e Exou Prope	Top Hit Database Source	·	SWISSPROT D	SWISSPROT L	SWISSPROT H		SWISSPROT	O LN	OL LN	SWISSPROT LI	SWISSPROT R	SWISSPROT R		SWISSPROT R	П	SWISSPROT D	_	SWISSPROT P	EST_HUMAN Q						EST_HUMAN 6	NT C	NT	_		٦	\neg	EST_HUMAN P	
Guic	Top Hit Acesslan No.	46.1				6.5E+00 AF175425.1									_		10.1		10.1								5.0E+00 Z83860.1				- [4.8E+00 AW750067.1	
	Most Similar (Top) Hit BLAST E Value	5.7E+00	5.6E+00 P75080	5.6E+00 Q55276	5.5E+00 P47447	6.5E+00	5.5E+00	5.4E+00	5.4E+00 X02212.1	5.4E+00 Q91062	5.4E+00 P40379	5.4E+00	5.4E+00 Q17094	5.4E+00 Q17094	5.3E+00	5.3E+00	5.3E+00	5.3E+00 Q27905	5.2E+00	5.2E+00	5.2E+00 Q10136	5.1E+00 016005	5.1E+00 P09182	5.0E+00	5.0E+00	5.0E+00	5.0E+00		4.9E+00	4.8E+00	4.8E+00	4.8E+00	4.7E+00
	Expression	0.95	1.13	2.59	0.69	1.28	3.09	1.14	1.14	1.54	0.83	0.83	1.83	1.83	1.32	3.23	0.49	3.2	16.0	0.95	. 2	6.0	1.19	0.72	0.59	3.07	8.95		0.71	10.88	0.47	5.28	1.86
	ORF SEQ ID NO:	32817		36458	31901		36455	32514	32515		34534	34535	35784	35785	30102		-	37548				34698	35577	31944		36197	37214		1		33879		25731
	Exon SEQ ID NO:	19752	20142	23223	18934	53369	L.	19492	19492	20465	21390	21390	22584	22584	17466	20673	21573	24225	18177	22919				18969		22977	23922	ł	- 1	ı	l		13090
	Probe SEQ ID NO:	7061	7468	11456	6157	10678	11464	6830	6830	7769	8698	8698	9836	9836	4734	7978	8882	11628	5377	10271	11150	8861	9725	6193	10094	10330	11260		10132	4039	8054	8439	283

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					``>	21 1100 00	טווקים באסוון
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
284		25731	1.89	4.7E+00	+00 BF240552.1	EST HUMAN	801875654F1 NIH_MGC_55 Homo saplens cDNA clone IMAGE:4099716 5'
3268	16030		2.38	4.7E+00	+00 AL163280.2	L	Homo sapiens chromosome 21 segment HS21 C080
9095	21783	34948	1.18	4.6E+00	+00 BE646437.1	EST_HUMAN	7e86g10.x1 NGL CGAP, CLL1 Homo septiens cDNA clone IMAGE:3292098 3' similar to TR: 075140 075140 KIAA0645 PROTEIN ;contains element PTR5 repetitive element ;
9095	21783	34949	1.18	4.6E+00	+00 BE646437.1	EST HUMAN	7e88g10.x1 NCI_CGAP_CLL1 Homo septiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN ;contains element PTR5 repetitive element:
10287	20045		200	20,100			Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
1020			10.0	4.00-400	T	2	genes, complete cas
A LINGS	┙		2.31	4.6E+00	4.6E+00 D63999.1	LZ.	Synechocystis sp. PCC6803 complete genome, 18/27, 2267260-2392728
11605			2.59	4.5E+00	٦	LN	Archaeoglobus fulgidus section 63 of 172 of the complete genome
11762		37685	1.78	4.5E+00		EST_HUMAN	602123238F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4280216 5
3035	15801	28447	0.96	4.4E+00	4.4E+00 BF530893.1	EST_HUMAN	602072585F1 NC _CGAP_Brn67 Homo saplens cDNA clone MAGE:4215284 5
3035		28448	96.0	4.4E+00	Γ	EST_HUMAN	602072586F1 NCI_CGAP_Brn87 Homo saplens cDNA clone IMAGE:4215284 5'
6109			1.66	4.4E+00		N	Murine I gene for MHC class II(Ia) associated invariant chain
6027	18807		0.68	4.3E+00	7.	Z	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7338			2.03	4.3E+00 Y13402.1		N	Plasmodium faldiparum R29R+var1 gene, exon 1
7515	20186	33280	0.65	4.3E+00	2.1	LN	Treponema pallidum section 38 of 87 of the complete genome
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
10769	23453	36696	7.64	4.3E+00/	+00 AF240786.1	NT	genes, complete cds
5430	18229		3.44	4.2E+00	+00 P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP)
2207		31206	0.87	4.2E+00		SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
6874		32627	2.62	4.2E+00	+00 P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6874		32628	2.62	4.2E+00	+00 P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
8829		34697	4.68	4.2E+00	+00 Al809013.1	EST_HUMAN	wf67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692.37
9818		35672	1.08	4.2E+00	+00 P31368	SWISSPROT	NUBBIN PROTEIN (TWAIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
10049	22697		0.48	4.2E+00	+00 P40886	SWISSPROT	HEXOSE TRANSPORTER HXT8
5846		31569	0.56	4.1E+00(SWISSPROT	CELLULAR TUMOR ANTIGEN P53
5846		31570	0.56	4.1E+00 (SWISSPROT	CELLULAR TUMOR ANTIGEN P53
7012		32760	0.84	4.1E+00	+00 BE253668.1 E	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7111		32863	0.65	4.1E+00	+00 BF247939.1 E	EST_HUMAN	601859030F1 NIH_MGC_58 Home sapiens cDNA clone IMAGE:4069758 5'
7559		33332	8.73	4.1E+00 (+00 023810	SWISSPROT	YY1 PROTEIN PRECURSOR
7681	20345		0.62	4.1E+00 /	23.1	NT	Patinopecten yessoensis mRNA for calcineurin A, complete cds
7683	20347	33459	4.32	4.1E+00 F	+00 P28964	SWISSPROT	GENE 68 PROTEIN

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Poche SEQ ID NO. Expression NO. (Top HI) Flag Top HI No. Top HI Delabase No. Top HI Source No. Top H						,		
20347 33460 4.32 4.1E+00 P28984 SWISSPROT 20512 33638 2.53 4.1E+00 P1283 SWISSPROT 22118 35296 0.57 4.1E+00 P48414 SWISSPROT 22363 0.48 4.1E+00 P46414 SWISSPROT 23672 1.169 4.1E+00 P688580.1 EST_HUMAN 19500 32524 0.77 4.0E+00 D62653 SWISSPROT 22494 3695 0.74 4.0E+00 D62653 SWISSPROT 22713 3695 0.44 4.0E+00 D62653 SWISSPROT 22713 3695 0.44 4.0E+00 D62653 SWISSPROT 22713 3695 0.44 4.0E+00 D62653 <	Probe SEQ ID NO:	SEQ ID NO:	ORF SEO ID NO:	Expression Signal		Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
20512 33638 2.53 4.1E+00 U57503.1 NT 22118 35295 0.57 4.1E+00 P11263 SWISSPROT 22284 35409 2.46 4.1E+00 P46414 SWISSPROT 22853 0.48 4.1E+00 P96414 SWISSPROT 23483 3.06 4.1E+00 P96416 SWISSPROT 16280 32524 0.77 4.0E+00 P62653 SWISSPROT 19500 32524 0.77 4.0E+00 D62653 SWISSPROT 22494 36695 0.44 4.0E+00 D62653 SWISSPROT 22743 36691 0.44 4.0E+00 D62653 SWISSPROT 22744 3.6E+00 D62653 SWISSPROT	7683	1		4.32	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
22118 35295 0.57 4.1E+00 P11253 SWISSPROT 22224 35409 2.46 4.1E+00 BF692426.1 EST_HUMAN 22483 0.48 4.1E+00 P46414 SWISSPROT 23483 3.06 4.1E+00 P8229 SWISSPROT 23572 1.56 4.0E+00 P3828 SWISSPROT 16580 32524 0.77 4.0E+00 D62653 SWISSPROT 19500 32525 0.75 4.0E+00 D62653 SWISSPROT 24464 36891 0.44 4.0E+00 D62653 SWISSPROT 22494 36891 0.44 4.0E+00 D62663 SWISSPROT	7817	ı		2.53	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
22224 35409 2.46 4.1E+00 BF692426.1 EST_HUMAN 22863 0.48 4.1E+00 P46414 SWISSPROT 23463 3.06 4.1E+00 P46414 SWISSPROT 16289 3.06 4.1E+00 P46414 SWISSPROT 19500 32524 0.77 4.0E+00 O62653 SWISSPROT 19500 32524 0.75 4.0E+00 O62653 SWISSPROT 19500 32524 0.75 4.0E+00 O62653 SWISSPROT 19500 32524 0.75 4.0E+00 O62653 SWISSPROT 19778 32843 1.44 4.0E+00 O62653 SWISSPROT 22434 36955 0.44 4.0E+00 O62653 SWISSPROT 22743 35931 0.63 4.0E+00 D61309 SWISSPROT 22743 35934 0.63 4.0E+00 D61309 SWISSPROT 16250 28904 4.61 3.9E+00 P7564 SWISSPROT	9440	L		0.57	4.1E+00	P11263	SWISSPROT	50S RIBOSOWAL PROTEIN L4
22863 0.48 4.1E+00 P46414 SWISSPROT 23483 3.06 4.1E+00 P96414 SWISSPROT 23572 11.69 4.1E+00 P96716 SWISSPROT 16289 0.36 4.0E+00 P38229 SWISSPROT 19500 32524 0.77 4.0E+00 O62653 SWISSPROT 19500 32524 0.75 4.0E+00 O62653 SWISSPROT 19500 32525 0.77 4.0E+00 O62653 SWISSPROT 24444 32634 1.44 4.0E+00 O62653 SWISSPROT 22743 35695 0.44 4.0E+00 O62653 SWISSPROT 22743 35695 0.44 4.0E+00 O62653 SWISSPROT 22744 36966 0.44 4.0E+00 O62653 SWISSPROT 22713 35931 0.63 4.0E+00 O62653 SWISSPROT 23220 36454 1.53 4.0E+00 O74660 O74660 O76664 <	9571			2.46	4.1E+00	BF692425.1	EST_HUMAN	602247938F1 NIH_MGC_62 Homo seplens cDNA clone IMAGE:4333209 5'
23433 3.06 4.1E+00 P0716 SWISSPROT 23433 3.06 4.1E+00 P0716 SWISSPROT 16289 0.96 4.0E+00 P08229 SWISSPROT 19500 32524 0.77 4.0E+00 P08283 SWISSPROT 19500 32524 0.77 4.0E+00 P06263 SWISSPROT 19500 32524 0.77 4.0E+00 P06263 SWISSPROT 19500 32525 0.77 4.0E+00 P06263 SWISSPROT 19708 32643 1.44 4.0E+00 P06263 SWISSPROT 27494 35695 0.45 4.0E+00 P06263 SWISSPROT 27713 36936 0.44 4.0E+00 P06363 SWISSPROT 27713 36936 0.44 4.0E+00 P06363 SWISSPROT 2713 36454 1.53 4.0E+00 P06363 SWISSPROT 16250 28904 4.61 3.9E+00 P07564 SWISSPROT 16250 28904 4.61 3.9E+00 P07564 SWISSPROT 18369 31279 2.91<	40204			0.48	4 15+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
2470 1,00 4,11-00 BE88580.1 EST HUMAN 1620 32524 0,77 4,06+00 P688580.1 EST HUMAN 16500 32524 0,77 4,06+00 O62653 SWISSPROT 19500 32524 0,77 4,06+00 O62653 SWISSPROT 19500 32524 0,75 4,06+00 O62653 SWISSPROT 19500 32524 0,75 4,06+00 O62653 SWISSPROT 19500 32524 0,75 4,06+00 O62653 SWISSPROT 21434 36695 0,44 4,06+00 O62653 SWISSPROT 22713 35696 0,44 4,06+00 O61309 SWISSPROT 22713 35691 0,44 4,06+00 P7564 SWISSPROT 22713 37446 2,27 4,06+00 P07564 SWISSPROT 16250 28904 4,61 3,96+00 P6564 SWISSPROT 18369 31279 2,91 3,96+00	2000	. I.		3.06	7 11	D00718	CWISSPROT	HYPOTHETICAL PROTEIN HVI E1
16289 0,95 4,0E+00 P38229 SWISSPROT 19500 32524 0,77 4,0E+00 O62653 SWISSPROT 19500 32524 0,77 4,0E+00 O62653 SWISSPROT 19500 32524 0,75 4,0E+00 O62653 SWISSPROT 19500 32524 0,75 4,0E+00 O62653 SWISSPROT 21464 34611 0,45 4,0E+00 O62653 SWISSPROT 22494 35695 0,44 4,0E+00 O61309 SWISSPROT 22713 35931 0,48 4,0E+00 O61309 SWISSPROT 23220 36454 1,53 4,0E+00 P7564 SWISSPROT 16250 28904 4,61 3,9E+00 P7564 SWISSPROT 17026 28904 4,61 3,9E+00 P7564 SWISSPROT 18369 31279 2,91 3,9E+00 P7564 SWISSPROT 18369 31279 2,91 3,9E+00 P	10892	ł		11.69	4.16+00	BE885880.1	EST HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone !MAGE:3909051 5'
19500 32524 0,77 4,0E+00 O62653 SWISSPROT 19500 32525 0,77 4,0E+00 O62653 SWISSPROT 19500 32524 0,75 4,0E+00 O62653 SWISSPROT 19500 32525 0,75 4,0E+00 O62653 SWISSPROT 21464 34611 0,45 4,0E+00 O63030 SWISSPROT 22743 35695 0,44 4,0E+00 O61309 SWISSPROT 22713 35931 0,63 4,0E+00 P14546 SWISSPROT 23220 36454 1,53 4,0E+00 P7564 SWISSPROT 16250 28904 4,61 3,9E+00 X64518.1 NT 17026 28904 4,61 3,9E+00 A76564 SWISSPROT 18369 31279 2,91 3,9E+00 A65646.1 NT 18369 31279 3,9E+00 B6814357.1 EST_HUMAN 18369 31279 2,91 3,9E+00 B68	3533	1		0.95	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
19500 32525 0.77 4.0E+00 O62653 SWISSPROT 19500 32524 0.75 4.0E+00 O62653 SWISSPROT 19500 32525 0.75 4.0E+00 O62653 SWISSPROT 21464 34611 0.45 4.0E+00 O62653 SWISSPROT 22494 35695 0.44 4.0E+00 O61309 SWISSPROT 22713 35931 0.63 4.0E+00 O61309 SWISSPROT 23220 36454 1.53 4.0E+00 P14546 SWISSPROT 24137 37446 2.27 4.0E+00 P07564 SWISSPROT 16250 28904 4.61 3.9E+00 X64518.1 NT 17026 28904 4.61 3.9E+00 A655466.1 NT 18369 31279 2.91 3.9E+00 BE814357.1 EST_HUMAN 18364 3.26+0 B814357.1 EST_HUMAN 18364 3.9E+00 B9299 SWISSPROT	5372	1		0.77	4.0E+00	062653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
19500 32524 0.75 4.0E+00 O62653 SWISSPROT 19600 32525 0.75 4.0E+00 O62653 SWISSPROT 21464 34611 0.45 4.0E+00 O63010 SWISSPROT 22494 36695 0.44 4.0E+00 O61309 SWISSPROT 22713 36931 0.63 4.0E+00 O61309 SWISSPROT 23220 36454 1.53 4.0E+00 P14546 SWISSPROT 24137 37445 2.27 4.0E+00 P07564 SWISSPROT 16250 28904 4.61 3.9E+00 A64518.1 NT 18369 31279 2.91 3.9E+00 A655466.1 NT 18369 31280 2.91 3.9E+00 BE314357.1 EST_HUMAN 18369 32367 0.55 3.9E+00 BE314357.1 EST_HUMAN 19354 3.26+00 D93299 SWISSPROT	5372	ı		0.77	4.0E+00	062653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
19500 32525 0.75 4.0E+00 O62653 SWISSPROT 21464 32843 1.44 4.0E+00 O33010 SWISSPROT 22494 35695 0.44 4.0E+00 O41309 SWISSPROT 22713 35694 0.63 4.0E+00 O61309 SWISSPROT 23220 36454 1.53 4.0E+00 P14546 SWISSPROT 23220 36454 1.53 4.0E+00 P07564 SWISSPROT 24137 37446 2.27 4.0E+00 P07564 SWISSPROT 16250 28904 4.61 3.9E+00 X64518.1 NT 17026 8.24 3.9E+00 X64518.1 NT 18369 31279 2.91 3.9E+00 BE814357.1 EST_HUMAN 18369 31280 2.91 3.9E+00 BE814357.1 EST_HUMAN 18364 32546 4.62 3.9E+00 B93299 SWISSPROT	6838	ı		0.75	4.0E+00	062653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
19778 32843 1.44 4.0E+00 033010 SWISSPROT 21464 34611 0.45 4.0E+00 014167 SWISSPROT 22434 35695 0.44 4.0E+00 061309 SWISSPROT 22713 35631 0.63 4.0E+00 D61456 SWISSPROT 23220 36454 1.53 4.0E+00 P14546 SWISSPROT 24137 37446 2.27 4.0E+00 P07564 SWISSPROT 16250 28904 4.61 3.9E+00 X64518.1 NT 17026 8.24 3.9E+00 X64518.1 NT 18369 31279 2.91 3.9E+00 BE814367.1 EST_HUMAN 18369 31280 2.91 3.9E+00 BE814367.1 EST_HUMAN 18364 3.2646 4.62 3.9E+00 P93299 SWISSPROT	6838			0.75	4.0E+00	062653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
21464 34611 0,45 4,0E+00 014167 SWISSPROT 22494 35695 0,44 4,0E+00 061309 SWISSPROT 22713 35931 0,63 4,0E+00 AE002132.1 NT 23220 36454 1,53 4,0E+00 P14546 SWISSPROT 24137 37444 2,27 4,0E+00 P07564 SWISSPROT 16250 28904 4,61 3,9E+00 R4518.1 NT 17026 8,24 3,9E+00 R455466.1 NT 18369 31279 2,91 3,9E+00 BE814367.1 EST_HUMAN 18369 31280 2,91 3,9E+00 BE814367.1 EST_HUMAN 18369 32846 4,62 3,9E+00 B29299 SWISSPROT	7089	1		4.1	4.0E+00	033010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
22494 35695 0,44 4,0E+00 O61309 SWISSPROT 22713 35931 0,63 4,0E+00 AE002132.1 NT 23220 36454 1,53 4,0E+00 P14546 SWISSPROT 24137 37444 2,27 4,0E+00 P07564 SWISSPROT 16250 28904 4,61 3,9E+00 X64518.1 NT 17026 8,24 3,9E+00 X64518.1 NT 18369 31279 2,91 3,9E+00 BE814357.1 EST_HUMAN 18369 31280 2,91 3,9E+00 BE814357.1 EST_HUMAN 18364 32546 4,62 3,9E+00 B924357.1 EST_HUMAN 18369 3,28e+00 B929 SWISSPROT	8772	l		0,45	4.0E+00	Q14167	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
22713 35631 0.63 4.0E+00 AE002132.1 NT 23220 36454 1.53 4.0E+00 P14546 SWISSPROT 24137 37444 2.27 4.0E+00 P07564 SWISSPROT 16250 28904 4.61 3.9E+00 K64518.1 NT 17026 8.24 3.9E+00 K64518.1 NT 18369 31279 2.91 3.9E+00 AF055466.1 NT 18369 31280 2.91 3.9E+00 BE814367.1 EST_HUMAN 18369 31280 2.91 3.9E+00 BE814367.1 EST_HUMAN 18369 328640 0.55 3.9E+00 B92299 SWISSPROT	9843	1		0.44	4.0E+00	061309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
23220 36454 1.53 4.0E+00 P14546 SWISSPROT 24137 37444 2.27 4.0E+00 P07564 SWISSPROT 24137 37445 2.27 4.0E+00 P07564 SWISSPROT 17026 28904 4.61 3.9E+00 X64518.1 NT 17026 8.24 3.9E+00 X64518.1 NT 18369 31279 2.91 3.9E+00 AF055466.1 NT 18369 31280 2.91 3.9E+00 BE814367.1 EST_HUMAN 18369 32367 0.55 3.9E+00 U91328.1 NT 19354 32546 4.62 3.9E+00 U91328.1 NT	10065	_		0.63	4.0E+00	AE002132,1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
24137 37444 2.27 4.0E+00 P07564 SWISSPROT 24137 37445 2.27 4.0E+00 P07564 SWISSPROT 16250 28904 4.61 3.9E+00 X64518.1 NT 17026 8.24 3.9E+00 X64518.1 NT 18369 31279 2.91 3.9E+00 BE814367.1 EST_HUMAN 18369 32367 0.55 3.9E+00 U91328.1 NT 19354 32367 0.55 3.9E+00 U91328.1 NT 19354 32546 4.62 3.9E+00 P39299 SWISSPROT	11453			1.53	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
24137 37444 2.27 4.0E+00 P07564 SWISSPROT 24137 37445 2.27 4.0E+00 P07564 SWISSPROT 16250 28904 4.61 3.9E+00 X64518.1 NT 17026 8.24 3.9E+00 X64518.1 NT 18369 31279 2.91 3.9E+00 BE814357.1 EST_HUMAN 18369 32367 0.55 3.9E+00 U91228.1 NT 19354 32367 0.55 3.9E+00 U91228.1 NT 19518 32546 4.62 3.9E+00 P39299 SWISSPROT								GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS
24137 37445 2.27 4.0E+00 P07564 SWISSPROT	11537			2.27	4.0E+	P07564	SWISSPROT	NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
24137 37445 2.27 4.0E+00 P07564 SWISSPROT. 16250 28904 4.61 3.9E+00 K64518.1 NT 17026 8.24 3.9E+00 R6814357.1 NT 18369 31279 2.91 3.9E+00 BE814357.1 EST_HUMAN 18369 32367 0.55 3.9E+00 BE814357.1 EST_HUMAN 19354 32367 0.55 3.9E+00 U91328.1 NT 19518 32546 4.62 3.9E+00 P39299 SWISSPROT								GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS
16250 28904 4,61 3.9E+00 X64518.1 NT 17026 8.24 3.9E+00 AF055466.1 NT 18369 31280 2.91 3.9E+00 BE814357.1 EST_HUMAN 18369 31280 2.91 3.9E+00 BE814357.1 EST_HUMAN 19354 32367 0.55 3.9E+00 U91328.1 NT 19518 32546 4.62 3.9E+00 P39299 SWISSPROT	11537				4.0E+00	P07564	SWISSPROT .	NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
17026 8.24 3.9E+00 AF055466.1 NT 18369 31279 2.91 3.9E+00 BE814357.1 EST_HUMAN 18369 31280 2.91 3.9E+00 BE814357.1 EST_HUMAN 19354 32367 0.55 3.9E+00 U91328.1 NT 19518 32546 4.62 3.9E+00 P39299 SWISSPROT	3494	<u> </u>		4.61	3.9E+00	X64518.1	LN	N.tabacum chitinase gene 50 for class I chitinase C
18369 31279 2.91 3.9E+00 BE814357.1 EST_HUMAN 18369 31280 2.91 3.9E+00 BE814357.1 EST_HUMAN 19354 32367 0.55 3.9E+00 U91328.1 NT 19518 32546 4.62 3.9E+00 P39299 SWISSPROT	4287			8.24		AF055466.1	ΙN	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
18369 31280 2.91 3.9E+00 BE814357.1 EST_HUMAN 19354 32367 0.55 3.9E+00 U91328.1 NT 19518 32546 4.62 3.9E+00 P39299 SWISSPROT	5572	1				BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
19354 32367 0.55 3.9E+00 U91328.1 NT 19518 32546 4.62 3.9E+00 P93299 SWISSPROT	5572	1	H		3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
19518 32546 4.62 3.9E+00 P39299 SWISSPROT	6591			0.55	3.9Ē⁴	U91328.1	FX	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
	6774	, ,			Ш	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION

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Single Exon Probes Expressed in Brain	Hit Top Hit Descriptor Ce	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2	X.laevis mRNA for M4 muscarinic receptor	Homo sapiens NF2 gene	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome			MAN HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148	Streptococcus oralis partial xpt gene for xanthine phosphoribosytransferase, strain NCTC7864	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39	Thermoplasma acidophilum complete genome; segment 3/5	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds	T	Т	MAN AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'			MAN HUM000TB08 Liver HepG2 cell line. Homo saplens cDNA clone tb08			Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome	Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds; and the translation start site has been verified (glpD), the translation start site has been verified (glpD), and repressor protein (glpR) genes.	complete cds	Cryptosportdium felis heat shock protein 70 (HSP70) gene, partial cds	Borrella burgdorferi (strain 25015) outer surface protein (ospC) gene, pertial ods	MAN y940c08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34940 5'	Г	2p88b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;		╗	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
ngle Exon	Top Hit Database Source	N.	NT	۲	NT	SWISSPROT	EST_HUN	EST_HUMAN	TN	TN	TN	Li 4	Z Z	EST HUMAN	EST_HUMAN	EST_HUMAN	١	EST_HUMAN	EST_HUMAN	EST_HUMAN	INT	TN		뉟	μ	Ε	EST_HUMAN	SWISSPROT	EST HUMAN		EST_HUMAN	ΝŢ
รัก -	iter Top Hit Acession	-00 M23907.1	-00 X65865.1	-00 Y18000.1	-00 AE001562.1	-00 Q57830	-00 AI493849.1	-00 D44725.1	00 AJ390961.1	H00 AL161539.2	-00 AL445065.1		4903830 IN 4903830 IN 1	-00 BF669279.1	+00 BF669279.1	-00 AV761055.1	-00 AL161472.2	-00 BF316316.1	3.6E+00 D12367.1	-00 D12367.1	3.6E+00 AE004447.1	3.6E+00 AE004447.1		3.6E+00 M96795.1	-00 AF221538.1	3.5E+00 L42898.1	-00 R19745.1	-00 P24557	-00 AA190998.1		-00 AA190998.1	+00 AL161553.2
	Most Similar (Top) Hit BLAST E Value	3.9E+	3.9E+		3.8E+	3.8E+	3.8E+	3.8E+	3.8E+	3.7E+	3.7E+		3.7E+		3.7E+	3.6E+	· 3.6E+	3.6E+	3.6E+	3.6E+	3.6E+	3.6E+		3.6E+	3.5E+	3.5E+	3.5E+	3.6E+	3.5E+		3.5E+	3.5E+
	Expression Signal	4.3	1.86	3.3	6.0	96.0	99.0	1.1	0.62	12.29	1.03	ц ч	0.70	2.23	2.23	5.19	1.06	0.74	0.95	0.95	3.83	3.83		4.07	1.1	1.17	1.18	0.56	1.02		1.02	0.96
	ORF SEQ ID NO:	33022	34046	36403		32054	32626	34161		29379			34928	37363	37384	25986		30498	34280	34281	34378	34379			28652		31864		34763		34764	35227
	SEQ ID	19946	20910	23176	15347	19070		21024	22345	16748	19757	70070	21765	24057	24057	13359	17477	17983	21142	l	. 1	21235		23444	16003	18695	18896	21078	21621	1	1	22055
	Probe SEO ID NO:	7262	8216	11365	2635	6297	6673	8331	9694	4001	7066	0000	9000	11408	11408	579	4745	5174	8450	8450	8543	8543		10759	3241	5911	6118	8383	8930		8930	9393

Page 9 of 536 Table 4 Single Exon Probes Expressed in Brain

		Most Similar		ŀ	
SEQ ID ORF SEQ NO:	C Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
				NT	Bos taurus mRNA for Ran-binding protein 2, partial
				LN	Brassica napus RPB5d mRNA, complete cds
			P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
				SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
000	0.7			FX	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KOM, 11) name complete cits
			_	Į,	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
				LIZ	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
				LN	Saccharomyoes cerevisiae MSS1 gene, complete cds
				IN	Homo sapiens DiGeorge syndrome critical region, centromeric end
18759 3172				SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
18759 3172				SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
				NT	Homo saplens serine palmitoyl transferase, subunit il gene, complete cds; and unknown genes
			AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
23008 3622			AP001511.1	۲	Bacillus halodurans genomic DNA, section 5/14
13273 2590	1.64		X96422.1	NT	D.rerio zp-50 POU gene
13273 2590	6.0 80		X96422.1	NT	D.rerio zp-50 POU gene
			4502404	L	Homo sapiens carcinoembryonic antigen∡elated cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
		L	1	SWISSPROT	SQUALENE-HOPENE CYCLASE
L			P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
		·	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
18313 3121			P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
18988 3196			P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
18988 3196		3.2E+(P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
			P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
20336 3344			Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
20336 3344		3.2E+(Y13655.1	NT	Chlamydomonas reinhardtil chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
		3.2E+(P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SWALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
			M36383.1	NT	S.cerevisiae threonine deaminase (ILV1) gene, complete cds
22689 3590			AB016081.2	NT	Oryzias latipes OIGC6 gene for guanytyl cyclase C, complete cds
		3.25+(L33836.1	N	Sus scrofa choline acetyltransferase gene, promoter region
		3.1E+	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
١		3.1€±	P52178	SWISSPROT	TRIOSE PHOSPHALEPHOSPHALE LAANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CLPT)
	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	36283 26933 33021 33324 33324 34813 34850 34729 31722 31723 31723 31723 31723 31723 31723 31724 31724 3177 31214 31214 31216 3	36283 0.46 26933 2.94 33021 2.64 33021 2.64 33021 2.64 33021 2.64 33813 0.67 34813 0.67 34820 0.54 38030 2.97 31722 1.57 31722 1.67 31723 0.9 36223 0.9 25908 0.9 25908 0.9 25908 1.64 25908 1.64 25908 1.64 31215 2.7 31214 2.7 31348 2.65 33449 2.65 33449 2.65 33449 2.65 33449 2.65 33449 2.65 33449 2.65 33449 2.65 33449 2.65 33449 2.65 33449 2.65 33449 2.65 33449 2.65	S6283 O.46 3.5E+00 AJ133723.1 26633 2.94 · 3.4E+00 AJ254577.1 26633 2.94 · 3.4E+00 AP254577.1 33021 2.64 3.4E+00 P04052 33374 0.69 3.4E+00 P04052 34813 0.67 3.4E+00 AD250567.1 34850 0.54 3.4E+00 AP013167.1 31723 1.57 3.4E+00 AP01111.1 36030 2.97 3.4E+00 AP01111.1 36223 0.9 3.2E+00 AP01111.1 36224 0.9 3.2E+00 AP022.1 36224 0.9 3.2E+00 AP4924 31177 1.06 3.2E+00 AP4924 3124 2.7 3.2E+00 AP4924	S6283 0.46 3.5E+00 AJ33723.1 NT 26833 2.94 3.4E+00 AF284577.1 NT 26833 2.94 3.4E+00 AF284577.1 NT 33021 2.64 3.4E+00 P04052 SWISSPROT 33021 2.64 3.4E+00 P04052 SWISSPROT 34813 0.67 3.4E+00 P04052 SWISSPROT 34850 0.67 3.4E+00 P04052 SWISSPROT 34850 0.67 3.4E+00 P04052 SWISSPROT 34850 0.67 3.4E+00 P04056 NT 34850 0.67 3.4E+00 P04056 NT 31723 1.67 3.3E+00 P010689 SWISSPROT 31724 0.9 3.3E+00 P010689 SWISSPROT 31777 1.06 3.2E+00 P64024 SWISSPROT 31746 1.06 3.2E+00 P64024 SWISSPROT 31214 2.7 3.2E+00 P64024 SWISSPROT 31214 2.7 3.2E+00 P64024 SWISSPROT 31264 1.78 3.2E+00 P10265 SWI

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Top Hit Descriptor	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)	STRUCTURAL POLYPROTEIN (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2;	INONAL ROCTORAL PROTEIN VP4; MINOR STRUCTORAL PROTEIN VP3	STRUCTURAL POLYPROTEIN (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]	602017413F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4153059 5	Buxus harlandii maturase K (matk) gene, partial cds; chloroplast gene for chloroplast product	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52	Mus musculus endomucin (LOC53423), mRNA	601342758F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3684807 5	Mus musculus endomucin (LOC53423), mRNA	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2	Ipomoea purpurea chalcone synthase (CHSB) gene including complete 5'UTR and complete cds	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	xc88e12.x1 NCI_CGAP_Bm35 Homo sepiens cDNA clone IMAGE:2591374 3' similar to gb:M17733 THYMOSIN BETA-4 (HUMAN);	CM0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds	Mus musculus SRV-box containing gene 13 (Sox13), mRNA	Mus musculus SRY-box containing gene 13 (Sox13), mRNA	Mycobacterium fortuitum furA II gene	Hamo saplens Surf-5 and Surf-6 genes	Mus musculus SH2-containing Inositd 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds	faba bean necrotic yellows virus C2-Eg gene, Isolate Egyptian EV1-93	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
Top Hit Database Source	SWISSPROT	SWISSPROT	100000	OWISSERSOI	SWISSPROT	EST HUMAN	N F	5	Z	EST_HUMAN	LN FA	Ν	님	۲	닐	N⊤	EST HUMAN	EST HUMAN	N	NT	L	TN	LN	IN	님	TN	NT	IN	TN	NT	LN
Top Hit Acession No.	+00 014514	+00 P46589	000044	+00 F 05844	+00 P05844	+00 BF344171.1	H00 AF186398.1	+00 AL161552.2	8393724 NT	+00 BE565182.1	8393724 NT	B679306 NT	8679306 NT	H00 L14005.1	+00 U15947.1	+00 AL116459.1	+00/AW088191.1		+00 AF068749.1	6755601 NT	6755601 NT	+00 Y17062.1	+00 AJ224639.1	AF235502.1	2.6E+00 AJ132180.1	4J132180.1	+00 AL161540.2	9055193 NT	+00 AF143675.1	11419220 NT	+00 AJ271844.1
Most Similar (Top) Hit BLAST E Value	2.9E+00	2.9E+00	00.50	Z.8E+00	2.9E+00	2.9E+00	2.8E+00	2.8E+00	2.8E+00	2.8E+00	2.8E+00	2.7E+00	2.7E+00	2.7E+00	2.7E+00	2.7E+00	2.7E+00/	2.7E+00	2.6E+00	2.6E+00	2.6E+00	2.6E+00	2.6E+00	2.8E+00	2.6E+00/	2.6E+00 /	2.6E+00	2.6E+00	2.6E+00	2.6E+00	2.5E+00/
Expression Signal	5.21	6.84	7.9 0	70.0	0.67	1.03	4.4	2.74	5.72	0.54	1.32	13.51	13.51	1.17	9.0	1.83	0.73	1.75	5.15	1.68	1.68	0.59	0.82	6.04	1.13	1.13	2.83	1.67	1.32	3.17	3.73
ORF SEQ ID NO:	32862		70200			33819	26872		32968		32968		25673	31154			33519		28894	31149	31150			 ;	33778	33777	35395		36878		26878
Exon SEQ ID NO:		20037	29700		20463	20691	14187	14375	19892		19892	13036	13036	18263		21558	20403	1	li	18259		l	25424	20266	20853	20653	22210	22901	23630		14195
Probe SEQ ID NO:	7110	7356	7787		7927	9662	1440	1629	7207	9513	10588	224	224	5464	8045	8867	9332	10397	4626	5460	5460	5738	7454	7600	7958	7958	9557	10253	10953	12560	1448

WO 01/57275 PCT/US01/00667

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Single Exon Probes Expressed in Brain	Top HIt Descriptor	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4	TEICHOIC ACID BIOSYNTHESIS PROTEIN F	Vibrio cholerae ctxA gene and ctxB gene for cholera toxins, complete cds	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA	Rice DNA for aldolase C-1, complete cds	601175779F1 NIH_MGC_17 Hamo sapiens cDNA clone IMAGE:3531090 5	DNAJ PROTEIN	Mus musculus EiF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds	Chicken alpha-3 collagen type VI mRNA, 3' end	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)	602120856F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4278012 5	602120856F1 NIH_MGC_56 Home sapiens cDNA clone IMAGE:4278012 5	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD2/)(114)	OD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (114)	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome	RC2-PT0004-031299-011-d05 PT0004 Homo saplens cDNA	ENDOCHITINASE B PRECURSOR (CHN-B)	SKIN GRANULE PROTEIN PRECURSOR	SKIN GRANULE PROTEIN PRECURSOR	H.sapiens CTGF gene and promoter region		hre3f06.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:3133187 3'	hre3f06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3	DENITRIFICATION REGULATORY PROTEIN NIRQ	Fregaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allete, complete cds	G.domesticus artificial single chain antibody gene (L3)	Bos taurus partial cytb gene for cytochrome b			
Jie Exon Prop	Top Hit Database Source	NT	SWISSPROT	SWISSPROT	SWISSPROT	SWISSPROT	NT	EST_HUMAN	NT	NT	EST HUMAN	SWISSPROT	L	IN	NT	SWISSPROT	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	۲	EST_HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	NT	SWISSPROT	EST_HUMAN	EST_HUMAN	SWISSPROT	۲۷	NT	N
Surs	Top Hit Acession No.	-00 AJ271844.1	00 P13485	13485	+00 P13485	13485	-00 D30052.1	-00 AW949158.1	4502902 NT	-00 D50307.1	-00 BE297758.1	240170	:+00 AF289665.1	H00 M24282.1	4503352 NT	100 P02843		12.1		+00 P26842	+00 AE001486.1	H00 AW875126.1	F00 P24091	+00 P13673	+00 P13673	ноо X92511.1	+00 P09099	+00 BE326702.1	+00 BE326702.1	+00 Q51481	+00 AF158652.2	+00 Z46724.1	+00 AJ401081.1
	Most Similar (Top) Hit BLAST E Value	2.5E+00 /	2.5E+00 F	2.5E+00 F	2.6E+00 F	2.6E+00 F	2.5E+00	2.5E+00 /	2.5E+00	2.5E+00	2.5E+00	2.5E+00	2.5E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.4E+00	2.3E+00	2.3E+00
	Expression Signal	3.73	2.22	222	1.63	1.63	0.64	0.99	0.58	1.53	0.67	1.34	3.08	1.13	60.9	4.16	0.78	0.78	2.4	2.4	2.63	1.61	7.38	2.56	2.58	1.86	6.55	1.62	1.62	0.87	2.16	13.6	1,35
	ORF SEQ ID NO:	26879		31435		31435	32406	33431	33477	34841	35608			28428	30203	31657	33040	33041	33865	33866			34563	35788		35868		36079	36080	36364	37327	26650	Ш
	Exon SEQ ID NO:	14195	ı		1	1	19392	20323	20383	21691	22403	24128	24498	15778	17579		l	19964	20734	20734	20804		l _	<u> </u>	_	L	1_	1	22868	23136	24022	L	Ш
	Probe SEO ID NO:	1448	5723	5723	6367	6367	9830	7859	7700	9004	9752	11528	11943	3012	4849	6920	7280	7280	8039	8039	8110	8549	8727	9838	9938	10007	10143	10220	10220	10490	11331	1231	4102

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	Top Hit Descriptor	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)	M.mazei dnak and dnaJ genes homologues coding for DnaK and DnaJ	Polypterus amatipinnis mitochondríon, complete genome	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)	ANNEXIN VII (SYNEXIN)	602069121F1 NIH_MGC_58 Homo sepiens cDNA clone IMAGE:4068173 5'	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds	Rat gene for regucalcin, exon1 (non-coding exon)	Rat gene for regucalcin, exon1 (non-coding exon)	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA, (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- BINDING REPEATS) (LR11) (>	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LOLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LOLR REPEA	RC3-CT0254-300800-022-e06 CT0254 Homo saplens cDNA	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'	MINOR VIRION STRUCTURAL PROTEIN MU-2	INSULIN-LIKE GROW TH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)	nl95b02.s1 NCI_CGAP_Co10 Homo saplens cDNA clone IMAGE:1058379 3'	zn97f04.r1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:566143 5'	zx05g10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5	ALANINE RACEMASE	bb17h12.x1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
	Top Hit Datebase Source	EST_HUMAN	L	SWISSPROT	LN	LN	SWISSPROT	Γ		EST_HUMAN	EST_HUMAN	LN	NT	NT	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN
	ession		54	П	\Box	7		✝			_		_				Т-									
	Top Hit Acession No.	N86245.1	6978554 NT	P07199	X60265.1	5835317 NT	011127	007076	BF541987.1	BF541987.1	BE895237.1	AF020528.1	D67071.1	D67071.1	088307	088307	BE927220.1	BE927220.1	BE250383.1	Q00335	P51459	AA594574.1	AA137027.1	AA449012.1	P54918	BE301560.1
	Most Similar (Top Hit Ac BLAST E No.	2.3E+00 N86245.1		2.3E+00 P07199	2.3E+00 X60265.1	2.3E+00 583531	2.3E+00 Q11127	2.3E+00 Q07076	2.3E+00 BF541987.1	l					2.2E+00 088307	2 2E+00 () () () ()	2.2E+00 BE927220.1	2,2E+00 BE927220.1	2,2E+00 BE250383.1	2.2E+00 Q00335					2.2E+00 P54918	2.2E+00 BE301560.1
		0.95 2.3E+00 N86245.1		3.07 2.3E+00 P07199	1.01 2.3E+00 X60265.1	2.3E+00	1.8 2.3E+00 Q11127			l	6.84 2.3E+00 BE895237.1					12 73 2 2E+00 (O88307	1			3.87 2.2E+00 Q00335		3.94 2.2E+00 AA594574.1			0.72 2.2E+00 P54918	0.58 2.2E+00 BE301560.1
	Most Similar (Top) Hit BLAST E Value	0.95 2.3E+0	2.3E+00	3.07	33455 1.01 2.3E+00 X60265.1	34849 0.54 2.3E+00		3.83	3.03	3.03		0.95	5.01	5.01	30692 12.73		1.03	1.03	9.84	32010 3.87	32269 3.16	3.94	32975 0.9	33272 19.2	33365 0.72	33823 0.58
	Expression (Top) Hit Signal Value	2.3E+0	20035 33113 2.47 2.3E+00	25425 3.07	20343 33455 1.01 2.3E+00 X60265.1	21698 34849 0.54 2.3E+00	21757 34919 1.8	23395 36632 3.83	24373 37703 3.03	37704 3.03	24642 31099 6.84	16746 28378 0.95	29644 5.01	17017 29645 5.01	18064 30692 12.73	18064 30803 12.73	18554 31478 1.03	31479 1.03	18753 31714 9.84	19035 32010 3.87	19267 32269 3.16	3.94	19902 32975 0.9	20178 33272 19.2	20257 33365 0.72	0.58

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8001	20696	33824		2.2E+	-00 BE301560.1	EST HUMAN	bb17h12.xt NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE).
9241			,	2.2E+	-00 BE741678.1	EST HUMAN	601594733F1 NIH_MGC_9 Hamo sapiens cDNA clane IMAGE:3948561 5'
9468	25124		2,28	2.2E+00	-00 004708	SWISSPROT	TRANSPOSON TY1 PROTEIN A
9953	22601	35804	1.1	2.2E+00	-00 AI290373.1	EST_HUMAN	qm69b03.x1 Soares, placenta, 8to3weeks, 2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893965.3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
9953	22601	35805	1.1	2.2E+00	-00 A1290373.1	EST HUMAN	qm69b03.x1 Soares_placenta_8tc9weeks_ZNbHP8tc9W Homo septens cDNA clone IMAGE:1893965 3' similar to cb:Y00433 GLUTATHIONE PEROXIDASE HIMANY
9666	22644	35856	7		00 BF246782.1	EST HUMAN	601855591F1 NIH MGC 57 Homo sapiens cDNA clone IMAGE 4075391 51
10353	23000	36217		2.2E+00	00 AF183416.1	TN	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolon mRNA complete cols
11418	23185	36415		2.2E+00 P07911	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11616	24214	37539	5.89	2.2E+00		SWISSPROT	EARLY E1A 28 KD PROTEIN
929	15545	25967	8.3	2.1E+00	2.1E+00 AF132612.2	Z	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3675	16330		1.08	2.1E+00	AW 449366.1	EST_HUMAN	UI-H-Bi3-aki-e-08-0-UI,s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6041	18821		0.89	2.1E+00		SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
67.10	19625	32669	3.95	2.1E+00		SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
6946	19428	32443	5.72	2.1E+00	00 N29575.1	EST HUMAN	W08a10.s1 Seares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654 TRANSCRIPTION INITIATION FACTOR TFIID /HIMANN
8395	21088		1.97	2.1E+00	15	EST HUMAN	AU123630 NT2RM2 Homo saplens cDNA clans NT2RM200671 5'
1174	13927	26591	1.44	2.0E+00		N⊤	Homo saplens p22Dokdel (DOKDEL) mRNA, complete cds
1174	13927	26292	1.44	2.0E+00		N	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1312	14060	26735	76.0	2.0E+00	00 AF204927.1	NT	Oryctolagus cuniculus Na+,K+-ATPase beta 1 subunit mRNA, complete cds
1569	14316		2.61	2.0E+00 P25582		SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2145	14875	27609	5.98	2.0E+00		IN	R.norvegicus mRNA for collagen alpha1 type /
2145	14875	27810	5.98	2.0E+00		NT	R.norvegicus mRNA for collagen alpha1 type i
4080	16824	29450	2.2	2.0E+00	00 AW664496.1	EST_HUMAN	h13c05 x1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN):
4080	16824	29451	2.2	2.0E+00	00 AW664496.1	EST HUMAN	h13605,x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GI YCFRAI DEHYDE 3-PHOSPHATE DEHYDROGENASE 1 INFO AUTMANY
0772	20.50		000	100	Γ		STRUCTURAL POLYPROTEIN [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE
R# /	67170		0.92	2.0E+00		SWISSPROT	GLYCOPROTEINS E1 AND E2]
526/	20618	33745	3.17	2.0E+00	T	Ł	Escherichia coli 0157 DNA, map position at 46 min., complete cds
626/	81007	33/46	3.17	2.0E+00	T		Escherichia coli 0157 DNA, map position at 46 min., complete cds
/9Z9	20615	33747	3.17	2.0E+001	2.0E+00 AB008676.1	۲ <u>۷</u>	Escherichla coli 0157 DNA, map position at 46 min., complete cds

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seu III bi aili	Top Hit Descriptor	D PRECURSOR	Homo sapiens PRO0530 mRNA, complete cds	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 0-FRUCTOSYL TRANSFERASE)	Homo sapiens chromosome 21 segment HS21 C080	oz43h05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA	CM0-BT0282-171299-127-e05 BT0282 Homo saplens cDNA	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters	Mus musculus T-cell acute lymphocytic leukemia 1 (Tal1), mRNA	602071917F1 NCI_CGAP_Brn67 Hamo saplens cDNA clone IMAGE:4214669 51	Hippoglossus hippoglossus interferon Inducible Mx protein (Mx) mRNA, complete cds	601894255F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4140084 5'	M.musculus Ank-1 mRNA for erythroid ankyrin	M.musculus Ank-1 mRNA for erythroid ankyrin	PROTEIN DLX-3	PROTEIN DLX-3	s HSPC262 mRNA, partial cds	EST365751 MAGE resequences, MAGC Homo sapiens cDNA	6787 Human retina cDNA Tsp509l-cleaved subilbrary Homo sapiens cDNA not directional	tu82d07.xt NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.t1 MSR1 repetitive element ;	qf50b01.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1753417 3' similar to contains L1.t1 L1	ומוו	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
olligie Exoli Flobes Expressed III braili	·	CHITINASE D PRECURSOR	o sapiens PRO0530 mRNA, corr	IDINE DEAMINASE (CYTIDINE	mydomonas reinhardtii alternative	us norvegicus Actin-related protei	LEVANSUCRASE (BETA-D-FRUCT TRANSFERASE)	o sapiens chromosome 21 segmi	h05.x1 Soares_NhHMPu_S1 Hor	LEVANSUCRASE (BETA-D-FRUCT TRANSFERASE)	-BT0282-171299-127-905 BT028	-BT0282-171299-127-e05 BT028	IP TRANSCRIPTION FACTOR	OTHETICAL 38.0 KD PROTEIN	OTHETICAL 38.0 KD PROTEIN	musculus T cell receptor gamma	musculus T-cell acute lymphocyt	171917F1 NCI_CGAP_Brn67 Hor	oglossus hippoglossus interferon	94255F1 NIH_MGC_17 Homo si	usculus Ank-1 mRNA for erythrol	usculus Ank-1 mRNA for erythrol	HOMEOBOX PROTEIN DLX-3	HOMEOBOX PROTEIN DLX-3	Homo saplens HSPC262 mRNA, partial cds	365751 MAGE resequences, MA	' Human retina cDNA Tsp509I-cli	tu82d07.x1 NCI_CGAP_Gas4 Homo MSR1 repetitive element;	201.x1 Soares_testis_NHT Homo	lepenave element,	o sapiens lens epithellum-derived
ם באטוו דוטאס	Top Hit Database Source	SWISSPROT CHI	NT	SWISSPROT CY	NT		SWISSPROT TRA		EST_HUMAN oz4	SWISSPROT TRA	Т	Γ		SWISSPROT HY	SWISSPROT HY			EST_HUMAN 602	NT Hip	T HUMAN	NT M.m	NT N	SWISSPROT HO	ISSPROT	NT	EST_HUMAN EST	HUMAN	tu82 EST HUMAN MSI		EST HOWAN IED	╗
Billo	Top Hit Acession No.		100 AF111849.1	+00 P44325 S	100 AF314254.1	9506404 NT	-00 Q60114 S	100 AL163280.2 N	-00 AI141067.1 E		16.1		-00 Q9TTR8 S	-00 Q03703 S	-00 Q03703	-00 AF021335.1 N	8755715 NT	-00 BF530830.1 E		1.1		-00 X69063.1	-00 O60479 S		-00 AF161380.1 N	-00 AW953681.1 E	.00 W 22424.1	00 Al678443.1 E			+00 AF199339.1 IN
	Most Similar (Top) Hit BLAST E Value	1.8E+00	1.8E+00	1.8E+00	1.8E+00	1.8E+00	1.7E+00	1.7E+00 /	1.7E+00	1.7E+00 (1.7E+00 (1.7E+00	1.7E+00	1.7E+00 /	1.7E+00	1.7E+00	1.7E+00 /	1.7E+00	1.7E+00	1.7E+00	1.7E+00	1.75+00	1.7E+00 /	1.7E+00/	1.7E+00 \	1.7E+00	1	1.75+00/	1.6E+00/
	Expression Signal	0.75	3.2	0.63	6.29	3.9	2.21	2.29	2.68	0.81	1.7	1.77	3.28	1.11	1.11	0.91	1.13	0.59	0.6	2.3	0.59	0.69	2.18	2.18	1.15	0.48	2.57	<u>1</u>	3	Ď.	18.51
	ORF SEQ ID NO:	35605					26502	27734	27833	29792	31223	31224	31666	32871	32872	33573	33755	33781	34268		34440	34441	34892	34893			37514	31074	o E	0/800	27491
	Exon SEQ 1D NO:	22400	22831	23098	25236	24763	13844	14995	15094	17162	1			19806	19806		20627			1		21297	25123	25123	22159	22719	24195	24684	1	ł	14762
	Probe SEQ ID NO:	9749	10183	10452	12276	12359	1086	2269	2372	4426	5525	5525	5927	7118	7118	7753	7932	7961	8440	8526	8605	8605	9047	9047	9266	10071	11596	12231		12/1/21	2027

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2036	14771	27500	3.75	1.6E+00	00 AF077374.1	NT	Homo saplens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2042	14776	27505	1.54	1.6E+00	1.6E+00 Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
2282	15007			1.6E+00		NT	B.napus gene encoding endo-polygalacturonase
2961	15727	28377	1.61	1.6E+00	00 W 58426.1	EST_HUMAN	zd25f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN);
4011	16757		5,68	1.6E+00		EST_HUMAN	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4319	17058	29682	1.9	1.6E+00		TN	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4319	17058	29683	1.9	1.6E+00	1.6E+00 AF155827.1	TN	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4942	17669	30277	0.84	1.6E+00	1.6E+00 AF075394.1	LΝ	Uroteuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
	ł						Uroteuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial
4942	17669	30278	0.84	1.6E+00	4.1	L	protein, partial cds
5024	17745			1.6E+00	1.6E+00 Y11344.1	LN	Mus musculus ST6GalNAcIII gene, exon 2
5024	17745	30357	2.86	1.6E+00	1.6E+00 Y11344.1	LN	Mus musculus ST6GalNAcili gene, exon 2
5737	18529	31450	2.18	1.6E+00	1.6E+00 L04808.1	LN	Brachydanio reno MHC class II DA-beta-2*01 gene, 3' end
5823	18612	31543	62'0	1.6E+00	1.6E+00 AF005631.1	TN	Homo sapiens transglutaminase type I (Tgasel) gene, promoter region
8378	19147	32146	69.0	1.6E+00		EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
6610	19373		1.06	1.6E+00	1	EST HUMAN	UI-H-BIZ-ahr-b-04-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens oDNA clone IMAGE:2727511 3'
7145	19832	32901	2.73	1.6E+00	1.6E+00 BE897267.1	EST_HUMAN	RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
7929	20624		1.19	1.6E+00		SWISSPROT	VIRULENCE FACTOR MYIN HOMOLOG
8277	20971	34112	3.28		AJ297131.1	TN	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
8628	21490	34636	0.83	1.6E+00		NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8628			0.83		37222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8970	21660	34810	0.47	1.6E+00	1.6E+00 BE388331.1	EST_HUMAN	601283925F1 NIH_MGC_44 Hamo sapiens cDNA clone IMAGE:3605647 5'
0986	25121		1.94			NT	M.musculus COL3A1 gene for collegen alpha-/
9360	25121	33550	1.94	1.6E+00		LN	M.musculus COL3A1 gene for collagen alpha-l
9487	22140		0.56		3.1	ΝΤ	Thermoanaerobacter ethanolicus D-xylose-binding protein (xylF) gene, complete cds
9634	22286	35480	1.32		1.6E+00 T41290.1	EST_HUMAN	ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV
							Drosophila melanogaster signal transducting adaptor protein (STAM), serine threonine kinase lal (IAL), and
10047			0.5			۲	zinc finger protein (DNZ1) genes, complete cds
10085		35947	1.15		1.6E+00 AW835644.1	EST HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
10085	22733		1.15			EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
10242					1.6E+00 AF037352.1	۲	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10491	23137	36365	0.45			N	Glugea plecoglossi beta-tubulin 2 (btub2) gene, partial cds

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	-	_	_		_	_		_		_					_	_									•					
Top Hit Descriptor	CAPSID PROTEIN P40 (CONTAINS: ASSEMBLIN (PROTEASE) : CAPSID ASSEMBLY PROTEIN	nc16b02.s1 NCI_CGAP_PrI Homo sapiens cDNA clone IMAGE:1008267 sImilar to contains element MER4 repetitive element:	Homo sapiens transdutaminase type I (Trasel) dene promoter region	Homo sapiens unknown mRNA	Rattus naviedicus jun dimerization protein 2 (Idn. 2) mRNA complete ade	Chlamydophila pneumoniae AR39, section 32 of 94 of the complete genome	Mus musculus a dishtegrin and metalloproteinase domain (ADAM) 15 (meteroldin) (Adam48) mBNA	Potato virus A RNA complete genome, Isolate U	Mus musculus T-cell lymphoma Invasion and metastasis 1 (Tiam1). mRNA	Potato virus A RNA complete genome, Isolate U	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1	#t12f10.x1 NCI_CGAP_GC6 Hamo saplens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1.	TO THE TOTAL TOTAL THE TOT	แนวบนา NCL_CGAP_GC6 Hama sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1.;	9910e02.r1 Soares Infant brain 1NIB Homo sablens cDNA clone IMAGE:31693 5	601478745F1 NJH MGC 68 Homo seplens cDNA close IMA GE-3884 FKK R	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAI 5 INTERGENIC REGION PRECLIPSOD	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECLIRSOR	ak26f10.s1 Soares testis NHT Homo saplens cDNA clone IMAGE:14071153'	an07b11.s1 Stratagene schizo brain S11 Homo saplens cDNA clone IMAGE:1684893 3' similar to	Homo sapiens WDR4 gene for WD repeat protein complete cds	601509586F1 NIH MGC 71 Home sapiens CDNA clone IMAGE:3014184 F	Mouse germline IdM chain dene, mu-delta region	Homo saplens hGPIb alpha gene for platelet dixconotein ib alpha complete cite	601882662F1 NIH MGC 57 Homo saplens CDNA clone IMAGE 4095435 F	M03h01.r1 Soares placenta Nb2HP Homo saplens cDNA clone IMAGE-147697 5'	QV3-CT0192-261099-008-d09 CT0192 Homo saplens cDNA	RC0-TN0078-150900-034-g05 TN0078 Homo saplens cDNA	602035771F1 NCI_CGAP_Bm64 Homo saplens cDNA clone IMAGE:4183865 5	ze38g06.r1 Soares retina N2b4HR Homo saplens cDNA clone IMAGE:361306 5
Top Hit Database Source	SWISSPROT	EST HUMAN	IN IN	L	L	LN	Į.	TN	Ę	NT	N _T	EST HUMAN		EST HUMAN	Г	Г		Г	EST_HUMAN	EST HUMAN	Т	T HUMAN			EST HUMAN	Г		EST_HUMAN	Ι'''	EST_HUMAN
Top Hit Acession No.	00 P54817	1.6E+00 AA216387.1		Γ		1.5E+00 AE002201.2	6752961 NT	1.5E+00 AJ131402.1	6678350 NT	1.5E+00 AJ131402.1		1.5E+00 Al655301.1	T	1.5E+00 Al655301.1		1.5E+00 BE785356.1			59.1	1.5E+00 Aloo3254.1				5.1	Γ	Γ		Γ	1.5E+00 BF337944.1	
Most Similar (Top) Hit BLAST E Value	1.6E+00	1.6E+00	1.6E+00/	1.6E+00	1.5E+00	1.5E+00	1.5E+00	1.5E+00 /	1.5E+00	1.5E+00	1.5E+00	1.5E+00		1.5E+00/	1.5E+00 R17879.1	1.5E+00 E	1.5E+00 P47179	1.5E+00 P47179	1.5E+00	1.5E+00	1.5E+00 A	1.5E+00 E	1.5E+00 K02138.1	1.5E+00 A	1.5E+00 B	1.5E+00 R	1.5E+00 A	1.5E+00 B	1.5E+00 B	1.5E+00 A
Expression Signal	1.95	1.27	5.27	3.46	5.31	2.2	2.03	1.95	2	1.85	0.72	0.83		0.83	3.02	1.37	23.98	23.98	19:0	0.76	0.64	0.89	0.84	0.48	0.46	0.64	1.39	6:38	1.77	1.66
ORF SEQ ID NO:	36602	36657	31543	37626	25476			27867	27975	27867	28785	31350		31351	32068		32814	32815	33006	33257		33848	34377		34876	35217	35374	35618		35958
Exon SEQ ID NO:	23361	23416	18612	24300	12859	13037	13384	15131	15235	15131	16127	18437		18437	19083	19720	19751	19751	19830	20166	20390	20716	21234	21605	21722	22045	22188	22411	22600	22744
Probe SEQ ID NO:	10670	10728	10747	11705	31	225	808	2410	2519	3135	3368	5642		5642	6312	7028	2060	7060	7245	7483	7727	8021	8542	8914	9032	9383	9535	9760	9952	10096

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Single Exon Probes Expressed in brain	Most Similar Top Hit Acession Top Hit Bescriptor Top Hit Descriptor Source Source	1.5E+00 AA017689.1 EST_HUMAN	1.5E+00 AL134197.1 EST_HUMAN	1.5E+00 X07380.1 NT	1.5E+00 AI400798.1 EST_HUMAN	1.5E+00(A/400798.1 EST_HUMAN	1.5E+00 D63480.1 NT	1.5E+00 AL445065.1 NT	1,4E+00 7661685 NT		1.4E+00 U67922.1 NT	1.4E+00 X74463.1 NT		1.4E400-A1004304,Z	1.4E+00 AF064564.2 NT	1.4E+00 BF681547.1 EST_HUMAN	L	1.4E+00 AB032983.1	2 1.4E+00 Q13472 SWISSPROT DNA TOPOISOMERASE III ALPHA	1.4E+00 AB020712.1 NT	1.4E+00 Q92777 SWISSPROT	1.4E+00 Q92777 SWISSPROT	1.4E+00 AJ133269.1 NT		1 4F+00 P55268 SWISSPROT	1,4E+00 P55268 SWISSPROT	1.4E+00 P07683 SWISSPROT	1.4E+00 AJ271735.1 NT	1.4E+00 R20459.1	1.4E+00 BE064667.1 EST_HUMAN	1.4E+00 AF134844.1
	Most (Togression Signal Ve	1.66 1	4.46	6.55	2.1	2.1	1.44		2.76	2.76	6.92	2.21		7.0.7	2.61	1.81	1.61	5.57	2.72			2.67	2.07	1 17	L			4.47	1.73		0.51
	ORF SEQ ID NO:		37282		37549	37550	30713		3 25472	3 25473	_	28125		17707	28222		30754		3 31936		32074	32075	32946	32062			, l	<u>ا</u>	1 34829		34985
	Exon SEQ ID NO:	22744	23982	24130	24226	24226	_	24815	12856	12856	15057	15384	l	13481	15481	17280	18093	18240	18963	25420	19089	19089	19872	10887	1_			21385			21819
	Probe SEQ ID NO:	10096	11375	11530	11629	11629	12222	12445	28	28	2333	2675	92.20	9//7	2776	4545	5288	5441	6186	6202	6318	6318	7186	7204	725g	7258	8233	8693	8991	608	9131

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				Most Similar			
SEQ ID NO:	SEO D NO:	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10108	22756		62.0	1.4E+00	·00 BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10151	Щ			1.4E+00	+00 BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-CO4 HT0198 Hamo sapiens cDNA
10151	22799	36016	0.61	1.4E+00	+00 BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10424	23070		1.06	1.4E+00	+00 D63441.1	ΙΝ	Pandorina colemaniae chloroplast rbcL gene for ribulose bisphosphate carboxylase, partial cds
10424		36282	1.06	1.4E+00	+00 D63441.1	ΤN	Pandorina colemaniae chloroplast rbcL gene for ribulose bisphosphate carboxylase, partial cds
11003	23675	36931	1.34	1.4F+00	HO0 AA195528 1	FST HUMAN	z36e09.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element MER22 repetitive element:
11188			6.16	1.45+00	-00 AB006682.1	LZ	Homo sapiens APECED mRNA for AIRE-1, complete cds
11381			4.42	1.4E+00	+00 BE962107.2	EST HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11381	23988	37289	4.42	1.4E+00	+00 BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:38458053'
11404	24053	37357	3.46	1.4E+00	HOO U30790.1	ΤN	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunif (pcg1) gene, complete cds
11404	24053	37358	3.46	1.4E+00	100 U30790.1	N	Pneumocystis carinil f. sp. ratti guanine nucleotide binding protein alpha subunit (pcq1) gene, complete cds
12079	25256		1.48	1.4E+00	-00 AL161500.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
292			1.81	1.3E+00	-00 273640.1	N.	M.mucedo gene encoding 4-Dihydromethyl-trisporate dehydrogenase
882		26320	3.42	1.3E+00	-00 AJ271192.1	IN	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1107	13864		20.26	1.3E+00	-00 Y19213.1	۲N	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
1274		26692	13.71	1.3E+00	4507998 NT	ΝΤ	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1274	14024	26693	13.71	1.3E+00	4507998 NT	F	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1334			1.26	1.3E+00		NT	Coix lacryma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1605	14351		2.27	1.3E+00	1.3E+00 AE002338.2	TN	Chlamydia muridarum, section 66 of 85 of the complete genome
3330	14067		•	4 0 0	A D020447 4	H	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP)
2405	1	27862	1.27	137.00	Γ	SWISSPROT	LAMININ AI PHA-1 CHAIN PRECIESOR (LAMININ A CHAIN)
2553	L		1.75	1.3€+00	35.2	EST HUMAN	601661233R1 NIH MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2940	15705	28354	0.73	1.3E+00	6755621 NT	LN	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
							Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyta membrane
2584	16330	78087	C	in c	00 A E0 48 40 4 4	Fix	protein (Pob), synaptic vesicle-associated integral membrane protein (VAMP-1), proceilagen C-proteinase
5427		30938	60.0	37.40		SWISSPROT	PHENOL HYDROXY ASE PS PROTEIN (PHENOL 2 MONOOXY SENASE PS COMBONENT)
5822	L	31330	90	1 3 11 100	-	TN	Himan setration 17 hata dahudranasa sana pamahda ada
2883	L_	31590	0.81	1.31	_	EST HUMAN	602145264F1 NIH MGC 48 Homo sabiens cDNA clone IMAGE 4309095 5
5928		31667	7.57	1.3E+00	Ļ	EST_HUMAN	PMo-CT0289-291199-004-f08 CT0289 Homo saplens cDNA
					1		

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	Γ	_				
Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
18712			1.3E+00	1.3E+00 AW362834.1	EST_HUMAN	PM0-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
19093	32081	1.34	1.3E+00	1.3E+00 M33496.1	LN⊤	D.melanogaster no-on-transient A gene product, complete cds
19414		0.75	1.3E+00 Q00156	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
19573	32606	0.62	1.3E+00	M13918.2	LN	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
19554		1.17	1.3E+00	1.3E+00 BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE;3447965 5'
19692	32743	0.81	1.3E+00	00 BE243571.1	EST HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project≕TCBA Homo sapiens cDNA clone TCBAP0959
20030	33417	101	1.35+00	00 P24540	TORGREGA	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
20891			1,3E+00	1.3E+00 AJ009912.1	ĻΝ	Sus scrofa plp gene
21039	L		1.3E+00	1.3E+00 BE963379.2	EST HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA cione IMAGE:3866195 3'
21151			1.3E+00	1.3E+00 BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Hamo saplens cDNA clone IMAGE:3950532 3'
21303		1.78	1.3E+00	9910247 NT	LN.	Hono sapiens GL004 protein (GL004), mRNA
21381	34525	62.0	1.3E+00	1.3E+00 Al927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_KId11 Homo sapiens cDNA clone IMAGE:2462100 3'
22093		5.24	1.3E+00	1.3E+00 AF042084.1	ĽN	Homo saplens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
22102	35273	2.56	1.3E+00	1.3E+00 X72019.1	Į.	S.alba phr-1 mRNA for photolyase
22102	35274		1.3E+00	1.3E+00 X72019.1	LN⊤	S.alba phr-1 mRNA for photolyase
22177	35361		1.3E+00	00 AF059250.1	N⊤	Homo saplens lipoxygenase (ALOX12B) mRNA, complete cds
22222	35407	1.56	1.3E+00	00 000754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
22303		1.14	1.35+00	1.3E+00 AI927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2462100 3'
2377			1.3E+00	1.3E+00 AJ223962.1	ΝT	Lactococcus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
22377	35579	62.0	1.3E+00	1.3E+00 AJ223962.1	N	Lactococcus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
22417	35624	4.53	1.3E+00	00 BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38661953'
22477		0.48	1.3E+00	00 AI559944.1	EST_HUMAN	tq77a12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
22698	35913	0.46	1.3E+00	1.3E+00 AF061251.1	۲	Eschericia coli serotype 0157:H7 O antigen gene cluster
22698			1.3E+00	00 AF061251.1	LN LN	Eschericia coll serotype O157:H7 O antigen gene cluster
22761	35974		1.3E+00	00 AE004392.1	LΝ	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
22778	35991	1.35	1.3E+00	1.3E+00 M29953.1	TN	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
23129		0.82	1.3E+00	1.3E+00 AL163302.2	LN	Homo sapiens chromosome 21 segment HS21C102
23157	36383	0.45	1.3E+00	00 Al990846.1	EST HUMAN	ws32e10x1 NCI_CGAP_GC6 Homb sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN Q16881 THIOREDOXIN REDUCTASE;
23286			1.3E+00	00 014117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)

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Single Exon Plobes Expressed in Drain	Top Hit Descriptor	MRNA 3'-END PROCESSING PROTEIN RNA15	Mus musculus desmin gene	xp09e03.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739868 3'	Human mRNA for KIAA0085 gene, partial cds	Bacillus subtilis genomic DNA 23.9kB fragment	Cava porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds							Г	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA	Elaeis oleifera sesquiterpene synthase mRNA, complete cds	pea seed-borne mosaic virus complete genome	pea seed-borne mosaic virus complete genome	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds	Homo sapiens mRNA for KIAA0874 protein, partial cds	Arabidopsis thallana DNA chromosome 4, contig fragment No. 63					Homo sapiens LHX3 gene, intron 2	Rattus rattus cardiac AE3 gene, excns 1-23	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21	Homa saplens post-synaptic density 95 (DLG4) gene, complete cds	T.pinnatum chloroplast rbcL gene, partial	Human extracellular calcium-sensing receptor mRNA, complete cds		Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds		QV4-BN0080-270400-190-a03 BN0090 Homo saplens cDNA
gie Exon Pi	Top Hit Database Source	SWISSPROT	TN	EST_HUMAN	NT	NT	ᅜ	EST_HUMAN	SWISSPROT	TN	EST_HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	TN	TN	TN	TN	TN	INT	TN	NT	SWISSPROT	NT	EST_HUMAN	LN	TN	INT	TN	INT	NT	EST_HUMAN	LN	NT	EST_HUMAN
	Top Hit Acession No.	+00 P25299	+00 Z18892.2	+00 AW274791.1	+00 D42042.1	+00 298682.1	+00 AF187873.1	+00 BF348043.1	+00 P33464	+00 AF187035.1	+00 AA676246.1	+00 P05228	+00 P05228	+00 P05228	8924234 NT	+00 AF080245.2	+00 AJ252242.1	+00 AJ252242.1	+00 AF140631.1	+00 AB020681.1	+00 AL161563.2	+00 AL161563.2	+00 P54910	+00 U75902.1	+00 BF373570.1	+00 AF188740.1	+00 M87060.1	+00 AL161509.2	+00 AF156495.1	+00 Y09200.1	+00 U20760.1	+00 AW813276.1	+00 AF016052.1	+00 X74885.1	+00 BE003113.1
	Most Similar (Top) Hit BLAST E Value	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.3E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00	1.2E+00
	Expression Signal	1.93	2.01	1.8	3.21	3.16	2.64	6.3	2.73	2.15	11.05	0.87	0.87	0.87	1.35	5.64	1.26	1.26	1.22	1.24	5.98	5.98	2.59	6.69	1.78	1.11	1.57	96.0	1.89	6.43	1.1	1.91	0.83	2.51	4.42
	ORF SEQ ID NO:	36744	36772		37433	37544		31035			26050	26239	26240	26241		28554	26600	26601	27463	28512	28573	28574		29091	28354	28766		29850	29892		30836	31158	31504	31801	31865
	Exon SEQ ID NO:	23505	23528	23968	24127	24221	24675	24780	25153	24848	13414	13578	13578	13576	13627	13893	13935	13935	14739	15873	15926	15926	16041	16452	16716	16110	17174	17222	17258	17283	18154	18266	18575	18840	18897
	Probe SEQ ID NO:	10822	10846	11307	11527	11624	12210	12388	12397	12489	635	804	804	804	858	1138	1183	1183	2003	3108	3163	3163	3280	3699	3967	4268	4438	4487	4523	4548	5351	5467	5784	0909	6119

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Single Exon Probes Expressed in Drain	t Similar Top Hit Acession Database Top Hit Descriptor Top Hit Descriptor Source	LN.	1.2E+00 X89084.1 NT C.glutamicum pta gene and ackA gene	1.2E+00 AA759254.1 EST_HUMAN ah84g12.s1 Sogres_testis_NHT Homo sapiens cDNA clone 1322374.3'	yy39b12.s1 Soares melanocyte 2NbHM Homo saplens cDNA clone IMAGE:273599 3' similar to gbJM87935JHUMAALU472 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:J04970	╅	276.1 EST HUMAN	1.2E+00 AB029010.1 NT Homo saplens mRNA for KIAA1087 protein, partial cds		1.2E+00 AJ271735.1 NT Homo sapiens Xq pseudoautosomal region; segment 1/2	1.2E+00 AV734585.1 EST_HUMAN AV734585 cdA Homo sapiens cDNA clone cdAAFH03 5'	,	Г	0 BE787646.1 EST_HUMAN	1.2E+00 AB033030.1 NT Homo sapiens mRNA for KIAA1204 protein, partial cds		P38427 SWISSPROT	7706271 NT	AW377210.1 [EST_HUMAN	EST HUMAN	NT	1.2E+00 D11745.1 [EST_HUMAN HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01	1.2E+00 X56832.1 NT H.saplens ENO3 gene for muscle specific enolase	TN	1 EST_HUMAN	1.2E+00 BE160761.1 EST_HUMAN PM1-HT0422-160200-007-910 HT0422 Homo sepiens cDNA	1.2E+00 U50147.1 NT Rattus norveglous synapse-associated protein 102 mRNA, complete cds	NT	5.1 NT	NT	EST_HUMAN	10 AW 575889.1
	Most Similar (Top) Hit BLAST E Value	1.2E+00 X8908	1.2E+00 X8908	1.2E+00 AA759	SCOOL TO A	1 2E +00 N3328	1.2E+00 AW81	1.2E+00 AB029	1.2E+00 AJ002	1.2E+00 AJ271	1.2E+00 AV73	1.2E+00 X7420	1.2E+00 J0521	1.2E+00 BE78	1.2E+00 AB03		1.2E+00 P3842	1.2E+00	1.2E+00 AW37	1.2E+00 H4850	1.2E+00 Z3285	1.2E+00 D117	1.2E+00 X5683	1.2E+00 AB00	1.2E+00 AW81	1.2E+00 BE16	1.2E+00 U501	1.2E+00 AL160	1.2E+00 AP00	1.1E+00 D8698	1.1E+00 AW96	1.1E+00 AW 57
	Expression Signal	1.54	1.54	39.54	ii ii	0.00	2.06		3.11	0.94	4.86	2.49		0.56	3.32		0.68	0.51	1.87	9.0	3.75			6.73				17.06	2.8		1.33	
	ORF SEQ ID NO:		31952	31989		32101			32512		33044	33323	33376	33492			34391			34991		35339	35684		37314		36434	30817			27200	
	Exon SEQ ID NO:	18974	18974	19015		10177			19490	19840	l	20220		20379	_		21253	21467	21614	21826		22158	22482	22872	24009	١.	23202	25227	24667	13237	14499	14629
	Probe SEQ ID NO:	6198	6198	6241	6	0347	6412	6815	6829	7153	7282	7550	7603	7715	8467		8561	8775	8923	9138	9538	9605	9831	10224	11318	11357	11435	12179	12199	451	1757	1892

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WO 01/57275 PCT/US01/00667

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8824	21516	34661	0.45		1.1E+00 Ai079946.1	EST_HUMAN	oz34f05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9337	20408		69'0	1.1E+00	1.1E+00 BE384876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9528	22181	35365	0.53	1.1E+00	1.1E+00 AJ245772.1	ΝŢ	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
9580	22233		1.2		1.1E+00 Y12227.1	۲	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
							Yersinia pseudotuberculosis psaE, psaE, adhesin (psaA), chaperone (psaB), and usher (psaC) genes,
9672		35520	1.14		1.1E+00 L76301.1	NT	complete cds
9732	22383	35585	1.37	1.1E+00	1.1E+00 AB023151.1	L	Homo sapiens mRNA for KIAA0934 protein, partial cds
2883	22488		4.59		1.1E+00 AL161515.2	IN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9898	22548	35742	18.34	1.1E+00	6754021 NT	F	Mus musculus guanine nucleotide binding protein (G protein), gámma 3 subunit (Gng3), mRNA
10398	23044	36260	F.	1.1E+00 P73769	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
	l						au\$1c11.yl Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518292 5 similar to gb:D10522
10504		363/5			AIB78921.1	ES HUMAN	numan minna for out-L protein, complete cas. (notwan);
10547	23243		2.25		1.1E+00 11067364	11067364 NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
							Klebsormidium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding
10606	23300		3.1	1.1E+00	1.1E+00 AF068942.1	NT	mitochondrial protein, partial cds
11023	23695				11439596 NT	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 11 (KCNJ11), mRNA
11026	23698		1.58		1.1E+00 L16877.1	TN	Homo sapiens cytochrome P4502C9 (CYP2C9) gene, 5' flank and exon 1
11042	17901		5.23		8922973 NT	LN	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11048	23718	36988	3.68	1.1E+	00 AF012862.1	LN LN	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
	1						
11048	23718	36989	3.68	1.1€+	00 AF012862.1	LΝ	Petroselinum crispum cytosolic glucose-8-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11328	24019	37323	4.58	1.1E+	-00 Ai809699.1	EST_HUMAN	wf76e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23615483'
11561	24160	37470	1.63		1.1E+00 D89501.1	ΝΤ	Human PBI gene, complete cds
11561	24160	37471	1.63		1.1E+00 D89501.1	N	Human PBI gene, complete cds
12153	24639		3.66		1.1E+00 P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12250	24697	31078	1.93		1.1E+00 AF216696.1	LN.	Taenia solium immunogenic protein Ts76 mRNA, partial ods
12378	25225		2.09		1.1E+00 AF234169.1	N	Dictyostelium discoideum isopentenyl pyrophosphate isomerase (Dipl) mRNA, complete cds
12388	25200		1.44	1.1E+00	8393196 NT	占	Rattus norvegicus C-reactive protein, member of the pentraxin family (Crp), mRNA
97	12923		2.46		1.0E+00 U23808.1	\L	Xenopus laevis rhodopsin gene, complete cds
111	12932	25569			1.0E+00 D88425.1	N	Cavia cobaya mRNA for serine/threoine kinase, complete cds
409	13194		2.25		1.0E+00 AB021684.1	TN	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
299	13344	25971	1.2	1.0E+	1.0E+00 AJ251660.1	NT	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
662	13438	26079	4.38	1.0년	100 AL163218.2	N	Homo sapiens chromosome 21 segment HS21C018

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Oligie Exoli Flobes Expressed III braill	Top Hit Descriptor	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds	V.carteri Algal-CAM mRNA	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete ods		DNA GYRASE SUBUNIT B	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)	HYPOTHETICAL 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME I	af26g08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204 ;contains element MER22 MER22 repatitive element;	Xenopus laevis rhodopsin gene, complete cds	Agaricus bisporus mRNA for tyrosinase	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA	Raftus norvegicus mRNA for N-acety/glucosaminy/transferase III, complete cds	Mus musculus dipeptidy aminopeptidase-like protein 6 (Dpp8) gene, partial cds; and proximal Rump white inversion breakpoint	Hordeum vulgare gene encoding cystelne proteinase	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 6	FIBER PROTEIN	UI-H-BI3-alx-d-09-0-UI:s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds	Homo saplens cell cycle protein (PA2G4) gene, exons 2 though 5	SRB-11 PROTEIN	V.carteri gene encoding valvoxapsin
אום בעחוו בנחמם	Top Hit Database Source	NT A	V	g IN	SWISSPROT D	Ι.	SWISSPROT 3	SWISSPROT 3	Γ	EST_HUMAN W	Ϋ́		I is		NT R	M TN	H	NT B	NT B	NT A	Г	T_HUMAN	NT N	H	ISSPROT	NT
110	Tap Hit Acession No.	1.0E+00 AF125984.1		1.0E+00 AB006531.1			00 P24008	00 P24008			+00 U23808.1	Γ	1.0E+00 AF223391.1	8922245 NT		00 AF092505.1		1.0E+00 AF248054.1	1.0E+00 AF248054.1			2.1		1		
	Most Similar (Top) Hit BLAST E Value	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00 P48355	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00 D10852.1	1.0E+00	1.0E+00 Z97022.1	1.0E+00 /	1.0E+00	1.0E+00 Z97341.2	1.0E+00 P04501	1.0E+00/	1.0E+00 U75902.1	1.0E+00/	1.0E+00 P46506	1.0E+00
	Expression Signal	0.95	3.03	0.93	1.18	1.18	3.82	3.82	1.17	1.24	1.24	1.04	0.78	0.79	0.93	0.74	3.53	4.97	4.97	1.53	4.7	1.49	1.95	0.91	1.06	1.33
	ORF SEQ ID NO:			27193		27948	28287	28288		28609		29063	29424				30629	31472	31473					32213		32634
	Exon SEQ ID NO:	13439	15567			15206	15645	15645	16733	15957	12923	16422	16795	16983	17680	17698	18008	18551	18551	18654	18804	18810	19166			19596
	Probe SEQ ID NO:	663	1365	1751	2489	2489	2878	2878	2967	3194	3585	3869	4050	4242	4964	4975	5200	5759	69/9	2867	6024	0030	6397	6447	6534	6679

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7038	19730	32788	1.09		1.0E+00 S52770.1	L	insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7378	20058		9.29	1.0E+(00 P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7611	Ľ					TN	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7626					1.0E+00 AA775191.1	EST_HUMAN	ac79b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868791 3'
7861	20556	33681	1.36		1.0E+00 BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5
7861		33682	1.36		7.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5
8041	17680		1.19	1.0E+	D10852.1	LN	Rattus norvegicus mRNA for N-acetylglucosaminytransferase III, complete cds
8248	20942	34079	2.02	1.0E+	1.0E+00 Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
	1						PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA
8248	20942	34080	2.02	1.0E+	00 002207	SWISSPROT	DEHYDROGENASE]
8376	21069		0.85	1.0E+	00 P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
	1 .						UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN
8408	21101	34237	0.5	1.0E+	00 Q9Y5T5	SWISSPROT	PROCESSING PROTEASE UBP-M)
8408	21101	34238	0.5	1.0E+	00 Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8436	26122		2.34	1.0E+00	00 BE147331.1	EST_HUMAN	RC1-HT0229-181099-011-e06 HT0229 Homo sapiens cDNA
8476	21168	34312	88.0	1.0E	U42720.2	L	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and \it Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes. >
8625				1.06	+00 M38427.1	N	Human immunodeficiency virus type 1 (HIV-1), Isolate SF33,
9171	L		2.43	1.0E+	00 BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5
9381	22043	35215				LN	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9381					6753429 NT	NT	Mus musculus chloride channel calcium activated 1 (Cica1), mRNA
9510					1.0E+00 AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'
9516					1.0E+00 ∪44952.1	N _T	Xenopus laevis zona pellucida C glycoprotein precursor (XIZPC) mRNA, complete cds
9516	22169	35352	1.43		1.0E+00 U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds

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[Τ	Γ	Γ	Т	Т	Т	Τ	Τ		Г	Г	T	Т	Т	Т	Т	Т	Г	Ī	Г	Г	Т	Π	Γ	Т	Г	Т	T	Г	Т	
Jingia Exoli Plobas Expressed in Diam	Top Hit Descriptor	Human Coronavirus gene for membrane protein	Human Coronavírus gene for membrane protein	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA	oy/5d07.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665901 3'	AV758825 BM Homo sapiens cDNA clone BMFAWC04 5'	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:428906 5'	Human retinoblastoma susceptibility gene exons 1-27, complete cds	PBR1=proline-rich protein {intron 3} [human, Genomic, 898 nt]	263b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Alt repatitive element contains element of the contains all repatitive element.	Picea glauca EMB13 mRNA	Hordeum vulgare gene encoding cysteine proteinase	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 8 (NADH DEHYDROGENASE 1, CHAIN 9) (NDH-1, CHAIN 8)	Human adenovirus type 5, complete genome	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)	EST388293 MAGE resequences, MAGN Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C102	Apple mosaic virus RNA 2 putative polymerase gene, complete cds	SERINE/THREONINE PROTEIN KINASE MINIBRAIN	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II	Lycopersicon esculentum putative Mi1 copy 1 nematode-resistance gene	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8	B.aphidicola 16S rDNA (host T.suberi)	B.aphidloola 16S rDNA (host T.suberi)	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLCLUTAMATE SYNTHASE) (AGS) (NAGS)	Callithrix Jacchus UBE1 gene derived retroposon on the Y chromosome	Xenopus laevis rac GTPase mRNA, complete cds	PROBABLE ENDONUCLEASE IV (ENDODEOXYRIBONUCLEASE IV)	Enterobacterlaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
שופו באטוו הינט	Top Hit Database Source	N	IN	N	N.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	LΝ	FOT HIMAN	L	N	SWISSPROT	ΙΝ	SWISSPROT	EST_HUMAN	ΙZ	N	SWISSPROT	SWISSPROT	N	SWISSPROT	N	۲	ΙN	SWISSPROT	٦N	ΙΝ	SWISSPROT	FX
5	Top Hit Acessian Na.	+00 X15498.1	+00 X15498.1	5174562 NT	5174562 NT	+00 AI077920.1	+00 AV758825.1	+00 AA004982.1	+00 AA004982.1	+00 L11910.1	+00 S90825.1	+00 AA701494 1	+00 L47613.1	+00 297022.1	-00 060019	9626187 NT	+00 P15306	+00 AW976184.1	9.9E-01 AL163302.2	-01 AF174585.1	P49657	-01 വ9ങ്32	J65687.1	-01 0,28642	9.9E-01 AJ005029.1	111972.1	-01 Y11972.1	-01 P22567	-01 AJ003108.1	-01 AF174644.1	-01 067551	9.8E-01 AJ302158,1
	Most Similar (Top) Hit BLAST E Value	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.05+00	1.0E+00	1.0瓦+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	9.9E-01	9.9E-01	9.9E-01 P49657	9.9E-01	9.9E-01 U65667.1	9.9E-01	9.9E-01	9.9E-01	9.9E-01	9.8E-01	9.8E-01 /	9.8E-01 /	9.8E-01	9.8E-01
	Expression Signal	0.49	0.49	0.71	0.71	0.81	4.36	16.16	16.16	1.1	4.57	1.49	1.50	1.55	12.29	1.38	3.01	2:32	1.19	0.97	10.09	0.93	1.37	2,18	2.37	2.3	2.3	1.14	1.21	1.01	0.92	4.67
	ORF SEQ ID NO:	35609	35610					36237	36238	36270	36823	09898		30629	37763	37794			28097		31253	31498			36547	37508	37509	25926			29171	32852
	Exon SEQ ID NO:	22404	22404	22660	22860	22752	22873	23021	23021	23053	23573	23897	24122	18008	24422	24452	24568	24772	15353	16345	18344	18570	21830	22005	23308	24191	24191	13294	15020	15509	16533	19788
	Probe SEQ ID NO:	9763	9753	10012	10012	10104	10225	10375	10375	10407	10893	11025	11522	11744	11838	11868	12049	12370	2643	3591	5547	5779	9160	9455	10614	11592	11592	510	2295	- 2804	3781	7099

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Probe SEQ ID NO: 7089 7545	Exon SEQ ID NO: 19788 20215 20215	S C	Expression Signal 4.67 1.15	Mosl (Tc BL,	Similar Top Hit Acessian AST E No. eilue 8.8E-01 AJ302168.1 9.8E-01 BF034018.1 9.8E-01 BF034018.1	Top Hit Database Source NT EST_HUMAN EST_HUMAN	Top Hit Database Source Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983 EST_HUMAN 601456337F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3860049 5' EST_HUMAN 601456337F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3860049 5'
8619 10336 10916						SWISSPROT EST_HUMAN EST_HUMAN	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM) od55d04.s1 NCi_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3' 601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
10916	<u> </u>	36843	2.29		9.8E-01 BE268705.1 9.8E-01 Al680876.1	EST HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5' byd2c10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2272242 3' Homo sapiens XZ8 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a, C22+/Calmoulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM) adrended incolouin-dependent protein sinase I (CAMKI), are not a contained in the
7058	1_1		2 7				Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial ods Trifficium sestional strice mist resistance protein Y410 (Y410) sens complete ods
8407 11123 4425	21100	34236	1.08 1.3 3.64			NT EST_HUMAN FST_HUMAN	Inform assivant superustressance protein from (Triny) gare, connected as Salmonella typhimutim adenine-methyltransferase (mod) and restriction endonuclease (res) UH-HSH acid-e-07-0-UI st NCI_CGAP_SubB Homo sapiens cDNA clone IMAGE:3085140 3' PM2-UN0053-240300-005-ft 2 UM0636 Homo sapiens cDNA
5667 5667 5667 6648	1111						Parvovirus B19 DNA, patient C, genome position 2448-2994 Parvovirus B19 DNA, patient C, genome position 2448-2994 Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 6
8291 8750 11503	20985 21442 24104 24104	34589 37416 37417	2.33 0.59 3.47			NT NT EST HUMAN EST HUMAN	P. faic parum complete gene map of plastid-like DNA (IR-A) Rattus norvegicus (strain R21) Rps2r gene, complete cds AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5' AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11952					722	L L	Homo sapiens centrosomal protein 2 (CEP2), mRNA Sphyma tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partal ods
2480 2673 3762	15198 15382 16514	27938 28122 29150	1.05 0.97 2.04	9.56	7705591	NT SWISSPROT EST HUMAN	Homo sapiens CGI-125 protein (LOC51003), mRNA ENDOGLUCANASE I PRECURSOR (EGI) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE I) 601675639F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3958473 5
3762 8899 9003						EST_HUMAN EST_HUMAN EST_HUMAN	601975639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5' qd57d07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3' RC1-CT0295-241189-011-b02 CT0295 Homo sapiens cDNA

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		_	_	-		_		_		_	_	_	_	_	-	_	_	_													
Single Exon Probes Expressed in Brain	Top Hit Descriptor	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'	UI-H-BI2-ahp-f-03-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'	ya53d04.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:666313'	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds	Human Fc-gamma-receptorIIA (FCGR2A) gene, exon 4	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869929 5'	Homo saplens epidermal growth factor receptor (avian enythrobiastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA	Homo saplens phytanovi-CoA hydroxylase (PHYH) gene, exon 5	RC5-BT0503-271189-011-B01 BT0503 Homo saplens cDNA	Bovine papillomavirus type 2, complete genome	Bovine papillomavirus type 2, complete genome	Homo saplens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete eds	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds	0e09b03.s1 NCI CGAP Ovz Homo sapiens cDNA clone IMAGE:1385357	Xenopus keevis CCCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34	Aedes triseriatus putative large subunit ribosomal protein rpL34 mRNA, complete cds	Homo saplens chromosome Xq28 melanoma antigen family A2a (WAGEA2A), melanoma antigen family A12 (MAGEA2A), melanoma antigen family A12 (MAGEA2A), melanoma antigen family A12	(MALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5/	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Sic30a4), mRNA	601461153F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3864661 5'	N.crassa valyi-IRNA synthelase (cyt-20/un-3) gene	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65	Mus musculus carbonic anhydrase 4 (Car4), mRNA	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA	7058e06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219.3' similar to SW.NU5M_TRYBB P04540 NADH-IIRIQI IINONE OXIDOREDI ICTASE CHAIN F.	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
gle Exon Pro	Top Hit Database Source	EST HUMAN	EST_HUMAN	EST HUMAN	N	TN	NT	EST_HUMAN	ΙN	TN	EST_HUMAN	LN LN	TN	Į.	LZ	EST HUMAN	FN	TN	TN		Z L	EST_HUMAN	EST_HUMAN	FN.	EST_HUMAN	FN	NT	FN	Į.	HST HIMAN	EST_HUMAN
NIN	Top Hit Acession No.	BF218771.1	9.5E-01 AW 293799.1	9.5E-01 T67204.1	9.4E-01 AF165990.1	9.4E-01 AF080595.1	M90724.1	9.4E-01 BE781251.1	11419857 NT	AF242382.1	Σ.	9.3E-01 M20219.1		9.3E-01 AF213884.1		9.3E-01 AA847040.1		9.3E-01 AL161534.2	9.3E-01 AF271207.1		9.3E-01 U82671.2	-	-01 BF129973.1	7108410 NT	E-01 BF037586.1		-01 AL161565.2	TN 221677 NT	11430963 NT		-01 BE563811.1
	Most Similar (Top) Hit BLAST E Value	9.5E-01	9.5E-01	9.5E-01	9.4E-01	9.4E-01	9.4E-01	9.4E-01	9.4E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01	9.3E-01 L36189.1	9.3E-01	9.3E-01	9.3E-01	9.3E-01		9.3E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9.2E-01	9 2E-01	9.2E-01
	Expression Signal	1.68	2.42	1.55	3.33	2.08	0.67	1.92	1.79	1.05	1.38	0.88	0.88	1.56	3.99	1.65	1.04	0.95	3.12		1.48	2.93	0.97	1.15	7.36	0.61	0.92	1.07	3.18	1.9	1.63
	ORF SEQ ID NO:	37159		37718			34606				28095	29388	29389	31204	31298	33785		34673				28648			31631	32306	35399	35496	36031	36178	36473
	SEQ ID NO:	23872	23196	24385	15959	15975	21458	24670	25219	14468	16351	16761	16761	18303	18388	20661	21405	21527	24970		25049	15995	17553	18428	18683	19302	22213	22300	22813	22962	23239
	Probe SEQ ID NO:	11209	11429	11795	3196	3212	8764	12202	12557	1726	2640	4015	4015	5055	5592	7966	8713	8835	12681		12802	3233	4822	5831	5898	6537	9260	9648	10165	10315	10543

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Single Exon Probes Expressed in Brain	Тф Hit Descriptor	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'	ye52/01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element,	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (IT! HEAVY CHAIN H3)	ob71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336882 3'	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds	P80-COILIN	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds	Homo sapiens neurexin III-alpha gene, partial cds	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds	Xenopus laevis gene for aldolase, complete cds	Danio rerio semaphorin Z1a mRNA, complete cds	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene,	Somption of the state of the st	Oithona nana cytochrome-c oxidase subunit I (coxl) gene, pertial cds; mitochondrial gene for mitochondrial product	Xylella fastidiosa, section 90 of 229 of the complete genome	Chlamydophila pneumoniae AR39, section 21 of 94 of the complete genome	qb64d08.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:17048793'	PUTATIVE F420-DEPENDENT NADP REDUCTASE	Pseudorables virus Ea glycoprotein M gene, complete cds	Homo sapiens cell death-inducing DFFA-like effector B (CIDEB), mRNA	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1	Synechocystis sp. PCC8803 complete genome, 13/27, 1578593-1719643	Homo sapiens SOS1 (SOS1) gene, partial cds	Homo sapiens AT-binding trænscription factor 1 (ATBF1), mRNA
Jie Exon Probe	Top Hit Database Source	EST_HUMAN 6			EST_HUMAN A	EST_HUMAN A	Г	SWISSPROT	EST_HUMAN ol	NT R	SWISSPROT P	H	H N	NT	X	NT	F. (2)					Г	SWISSPROT P						
OID.	Top Hit Acession No.	9.2E-01 BF132402.1		8923056 NT	-01 T26418.1	9.1E-01 T26418.1			3.1			9.1E-01 AF050113.1	-01 AF099810.1			-01 AF086761.1		-01 X60986.1	1.		-01 AE002186.2			E-01 AF310617.1	7656978 NT			8.7E-01 AF106953.2	5901893 NT
	Most Similar (Top) Hit BLAST E Value	9.2E-01	9.1E-01	9.1E-01	9.1E-01	9.1E-01	9.1E-01 L36033.1	9.1E-01 Q61704	9.1E-01	9.1E-01 U72995.1	9.1E-01	9.1E-01	9.0E-01	9.0E-01	9.0E-01 D38621.1	9.0E-01	0 7	8.9E-01	8.9E-01	8.9E-01	8.9E-01	8.9E-01	8.8E-01	8.8E-01	8.8E-01	8.8E-01	8.8E-01	8.7E-01 /	8.7E-01
	Expression Signal	1.79	1.88	2.76	1.15	1.15	1.28	3.53	17.62	2.34	0.45	27.98	2.08	0.72	1.18	0.49	6 8	1.38	0.71	2.51	2.86	2.51	3.82	0.67	0.83	4.96	1.8	1.54	1.07
	ORF SEQ ID NO:	37639	27057		28614	28615	31821	32180	33241	33410	35940		29714	33052		35100	ς. α.		34154	37707			29873	30755	35992	36953		25877	27859
	SEQ ID NO:	24316	14368	14851	15983	15963	18854	19181			22723	25294	17085	19974	20004	21928	18406	18931	21018	24377	24627	25343	17240	18094	22779	23690	25382	13238	15122
	Probe SEQ ID NO:	11722	1621	2120	3200	3200	6075	6413	7475	7637	10075	12291	4346	7291	7321	9249	5840	6154	8325	11787	12138	12762	4505	5289	10131	11018	11968	452	2401

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Cyanidium caldarium gene for SigC, complete cds	Cyanidium caldarium gene for SigC, complete cds	Homo sapiens human immunodeficiency virus type I enhancer-binding protein 1 (HIVEP1), mRNA	Fowl adenovirus 8, complete genome	Human fibroblast growth factor receptor 3 (FGFR3) gene, Intron 7	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7	Mamestra brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds	Pyrococcus abyssi complete genome; segment 5/8	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds	Streptomyces antibioticus polyketide biosynthetic gene cluster	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40	nn01112.y5 NOL_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR	repetitive element ;	Drosophila melanogaster Lis1 homolog mRNA, complete cds	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome	Phytophthora infestans mitochondrion, complete genome	Homo sapiens FRA38 common fracile racion, diademasha trinhasahata hvirolasa (FHIT) nene, evan 5	Rattus noveglous mRNA for RPHO-1, complete cds	Mus musculus trophinin (Trin) gene, complete cds	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA	Amanita muscaria mRNA for SCIII25 protein	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA	S.cerewisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isoproplymalate (alpha-IPM)	synthetase (partial), and DNA polymerase alpha (partial)	601144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'	Homo sapiens mRNA for KIAA0630 protein, partial cds	Homo sapiens thioredoxin-related protein mRNA, complete cds	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
le Exon Prope	Top Hit Database Source	NT C	D ⊢N			H H	T E		.d LN				NT N		Г	EST_HUMAN re		NT	M LN				M	EST_HUMAN IIL	Г	EST_HUMAN C			T_HUMAN	I I			NT
Suis	Top Hit Acession No.	-01 AB006799.1	-01 AB006799.1	11418543 NT	-01 AF083975.2		E-01 L78726.1		-01 AJ248287.1		-01 AL161506.2		01 Y19177.1	-01 AL161540.2				-01 AF108133.1	-01 AE000903 1	2472	-01 AF020503.1	Γ	8.2E-01 AF145589.1	Г					8.2E-01 BE263145.1				01 AF223888.1
	Most Similar (Top) Hit BLAST E Value	8.5E-01	8.5E-01	8.5E-01	8.4E-01	8.4E-01	8.4E-01	8.4E-01	8.4E-01	8.3E-01	8.3E-01	8.3E-01	8.3E-01	8.3E-01	!	8.3E-01 /	8.3E-01	8.3E-01	8.3E-01	8.3E-01	8.3E-01	8.2E-01/	8.2E-01	8.2E-01	8.2E-01	8.2E-01		8.2E-01	8.2E-01	8.2E-01/	8.2E-01 /	8.2E-01	8.2E-01/
	Expression Signal	1.17	1.17	2.24	0.73	2.28	2.28	0.63	2.68	2.8	2.99	0.79	3.35	2.41		4.51	1.27	3.46	3.35	2.03	2	2.3	1.31	1.06	0.75	3.49		4.74	0.59	0.65	1.37	0.59	0.59
	ORF SEQ ID NO:	38105	36106		30067	30910	30911	33485		26151	28497	29177	29375	30511			35872	35978	36505		37227	27506			32631	32569		32926	34173	35770	35812	35985	35986
	Exon SEQ ID NO:	Li		25296				1			15856	16542	16741	17995				22766	23267		23935	14778	14815			19541		- 1	21036	•	- 1	22771	
	Probe SEQ ID NO:	10248	10248	12278	4702	5406	5406	7708	9858	724	3091	3790	3993	5187		9568	10010	10118	10572	10590	11274	2045	2083	2686	9299	6797		7169	8343	9924	6966	10123	10123

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					S	איני ווייעיין סופ	סיוקים באסון וסינים באטונים באינים
Probe SEQ ID NO:	Exon SEQ (D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10283						SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10283	22931		3.65			SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11641						LN	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
11735	24328				8.2E-01 P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11740	24333	37659			H87398.1	EST_HUMAN	yw14d02.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo seplens cDNA clone IMAGE:252195 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
12298		L			8,2E-01 AJ001261.1	N	Mus musculus mRNA for NIPSNAP2 protein
2762			1.08			F	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3451	16207		3.08			LZ L	Homo sapiens MHC class 1 region
3451	16207	28858	3.08			NT	Homo saplens MHC class 1 region
4863			0.74		8.1E-01 AF202634.1	NT	Drosophila melanogaster Na/K-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6223					U16790.1	L	Mus musculus putative collagen alpha-2 (凶) chain (COL11A2) gene, partial cds
6526					Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
6526	l	_		L		SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7229	19914	32987			77.1	TA	Homo saplens KIAA0417 mRNA, complete cds
7412		[_		L	8.1E-01 047477	SWISSPROT	CYTOCHROME B
							Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium
							channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-
7811	20506	33628	0.75		8.1E-01 AF022713.2	NT	enriched protein (gprs) gene, partial cd>
							Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium
						<u>!</u>	channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds, and putative serine-
133	Ţ	_	0.75	1	AF022713.2	Z	enraned protein (gpts) gene, partial cd>
8507				- [AP001517.1	L _Z	Bacillus halodurans genomic DNA, section 11/14
8507	21199	34345	0.93		8.1E-01 AP001517.1	NT	Bacilius halodurans genomic DNA, section 11/14
							xn01h03.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2892489 3' similar to SW:LYAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN ;contains MER22.b1 PTR5.rspetitive
8998			1.08			EST_HUMAN	element;
10025	22673		0.7	8.1E-01	8.1E-01 P06425	SWISSPROT	PROBABLE E4 PROTEIN
							KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' sImilar to
10311					8.1E-01 N84541.1	EST_HUMAN	EST(CLONE C-0PE11)
11464	24067	37374				EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11464						EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
12022		31110			AE001711.1	۲	Thermotoga maritima section 23 of 136 of the complete genome
172	12985		3.49	Ц	8.0E-01 AJ271510.1	Z	Staphylococcus aureus partial pta gene for phosphate actyltransferase allele 15

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Bos taurus futb and rtif genes	Rattus norvegicus protease (prosome, macropain) 28 subunit, alpha (Psme1), mRNA	602072473F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215091 5'	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds	Mus musculus gene for oviductal glycoprotein, complete cds	Nelsseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit	RC0-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA	Rice stripe virus RNA 3	OREB-BINDING PROTEIN	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds	Ureaplasma urealyticum section 31 of 59 of the complete genome	Homo saplens mRNA for KJAA1452 protein, partial cds	Haemophilus influenzae Rd section 54 of 163 of the complete genome	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'	Mus musculus embigin (Emb), mRNA	Mus musculus embigin (Emb), mRNA	Human mRNA for prostacyclin synthase, complete cds	P.sativum GR gene	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds		AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'	Streptococcus mutans DNA for sigma 42 protein, dTDP 4-keto-L-rhamnose reductase, complete cds	DYNEIN HEAVY CHAIN (DYHC)	Homo sapiens KIAA1072 protein (KIAA1072), mRNA					Sphenodon punctatus alpha enolase mRNA, partial cds
gie Exon Pro	Top Hit Database Source	N F2	NT	EST_HUMAN	NT	TN	TN	TN	EST_HUMAN	ħ	SWISSPROT	뇐	N	N	L L	TN	TN	N	EST_HUMAN	TN	. LN	NT	NT	LΝ	SWISSPROT	EST_HUMAN	F	SWISSPROT	N	SWISSPROT	EST_HUMAN	EST_HUMAN	FZ	본
uio	Top Hit Acession No.	8.0E-01 AJ132772.1	8394087 NT	8.0E-01 BF530962.1	8.0E-01 AF127897.1	8.0E-01 AB006193.1	8.0E-01 AL162758.2	8.0E-01 X83739.2	8.0E-01 AW901489.1	Y11095.1	292793	7.9E-01 D11476.1	7.9E-01 AE002130.1	AB040885.1	7.9E-01 U32739.1	7.9E-01 AB004816.1	7.9E-01 AF130459.1	AF228664.1	7.9E-01 BE263612.1	6753745 NT	6753745 NT	7.9E-01 D38145.1	7.9E-01 X90996.1	7.9E-01 U01912.1	P19719	7.9E-01 AV700860.1	7.9E-01 AB000631.1	P15305	7662471	719022	7.8E-01 Z43785.1	AW959567.1	7.8E-01 U87305.1	7.8E-01 AF115856.1
	Most Similar (Top) Hit BLAST E Value	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01	8.0E-01 Y11095.1	8.0E-01 Q92793	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01	7.9E-01 P19719	7.9E-01	7.9E-01	7.9E-01 P15305	7.9E-01	7.9E-01 P19022	7.8E-01	7:8E-01	7.8E-01	7.8E-01
	Expression Signal	13.81	1.12	1.91	1.2	1.35	1.52	6.05	, 2.25	0.98	2.78	1.16	1.14	22.69	1.2	5.66	2.4	3.01	0.85	1.13	1.13	0.67	2.79	4.04	4.47	0.91	1.94	0.52	2.74	2.02	2.24	7.47	0.73	2.28
	ORF SEQ ID NO:	25730	27031		28484	28716		29862		34254	36803	25870				27726	27727	28916		29935	29936	32000	33831	35304	35801	35849	36271	36389		37123		27737	30020	31724
	SEQ ID	13089	14341	14764	15841	16067	16443	17232	20584	21118	23556	13227	13473	14346	14398	14986	14987	16262	17008	17307	17307	19026	20703	22124	22597	22639	23054	23162	23609	23840	13625	14999	17387	18760
	Probe SEQ ID NO:	282	1595	2029	3075	3307	3690	4496	7889	8423	10876	441	869	1600	1652	2259	2260	3506	4268	4572	4572	6252	8008	9447	9949	9991	10408	10516	10929	.11173	928	2273	4653	5978

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Table 4
Single Exon Probes Expressed in Brain

Top Hit Descriptor	INTERLEUKIN & PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)	Thermoplasma acidophilum complete genome; segment 4/5	7154d05 x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'	D.dlscoideum racGAP gene	Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (!Aalpha) and major histocompatibility protein class II beta chain (!Ebeta) genes, complete cds;	butyrophilin-like (NG9), butyrophilin-li>	CITRATE SYNTHASE	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyftransferase 7 (GalNAc-T7) (GALNAC-T7), mRNA	Homo sapiens PRO1975 mRNA, complete cds	Cofurnix cotumix Japonica sub-species Japonica beta-actin mRNA, partial cds	Colurnix colurnix Japonica sub-species Japonica beta-actin mRNA, partial cds	RAFFINOSE INVERTASE (INVERTASE)	RAFFINOSE INVERTASE (INVERTASE)	yf24b02.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:1277553'	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds	Archaeoglobus fulgidus, complete genome	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete	cds	Arabidopsis thallana 3-methycrotonyl-CoA carboxylase non-blottnylated subunit (MCCB) mRNA, complete	COS	MATING-TYPE PROTEIN A-ALPHA 24	aq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879	aq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
Top Hit Database Source	SWISSPROT	L	EST HUMAN	Z	Ę	ISSPROT	NT	ΝT		Ā	SWISSPROT	LΝ	L	Z	Ę	SWISSPROT	SWISSPROT	EST_HUMAN	LN	LΝ		LN		٦			T_HUMAN	
Top Hit Acession No.	.8E-01 P05231	.8E-01 AL445066,1	.8E-01 BF108927.1	.8E-01 Y10159.1	4826873 NT	.8E-01 Q25452	8E-01 L29260.1	7E-01 AF184345.1		.7E-01 AF050157.1	7E-01 033915	839340B NT	.7E-01 AF118085.1	7E-01 AF199488.1	7E-01 AF199488.1	7E-01 P16553	7E-01 P16553	7E-01 R08600.1	7E-01 AB021134.1	11497621 NT		6E-01 AF059510.1	. 0.2000	GE-U1 AFUSSS1U.1	6E-01 P37938	.6E-01]AI253399.1	.6E-01 AI253399.1	6E-01 U72487.1
Most Similar (Top) Hit BLAST E Value	7.8E-01	7.8E-01	7.8E-01	7.8E-01	7.8E-01	7.8E-01	7.8E-01	7.7E-01		7.7E-01	7.7E-01	7.7E-01	7.75-01	7.7E-01	7.7E-01	7.7E-01	7.7E-01	7.7E-01	7.7E-01	7.7E-01		7.6E-01			7.6E-01	7.6E-01	7.6E-01	7.6E-01
Expression Signal	0.88	0.63	1.02	1.3	0.51	0.97	2.5	7.61		2.26	2.21	0.84	3.98	3.38	3.38	1.45	1.45	0.85	0.51	4.55		4.88		4,88	0.81	0.94	0.94	0.88
ORF SEQ ID NO:	31871	32136		34987	35083			25596			28163		28985	29738	29739	31165	31166	31594	35600			31751		-	32189	30555		32449
SEQ ID NO:	18902	19140	21082	21821	21910	22672	25275	12954		13483	15424	16111	16340	17103	17103	18272	18272	18653	22395	24844		18789	00107	- {	- 1		17920	19433
Probe SEQ ID NO:	6124	6371	8389	9133	9231	10024	12271	139		709	2717	3351	3586	4365	4365	5473	5473	5866	9744	12161		8009	000	8008	6425	6751	6751	6951

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Single Exon Propes Expressed in Brain	Top Hit Descriptor	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (PR27) gene, complete cds; and HSAR (HSar) gene, complete cds	Mus musculus advillin (Advil-pending), mRNA	Mus musculus advillin (Advil-pending), mRNA	Mus musculus cytochrome P450, 2b9, phenobarbitol inducible, type a (Cyp2b9), mRNA	MUSCARINIC ACETYLCHOLINE RECEPTOR M2	MUSCARINIC ACETYLCHOLINE RECEPTOR M2	H.aspersa mRNA for neurofilament NF70	H.aspersa mRNA for neurofilament NF70	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88	Homo saplens mRNA for KIAA0895 protein, partial cds	Homo sapiens chromosome 21 segment HS21C101	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11 5'	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds	Homo sapiens GCMa/GCM1 gene for chorion-specific transcription factor GCMa, complete cds	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome	th14b09.x1 NCI_CGAP_Brn25 Homo saplens cDNA clone IMAGE:2167577 3' similar to contains Alu	repentive element; contains element MIK repentive element;	TO SEPTICATE THE TOTAL OF THE PRICE OF THE P	nomo sapiens chromosome z1 segment noz11046	Arabidopsis tnaliana UNA chromosome 4, contig fragment No. 51	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51	602018456F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154340 5'	Raftus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated	u	601573028F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3834174 5'	zp67h01.s1 Strategene endothellal cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPQ_MOUSE P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT;	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
ie Exon Propes	Top Hit Database Source	TN (O)				SWISSPROT MI	SWISSPROT	Г				NT Ho	NT H	EST_HUMAN C1			보	NT Ge		EG HUMAN TEN					EST_HUMAN 60			EST_HUMAN 60	T_HUMAN	
Buis	Top Hit Acession No.	01 AF146793.2	6857752 NT	6857752 NT	6753577 NT	01 P30372		01 X86347.1	01 X86347.1	01 AL161592.2	Γ	-01 AL163301.2			7.5E-01 AF052730.1			01 AE000823.1		7.4E-01 Alb88146.1	T	T	7.4E-01 AL161551.2		7.4E-01 BF346266.1			7.4E-01 BE747503.1		-01 11424933 NT
	Most Similar (Top) Hit BLAST E Value	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.6E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01	7.5E-01	i i	7.45-01/	7 16 91	10-11	7.45-01	7.4E-01	7.4E-01		7.4E-01	7.4E-01	7.4E-01	7.4E-01
	Expression Signal	1.38	1.88	1.88	0.74	5.03	5.03	2.68	2.68	3.64	3.73	1.44	1.23	0.95	1.01	1.5	4.8	1.46		8)	35.	5.5	1.23	1.23	0.83		0.76	6.95	1,14	0.76
	ORF SEQ ID NO:	33784	33852	33853	34703	35015	35016	37325	37326				25979	28769	33186	37130		30975	00000	77607	20042	74067	33362	33563	34365			34834	34901	36164
	Exon SEQ ID NO:	20659	20721	20721	21557	21849	21849	24021	24021	24306	24489	13284	13351	16114	20098	23844	24682	25008	10001	15085	1	1	2043	20439	21223		21305	21684	21743	22949
	Probe SEQ ID NO:	7964	8026	8026	8866	9179	9179	11330	11330	11711	11931	200	929	3354	7421	11177	.12228	12742	,,,,,,	3,73	4777	2/2	1/43	7743	8531		8613	8994	9054	10302

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					T		1	T			T		T				T	T	T		T		T	T	T.	HdN)	T	T	T	T	T	3923
Chigo Lyon Tobos Lypressed III Digiti	Top Hit Descriptor	Oryzias latipes gene for membrane quanyly cyclase OIGC1 complete cds	Oryzlas latibes gene for membrane guandyd cyclase OIGC1 complate cals	Mus musculus complement component 1 Inhibitor (Caph) mPNA	tat3h01.x1 NCI CGAP Lvm5 Homo saniens CDNA clane IMAGE:-2443056 2	HYPOTHETICAL PROTEIN HKLF1 (IRL1) (TRI 1)	Borrella burgdorferi (section 52 of 70) of the complete genome	Homo sapiens HT017 mRNA, complete cds	FERRICHROME SIDEROPHORE PEPTIDE SYNTHETASE	Mus musculus antigen (CD72) gene	Mus musculus antigen (CD72) gene	Lycopersicon esculentum mRNA for ublauritin activation enzyme	Dimelanogaster ChomRNA for clathrin heavy chain	Valdinolyticus sucresa (scrR) dana complete cds	V. aldinolyticus sucrese (scrB) dene, complete cele	225508.81 Scares fetal liver solven 1NFI S. St Homo capiene cDNA class 1440 E-144705 21	225b08.s1 Soares fetal liver spleen 1NFI S. St Homo capiens CDNA clone IMACE:451799 5	Rettus narvedicus initiation factor. 2 kinase (AF-2a) mBNA complete out.	N. tabacum NelF-4A13 mRNA	Gallus gallus gene for melanocortin 2-recentor complete ode	Fowlbox virus, complete denome	Gardia intertinale variant enactific europea anatois (um 147 0)	Human mRNA for KIAA0309 dene hartial cds	Homo sapiens IA-2 gene, intron 18	L.mesenteroldes gene for sucrose phosphorylase (EC 2.4.1.7)	NUCLEOSIDE TRIPHOSPHATASE I (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE I) (NPH	Solanum tuberosum cold-stress inducible protein (C17) gene complete ade	Oryctolagus cuntculus RING-finger binding protein mRNA partial cde	AV743773 CB Homo saplens cDNA clone CBMAFD06 5'	602118381F1 NIH MGC 56 Homo sapiens cDNA clone IMAGE 4275381 5'	Rattus norvegicus cytocentrin mRNA, complete cds	Dbs=Dbl guanine nucleotide exchange factor homotog [mice, 32D murine hemopoietic cell line, mRNA, 3923 nt]
21 1 104 216	Top Hit Database Source	Į.	IN	Z	EST HUMAN	SWISSPROT	NT	LN LN	SWISSPROT	LN LN	Z	N	Į.	LZ	Į.	EST HUMAN		Z	E	N	Į		LN	Į.	LN	SWISSPROT	NT	LN	EST HUMAN	EST_HUMAN	NT	NT
	Top Hit Acession No.	-01 AB021490.2	7.4E-01 AB021490.2	6753217 INT	7.4E-01 Al472841.1	P09710	7.3E-01 AE001166.1	7.3E-01 AF225421.1	043103	7.3E-01 L35772.1			Γ			-				-			-01 AB002307.1	Γ	E-01 D90314.1		-	Ξ		-01 BF670061.1	-01 U82623.1	-01 S76838.1
	Most Similar (Top) Hit BLAST E Velue	7.4E-01	7.4E-01	7.4E-01	7.4E-01	7.3E-01 P09710	7.3E-01	7.3E-01	7.3E-01 043103	7.3E-01	7.3E-01	7.3E-01	7.3E-01	7.3E-01	7.3E-01	7.3E-01	7.3E-01	7.2E-01 L29281.1	7.2E-01	7.2E-01	7.2E-01	7.2E-01	7.2E-01	7.2E-01 /	7.2E-01	7.2E-01 F	7.2E-01	7.2E-01 /	7.2E-01	7.2E-01	7.2E-01	7.2E-01
	Expression Signal	1.65	1.85	3.62	1.78	0.8	0.7	4.37	1.01	5.92	5.92	19.0	99'0	7.84	7.84	3.83	3.83	3.89	2.32	1.27	1.38	2.58	1.06	0.7	2.65	0.74	0.88	1.11	0.48	2.33	4.02	1.27
	요 0	37582	37583						30373	32276	32277	32735	33118	33210	33211	37361	37362	-	27398	27920	28473	28851	28994		30083	30410	32864	34183		36100	36568	37049
	- v		24260	24467		15765	17310	17386	17759	19278	19276	25103	20040	20121	20121	24058	24056	13583	14685	15181	15829	16201	16354	16785	17450	17794	19800	21046	21553	22887	23330	23774
	Probe SEQ ID NO:	11665	11665	11900	12008	2999	4575	4652	5040	6511	6511	6994	7359	7445	7445	11407	11407	812	1930	2463	3063	3445	3601	4040	4718	5075	7112	8353	8862	10239	10839	11104

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Table 4
Single Exon Probes Expressed in Brain

ſ		Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	T-	T	Т	Т	Т	T-		Т	7	_	_	Г	T= 7
	Top Hit Descriptor	Aeropyrum pernix genomic DNA, section 6/7	Rana catesbetana mRNA for builfrog skeletal muscle calcium release channel (ryanodine receptor) alpha soform(RNR1), complete cds	Homo sapiens partial TCF-4 dene for T-cell transcription factor-4 exons 15-16	Mus musculus otogelin (Otog), mRNA	Mus musculus otogelin (Otog), mRNA	602155438F1 NIH_MGC_83 Homo saplens cDNA clone IMAGE:4296344 5	602155438F1 NIH MGC 83 Homo sapiens cDNA clone IMAGE:4296344 5'	Drosophila melanogaster 6-pyruvoyltetrahydropterin synthase (pr) gene, complete cds	yq89d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202961 3'	RC1-BT0567-301299-011-d09 BT0567 Homo saplens cDNA	RC1-BT0567-301299-011-d09 BT0567 Homo sapiens cDNA	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5	Human T-cell receptor germline gamma-chain J2 gene	2006h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3/	Homo sapiens mRNA for KIAA0614 protein, partial cds	Homo saplens mRNA for KIAA0614 protein, partial cds	yz73e07.s1 Soares multiple_solerosis_2NbHMSP Homo sepiens cDNA clone IMAGE:288708 3' simifar to contains Alu repetitive element;	yz/3e07.31 Soares_multiple_sclerosis_ZNbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to	Management Attangement of comment US24C404	Arabidoosis thaliana mRNA for chlorophyll b synthase complete cds	Escherichia coli K-12 MG1855 section 143 of 400 of the complete genome	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF,	and milD genes, complete ods	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF,	and multiply genes, complete cas	trailo reno complement actor o miny, complete cos	AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5'	AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5'	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
	Top Hit Database Source	F	·	Z	F	E	EST_HUMAN	EST_HUMAN	Z L	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	님	EST_HUMAN	L	FZ	EST_HUMAN	TOT LIBRARY	NEWOL PI	LN	LN		۲	Ŀ	- 1	- 2	EST HUMAN	EST HUMAN	NT
	Top Hit Acesslon No.	-01 AP000063.1		-	05360	7305360 NT	7.1E-01 BF681034.1	7.1E-01 BF681034.1		7.1E-01 H54244.1			-	7.1E-01 M12961.1	7.1E-01 AA421492.1		7.0E-01 AB014514.1	7.0E-01 N62412.1	7 0E-04 NE2412 4	2				-01 U53868.1	7 05.04	Ī	Ī		-01 AV763842.1	6.9E-01 U69674.1
	Most Similar (Top) Hit BLAST E Value	7.2E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.1E-01	7.0E-01	7.0E-01	7.0E-01	7.05.04	7.0F-01	7.0E-01	7.0E-01		7.0E-01	7 00	7.05.01	1.00-01	7.0E-01	7.0E-01	6.9E-01
	Expression Signal	2.9	12.73	11.76	3.18	3.18	1.63	1.63	7.68	0.56	0.93	0.93	1.43	1.22	2.21	0.99	0.99	1.13	4	1 78	1.11	11.76		0.57	7 57	0.00	2	1.94	1.94	11.02
	ORF SEQ ID NO:		76097	28470		29556			32580	33916	34469	34470		36172		26624	26625	27907	27908	-				35064	24085	38400	20050	3,000	37007	26380
	SEQ ID NO:	24798	13451	15825	16925			18645	19550						25205	13958	13958	15169	15169	17719	18649	20970		21895	21805	23472	200	63/34	23734	13715
	Probe SEQ ID NO:	12422	676	3059	4184	4184	5858	5858	. 6850	8091	8635	8635	9755	10309	12211	1207	1207	2450	2450	4996	5862	8276		9216	9216	10528	74067	001	11064	949

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
949	13715	26381	11.02	6.9E-01	6.9E-01 U69674.1	Ę	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial ods
1287	14037	26708	2.74	6.9E-01	6.9E-01 AA593530.1	EST_HUMAN	nn28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3213		28627	1.97	6.95-01	11 AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5694	18488			6.9E-01	11 AB035662.1	NT	Branchlostoma belcheri BbNA3 mRNA for notochord actin, complete cds
5900	18685		0.82		1 Y18278.1	N	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAR550, partial
6277	19050	32027	1.36		1 BE296188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IWAGE:3532328 5'
7697	20360	33474	0.65	6.9E-0	1 AF248863.1	TN	Strongylocentrotus purpuratus myosin V, complete cds
7879	20574	33700	2.96	6.9E-0	11 AL161573.2	INT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7879	20574	33701	2.96	6.9E-0	1 AL161573.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
6906	21758		0.79	6.9E-0	1 AF118046.1	TN	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9594	22247	35431	0.59	6.9E-01	1 AF206319.1	TN	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9594	22247	35432	0.59	6.9E-01	1 AF206319.1	LZ LZ	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
. 11223	23886	37172	2.38	6.9E-01	1 D89013.1	IN	Homo saplens DAN gene, complete cds
11223	23886	37173	2.38	6.9E-01	6.9E-01 D89013.1	FN	Homo sapiens DAN gene, complete cds
11878	25197		3.04	6.95-01	6.9E-01	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MEH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14)
937	13704	26369	1.05	6.8E-01	6.8E-01 AF017784.1	Į.	Giardia intestinalis carbamate kinase gene, complete cds
2680	15389		66.0	6.8E-01	6.8E-01 D90917.1	F	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2832	14356	27045	1 40	A BE	8 BE.04 0 8 8 5 4 7 5 4	HOU HOU	aj75a05,s1 Soares_parathyrold_tumor_NbHPA Home saplens oDNA clone INAGE:1402256 3' similar to
4533	17268	28904	1 45	8 8E-01	8 8E-01 100782 1	Т	Raffhooded) protecting game - even iii and flanks
9538	22191	35375	1.45	6.8E-01	6.8E-01/AB037766.1	LX	Homo saplens mRNA for KIAA1345 protein, partial cds
11027	23699	36962	1.92	6.8E-01	6.8E-01 AJ276675.1		Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11027	23699	36963	1.92	6.8E-01	6.8E-01 AJ276675.1	Į.	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11058	23728	37000	2.4	6.8E-01	6.8E-01 AF038939.1	N T	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11058	23728	37001	2.4	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11607	24205	37527	1.36	6.8E-01	6.8E-01 AF110520.1	IN	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11607	24205	37528	1 36	8 78 70	8 8E.01 AE110520 1	Ę	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosy transferase, and RPS,8 mans. Complete cites. Serm21 ages to a protein and protein and protein and protein and protein and protein protein and p
	2		200	225	10050		ייני כו כ שנייטין לסיוור ו שמונין אמונים .

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					Uio.	gie Exon Proi	Single Exon Probes Expressed in Brain
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
291	13097	25739	44.11	6.7E-01	AF213884.1	۲Z	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
330	13131	25766	21.34	6.7E-01	01 AF213884.1	· FZ	Homo saplens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2143	14873	27606	1.73		6.7E-01 AA451864.1	EST_HUMAN	2x12g12.s1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2163	15587	27628	2.51	6.7E-01	01 AF186073.1	Ę	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced.
2994	15760	28408	3.41	6.7E-01	FN 0858280	Ę	Mus musculus Wiskott-Aldrich syndrome protein (Wasp.) mRNA
4419				6.7E-01	21 X74421.1	Ę	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
5422		30932	0.94	6.7E-4	11 J04836.1	E	M barkeri AT Pase alpha and beta subunit (atpA and atpB) genes, complete cds
5422		30933	0.94	6.7E-(11 J04836.1	FN	M.barkerl ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6231	ı		1.18		9635035 NT	۲	Gallid herpesvirus 2, complete genome
6231	. 1	31982	1.18		LN 9635035 NJ	본	Gallid herpesvirus 2, complete genome
7215	١		4.34	6.7E-(01 AE004606.1	ΙN	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7240		33000	0.92	6.7E-(01 AE001486.1	ΙN	Hellcobacter pylori, strain J99 section 47 of 132 of the complete genome
10044			0.68	6.7E-(6.7E-01 M34046.1	LN LN	Human placental protein 14 (PP14) gene, complete cds
10873					6.7E-01 BF354649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11436	23203	36435	3.59	6.7E-01 014357	014357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI
11659		37578	1.66	6.7E-(01 AA342521.1	EST_HUMAN	EST48065 Fetal spleen Homo sapiens cDNA 3' end
2505		27964	1.29	6.6E-01	1 AF075240.1	LN	Homo sapiens SLIT1 protein (SLIL2) mRNA, partial cds
2704	- 1	28148	1.44	6.6E-01	11 AF199339.1	LN	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3650	J	29043	4.57	6.6E-01	11 Y07669.1	LN	Calbicans random DNA marker, 282bp
4089	16832		0.85		6 6F.01 104328 4	Ŀ	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis
5125	L	30461	1.13		AL 161572.2	LN	Arabidosis thaliana DNA chromosome 4 contin froment No. 68
6240]_	31988	4.29	6.6E-01	6.6E-01 6680577 NT	LN	Mus musculus kinesin light chain 2 (Kic2), mRNA
7585	20253	33359	3.76	6.6E-01	6.6E-01 AV660506.1	EST HUMAN	AV660506 GLC Homo saplens cDNA clone GLCGID043'
8464	21156	34299	0.52	6.6E-01	6.6E-01 AV704700.1	EST_HUMAN	AV704700 ADB Homo saplens cDNA clone ADBCAF11 5'
9564			2		AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12470		31033	1.48		6.6E-01 AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
610	13388	26019	18.23		M75140.1	TN	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds

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		Т	Т	T	T	Τ.	g	Т	7	T	T	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Τ	Т	Т	Т	Т	Т	Т	Т
	Top Hit Descriptor	H.vulgaris Na.K-ATPase alpha subunit mRNA, complete cds	Mus musculus gene for Tob2, complete cds	Homo saplens SPP2 dene for secreted phosphoprofein 24 precintage avons 1.8	Arabidopsis thaliana DNA chromosome 4, contin fragment No. 39	Phsseolits Winaris A TPace namme criticiti mDNA	TRANSCRIPTION REGULATORY PROTEIN SNF6 (SWISNF COMPLEX COMPONENT SNF6)	Homo sablens chromosome 24 soument US94 Ob 40	Chicken mRNA for 115-kDa melanosomal metrix powiate complete and	wc48a02.x1 NCI CGAP Pr28 Homo sepiens cDNA clone IMAGE・シスク1642 31	Vd2/b04,s1 Soares fets liver spleen 1NFI S Home senions cDNA clone IMAGE-1089-47 9	Mus musculus small GTP-binding protein RAB25 (Rab26) gene, complete cds	W1786.r1 Scares plecents 8to9weeks 2NbHP8to8W Homo series כ החוש ביירום אות ביירום אות ביירום אות ביירום אות היירום את היירום אות היירום את היירום אות היירום את	not5c07.s1 NCI CGAP Phet Home seniers child clare IMAGE:4400748 3	AU138078 PLACE1 Homo sabiens cDNA clone PI ACE1007840 5	Plasmodium berghel cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and oxtochrome b	Partor, mixed orbital angles at country minochonarial proteins, complete cas hv74a10.x1 NCI CGAP 1 i.24 Home saniers cDNA class 1846.CE 3476430 31	S.cerevisiae chromosome IV reading frame ORF VDI 097c	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds	Pseudomonas fluorescens tryptophan halogenase (pmA) gene, complete cds	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds	Homo sapiens mRNA for KIAA 1607 protein, partial cds	Treponema pallidum section 63 of 87 of the complete genome	Homo saplens ataxla telanglectasia (ATM) gene, complete cds	602150289F1 NIH_MGC_81 Homo saplens cDNA clone IMAGE:4291126 5	AV759212 MDS Homo sapiens cDNA clone MDSCGC09 5'	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)	Haemophilus Influenzae Rd section 4 of 163 of the complete genome	Shigella flexneri multi-antibiotic resistance locus	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
21 1125	Top Hit Database Source	F	E	IN	N	ΙΝ	TOGGSSIMIS	FN FN	LZ	EST HUMAN	EST HUMAN	\ F	EST HUMAN	EST HUMAN	EST HUMAN	I LV	EST HUMAN	ZI.	NT	NT	TN	TN	N	TN	EST_HUMAN	EST_HUMAN	SWISSPROT	NT	TN	TN	NT
	Top Hit Acession No.	M75140.1	6.5E-01 AB041225.1	-01 AJ272285.1	-01 AL161539.2	-01 U28921.1	01 P18480	-01 AL 163249 2	-01 D88348.1	-01 AI799882.1		<u>~</u>	01 H87583.1	01 AA601287.1	01 AU138078,1	01 AE014115 1	01 BE465050.1	01 274145.1	01 U48848.1	01 AF161184.1			01 AE001247.1			12.1	01 P05228				01 U75331.1
	Most Similar (Top) Hit BLAST E Value	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6.5E-01	6 5F-01	6.5E-01	6.5E-01	8.5E-01	6.5E-01	6.5E-01	6.5E-01	8.5E-01/	6.5E-01/	8 5F-01 1	6.5E-01	6.5E-01	6.4E-01	6.4E-01	6.4E-01	6.4E-01	6.4E-01	6.4E-01	6.4E-01	6.4E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01	6.3E-01 U
	Expression Signal	18.23	4.25	4.23	0.78	2.6	177	0.62	1.5	0.84	0.8	1.96	2.68	3.5	3.93	2.42	2.07	1.81	8.05	1.16	2.16	1.08	1.82	8.6	1.22	5.99	4.58	2.25	2.02	3.51	3.51
	ORF SEQ ID NO:		28833	29615		30329	30843	31337	32400	33340		36094	36460	36518		37518			25694	28043	28855	29230	34347	35848	35864		25858	25938	27623	28035	28036
	Exon SEQ ID NO:			16990	17016	17728	25067	18424				22881	23228	23280	23381	24198	24710	25148		- }	- 1	16583	21202	22837	22652	24777	13211	13306	14889	15297	15297
	Probe SEQ ID NO:	610	3426	4249	4277	5003	5357	5627	6625	7566	8737	10233	10529	10585	10690	11589	12267	12504	246	2583	848	3842	8510	888	1004	12382	425	522	2159	2683	2583

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5973	18755			6.3E-01	01 BE093906.1	EST_HUMAN	PM0-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6504	19269			6.3E-01	01 L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6504	19269	32272	0.84	6.3E-01	01 1.27798.1	LN	Streptococcus dysgalactiae (mag) gene, complete cds
8419	21112			6.3E-01	01 BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
8784	21476		0.95	6.3E-01	01 S62927.1	TN	glycoprotein Illa {Alu 1 and 3 fusion junction} [human, Genomic Mutant, 300 nt]
9120	21808		8.0	6.3E-01	01 BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102596 5
9320	21987		2.45	6.3E-01		LN	Varida virus, complete genome
9320	21987	35160	2.45	6.3E-01	9627521 NT	TN	Variola virus, complete genome
9838	22489		19:0	6.3E-01	01 AE002329.2	NT	Chiamydia muridarum, section 59 of 85 of the complete genome
10326	22973	36193	1.47	6.3E-01	01 273003.1	N	S.cerevisiae chromosome VII reading frame ORF YGR218w
10427	23073	36294	1.19	6.3E-01	01 AE000313.1	NT	Escherichla coli K-12 MG1655 section 203 of 400 of the complete genome
10456	23102		0.45	6.3E-01	01 AW 795395.1	EST_HUMAN	PM0-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
							nr09h06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 002916
10993	23667			6.3E-01	01 AA877715.1	EST_HUMAN	HLARK.;
11308	23967			6.3E-01	01 Al904160.1	EST_HUMAN	CM-BT043-090299-046 BT043 Homo saplens cDNA
11402	24051		1.66	6.3E-01	01 P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11581	24180				01 P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
11988	25355	30607	4.37	6.3E-01	9910293	LN	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12078			1.45	6.35-01	01 AF105227.1	NT	Homo sapiens 3-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12283	25272		2.93	6.3E-01	01 X83528.1	TN.	C.limicala pscD gene
5780		31499	2.31	6.2E-01	01 Q10135	SWISSPROT	HYPOTHETICAL 142,5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7394	20073		3.44	6.2E-01	01 AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
7443	25114	33200	1 33	A 2E 04	03 61 031137 3	F	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finner protein 185
8200	1			6.2E-01	01 H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:213542 3'
							Lycopersicon esculentum cytosolic Cu,Zn superoxide dismutase (Scd) gene, partial cds; and dehydroquinate
8755	-			6.2E-	01 AF034411.1	NT	dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9349		33540		6.2E-	01 BE562687.1	EST_HUMAN	601336146F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3690010 5
9410			2.55	6.2E-	01 M24461.1	ΙN	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
9878	22626	35834	6.2	6.2E-	01 AL161511.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10121	22769	35982	0.5	6.2E-01	11420793 NT	LN	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10121	22769	35983	0.5	6.2E-01	11420793 NT	F	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA

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		_		_	_	_	_	_	,—		-,-	_	_	_	_					_			_		_	_		
Single Exon Probes Expressed in Brain	Top Hit Descriptor	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA	Caenorhabditis elegans N2 CeMyoD (hlh-1) alternatively spliced genes, complete cds	Rat TRPM-2 gene, complete cds	Rat TRPM-2 gene, complete cds	xd60h03.x1 NCI_CGAP_Ov23 Homo saplens cDNA clone IMAGE:2597237 3' similar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)	Arabidopsis, thaliana putative zinc transporter (ZIP1) mRNA, complete cds	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA	Homo saplens G-protein coupled receptor EDG-7 mRNA, complete cds	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome	Home sapiens depamine transporter (SLO6A3) gene, complete cds	hysluronen-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]	hyaturonan-binding protein≕hepatocyte growth factor activator homolog fhuman. plasma. mRNA, 2408 nf	Mus musculus Col4a5 mRNA for type IV collagen alpha 5 chain, complete cds	M.mazel orfA, orfB, and orfC of archaeal ABC-transporter system	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28	D(2) DOPAMINE RECEPTOR	UI-H-BI1-aeb-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'	Musca domestica insecticide susceptible strain voltage sansitive sodium channel mRNA, complete cds
gie Exon Pro	Top Hit Database Source	SWISSPROT	SWISSPROT	LN T	TN	LN	LΝ	EST_HUMAN	SWISSPROT	NT.	L	Z	FN.	FZ	FZ	FZ	LN	Į.	FZ.	FZ	LN LN	N-	LN T	TN	F	SWISSPROT	EST_HUMAN	μ
UIO .	Top Hit Acession No.	-01 P27410	-01 P27410	6678076 NT	6.1E-01 M59940.1	6.1E-01 M64733.1	M64733.1	6.1E-01 AW105653.1	6.1E-01 D63769	35.1	11431065	11431065 NT	6.1E-01 AF236117.1	6.1E-01 AF236117.1		-01 AF119117.1	-01 \$83182.1	6.1E-01 S83182.1	6.1E-01 AB041350.1		Г	5802999 NT			Г		-01 AW139713.1	6.0E-01 U38813.1
	Most Similar (Top) Hit BLAST E Value	6.2E-01	6.2月-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	8.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.1E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01
	Expression Signal	5.2	5.2	4.38	1.15	4.02	4.02	0.84	0.72	3.27	1.09	1.09	18.74	18.74	0.93	1.06	2.57	2.57	2.28	1.57	1.24	3.09	1.91	0.92	1.09	2	2.86	2.78
	ORF SEQ ID NO:	36305	36308			32540		32702	32751	33962	34528	34529			35597	35797	37855	37656	30899		25903		28785	29180		30628	30839	32210
	Exan SEQ ID NO:	23080	23080	15114	18248	19514	19514	19656	19697	20826	21386	21386	21982	21982	22393	22594	24331	24331	25159	24977	13267	13331	14089	16547	16905	18007	18156	18213
	Probe SEQ ID NO:	10434	10434	2393	5449	67.70	6770	6920	7005	8132	8694	8694	9315	9315	9742	9948	11738	11738	12074	12694	482	248	1341	3795	4165	5199	5353	6445

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Top Hit Descriptor	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW 136) (CDV 136) (CDV 136) (CDV 137)	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	SEGMENTATION PROTEIN FUSHI TARAZU	SEGMENTATION PROTEIN FUSHI TARAZU	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)	Gallus gailus mRNA for Hyperion protein, 419 kD isoform	Gallus gallus mRNA for Hyperion protein, 419 kD isoform	tf08f07.x1 NCL_CGAP_Prz8 Homo sapiens cDNA clone IMAGE:2095621 3'	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA	z/96g05.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4627763'	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA	RC1-HT0375-030500-015-c03 HT0375 Hamo sapiens cDNA	Haemophilus influenzae Rd section 16 of 163 of the complete genome	Homo saplens chromosome 21 segment HS21C067	Homo saplens chromosome 21 segment HS21C067	Rattus norvegicus cenexin 2 mRNA, partial cds	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds	Homo saplens gene for histamine H2 receptor, promoter region and complete cds	G.gallus gene for skeletal alpha-actinin, exon EF2	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643	Legionella pneumophila gene for iron superoxide dismutase, complete cds	Chiamydia trachomatis strain K/UW31/Cx major outer membrane protein (omp1) gene, complete cds	EGPROTEIN	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)	THYMIDYLATE KINASE (DTMP KINASE)	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds	PM1-DT0041-190100-002-h03 DT0041 Homo saplens cDNA	Mus spretus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds	JSN1 PROTEIN
Top Hit Database Source	SWISSPROT	N	SWISSPROT	SWISSPROT	Ę	SWISSPROT	L'N	Ę	23.1 EST_HUMAN	LN	EST_HUMAN	Ę	EST_HUMAN	LN FN	ΙΝ	TN	LN	۲N	NT TN	NT	JN	NT	TN	SWISSPROT	SWISSPROT	SWISSPROT	Ν	EST_HUMAN	NT	SWISSPROT
Top Hit Acession No.	01 004912	01 AJ277661.1	01 P02835	01 P02835	01 AB008193.1	01 Q01497	-01 AJ131892.1	01 AJ131892.1	-01 AI420623.1	11421663	01 AA706087.1	FN 6065303	01 BE157617.1	01 U32701.1		-01 AL163267.2	-01 AF162756.1	-01 AF065440.2	5.9E-01 AB023486.1	-01 X68801.1		-01 D12922.1	-01 AF063204.2	-01 P06463	-01 P55284	-01 Q9X0i3	-01 AF197944.1	-01 AW937175.1	-01 AF064626.1	-01 P47135
Most Similar (Top) Hit BLAST E Value	6.0E-01		6.0E-01	6.0E-01	6.0E-01		6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	6.0E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01	5.9E-01
Expression Signal	0.68	66.9	4.39	4.39	1.61	1.46	1.49	1.49	3.77	2.25	2.6	3.04	2.06	1.36	2.29	2.29	4.21	1.55	1.32	0.61	0.46	0.48	0.82	0.74	1.15	2.5	1.72			
ORF SEQ ID NO:	32335	33013	33850		35574		36921	36922				30815		26407		28676		32139	32922			34370	35299		35951	36502	36507			
Exon SEQ ID NO:	19328	L_	20718		22374		23664	1				25208	l.	13745	16026	16026	16937	19142	19853	19979	20593	21228	22120	L	١_		23271	L.,	l	1
Probe SEQ ID NO:	6563	7254	8023	8023	9723	10173	10990	10890	11540	12354	12455	12639	12664	980	3264	3264	4196	6373	7166	7296	7898	8536	9443	9813	10088	10569	10576	10881	11149	11458

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Single Exon Probes Expressed in Brain	ilt Top Hit Acession Database Top Hit Descriptor Top Hit Descriptor Source	SE-01 P47135 SWISSPROT JSN1 PROTEIN		05.1 NT	SWISSPROT	SWISSPROT	-01 7305230 NT Mus musculus low density lipoprotein B (LdIb), mRNA	IN	-N	SWISSPROT	EST_HUMAN	Z	5.8E-01 S66091.1 NT cyclic AMP-regulated phosphoprotein [rate, mRNA, 1030 nt]	yng/b03.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178757 3' similar to -0.1 H41571.1 EST HUMAN Igb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN):	Г	EST_HUMAN	SWISSPROT		-01 AJZ70774.1 NT Homo saplens partial TCF-4 gene for T-oell transcription factor-4, exons 6-11	SWISSPROT	-01/Q20471 SWISSPROT PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	-01 6755253 NT Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA	SWISSPROT	-01 AB033503.1 NT Populus euramericana psacs-2 mRNA for 1-aminoxyclopropane-1-carboxylate synthase, complete cds	EST HUMAN	LHUMAN	-01 AL111440.1 NT Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
	Top Hit Ace No.	P47135	142320.1	AB017705.1	P34926	P40472	73(AB009077.1	AE002152.1	Q10699	D78659.1	D50601.1	S65091.1	H41571.1	AI280051.1	AI280051.1	P:14328	P14328	AJ270774.1	Q27368	Q20471	BF031606.1	AJ243213.1	BF700092.1	BF700092.1	P06727	P06727	978	Q9WTJ2	AB033503.1	BF035413,1	AA194201.1	AL111440.1
	Most Similar (Top) Hit BLAST E Value	5.8E-01	5.9E-01	5.9E-01	5.9E-01	5.85-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	6.8E-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	5.8E-01	5.7E-01	5.7E-01	5.7E-01	5.7E-01	5.7E-01	5.7E-01	5.7E-01	5.7E-01
	Expression Signal	1.58	2	4.35	5.72	1.36	1.01	4.37	0.82	0.62	1.09	99'0	2.48	2.61	0.64	0.64	3.41	3.41	8.97	0.89	0.51	0.81	7,56	3.97	1.99	1.12	1.12	0.69	1.62	2.82	5.13	0.81	1.33
	ORF SEQ ID NO:	37369	31109			27348	28021	29838		31131	31835	31870			33805	33806	33914	33915	34628	34707	34708		36837			26912	26913		28631		32011	32388	30568
	Exon SEQ ID NO:	24062	24549	24698				17213	18095	18243	18869	18994	19630	20482	20680	20680	20784	20784			1	- 1	Į	23638	23759	14227	14227	15804	15980	16251	19036	19374	17932
	Probe SEQ ID NO:	11458	12021	12252	12465	1902	2569	4478	5290	5444	6091	6220	6715	7877	7985	7985	8090	8080	8789	8871	8872	9496	10911	10962	11089	1480	1480	3038	3217	3495	6262	6611	6763

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	Top Hit Descriptor	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)	Mus musculus Konq1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts	10 sapiens cDNA	ontig fragment No. 32	ontig fragment No. 32	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066810 5	mo saplens cDNA	601654814R1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:3839763 31	, partial cds	partial cds	ontig fragment No. 13		GKCFSF05 5	GKCFSF05 5	ucin, partial cds	801514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5	ng75g10.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7		onlig fragment No. 13	NER	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA	GAG POLYPROTEIN ICONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P101	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30: NI ICI EODBOTEIN P101	Homo canions entracted for dealing in this 276 considers handled life /OKN/A1 - 1914	vor18a10.s1 Soares adult brain N2b5HR55V Homo sanions cDNA clare IMACE: 17828.9			IB1 gene, partial cds	neta subunit, complete cds	or82c01.y5 NCI_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:1802336 5'	Crimean-Congo hemorrhadic fever virus strain SPU 415/85 nucleoprotein nane, complete ede
Single Exoll Plopes Expressed in Brain	,	PYRROLINE-5-CARBOXYLAT	Mus musculus Konq1, Ltrpc5, N	HA0895 Human fetal liver cDNA library Homo sapiens cDNA	Arabidopsis thallana DNA chromosome 4, contig fragment No. 32	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32	602067712F1 NIH MGC 58 H	MR3-HT0736-180700-003-a02 HT0736 Homo sapiens cDNA	601654814R1 NIH_MGC_57 H	Homo sapiens mRNA for KIAA0740 protein, partial cds	Homo sapiens mRNA for KIAA0740 protein, partial cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13	Chicken TBP gene, exon8, complete cds	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 5	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 5	Homo sapiens MUC3A gene for Intestinal mucin, partial cds	601514007F1 NIH_MGC_71 H	ng75g10.s1 NCI_CGAP_Pr6 H	repetitive element;	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13	HIGH AFFINITY POTASSIUM TRANSPORTER	602132029F1 NIH_MGC_81 H	Raffus norvegicus Propionyl Co	GAG POLYPROTEIN (CONTAINS: INNE PROTEIN P30; NUCLEOPROTEIN P101	GAG POLYPROTEIN [CONTAINS: INNE	Homo sanions supervillar drallar	vo18a10.s1 Soares adult brain N	Rabbit oral papillomavirus, complete genome	FOS-RELATED ANTIGEN-1	Bos faurus MHC class II beta-chain BoLA-DIB1 gene, partial cds	Carassius auratus gene for gonadotropin II beta subunit, complete cds	or82c01.y5 NCI_CGAP_Lu5 Ho	Crimean-Condo hemorrhadic fev
gie Exon Pro	Top Hit Datebase Source	SWISSPROT	N	EST HUMAN	Ν	N	EST HUMAN	EST_HUMAN	EST_HUMAN	LN	N	N	F	EST_HUMAN	EST_HUMAN	N P	EST_HUMAN		EST_HUMAN	NT	SWISSPROT	EST_HUMAN	۲N	SWISSPROT	TOGGRANMA	LN LN	EST HUMAN	NT	SWISSPROT	LN	NT	EST_HUMAN	LN.
	Top Hit Acession No.	P00373	E-01 AJ251835.1	E-01 Al065061.1	5.7E-01 AL161532.2	5.7E-01 AL161532.2	5.7E-01 BF540962.1	BE715051.1	5.7E-01 BE959722.2	5.6E-01 AB018283.2	5.6E-01 AB018283.2	AL161501.2	5.6E-01 D83135.1	5.6E-01 AV684703.1	5.6E-01 AV684703.1	5.6E-01 AB038782.1	5.6E-01 BE888280.1			1.2	P50505	5.6E-01 BF573829.1	8393912 NT	-01 P03341	-01 P03341	TOPONE	H46219.1		5.5E-01 P48755	Γ	1	5.5E-01 AI791766.1	
	Most Similar (Top) Hit BLAST E Value	5.7E-01 P00373	5.7E-01		5.7E-01	5.7E-01	5.7E-01	5.7E-01	5.7E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01	5.6E-01		5.65-01	5.6E-01	5.6E-01 P50505	5.6E-01	5.5E-01	5.5E-01	5.5F-01	5 SE-01	5.5E-01	5.5E-01	5.5E-01	5.5E-01	5.5E-01	5.5E-01	5.5E-01
	Expression Signal	2.14	0.5	0.47	1.19	1.19	0.72	1.52	3.01	1.3	1.3	76.0	0.74	4.01	4.01	1.08	2.57		1.63	1.69	2.7	4.26	0.85	6.93	893	-	1.55	4.22	1.7	1.79	0.85	1.04	0.7
	ORF SEQ ID NO:	33438			35544		36351			28772	28773	29252	29578	34541	34542	35199				29252			26606	28149	28150	283301		28644	29073	30419		34178	
	Exon SEQ ID NO:			_			23121	24524	24958		١		16956				24457	-	1	- 1	ı		13941	15412	15412	15685	15828	15991	16431	17801	19873	21041	22319
	Probe SEQ ID NO:	7664	7870	8279	6696	6696	10475	11983	12658	3357	3357	3863	4215	8702	8702	9275	11884	7,007	1881	12352	12379	12773	1189	2705	2705	2919	3062	3228	3678	5082	7187	8348	2996

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Probe Expn ORF SEQ Expression (Top) Hit Acession Top Hit Acession <th>Hit Acession Top Hit Database No. Source Source Source Source SET HUMAN 28507.1 EST_HUMAN 7657266 NT 7657266 N</th> <th>Top Hit Descriptor EST02835 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCQ35 601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3' Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA P seudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes P seudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes OV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA Chlamydophila pneumonlae AR39, section 74 of 94 of the complete genome Drosophila melanogaster mRNA for 15,15 beta carolene cloxygenase (beta-clox gene) Rattus rattus UDP glucuronosyltransferase gene, complete cds</th>	Hit Acession Top Hit Database No. Source Source Source Source SET HUMAN 28507.1 EST_HUMAN 7657266 NT 7657266 N	Top Hit Descriptor EST02835 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCQ35 601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3' Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA P seudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes P seudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes OV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA Chlamydophila pneumonlae AR39, section 74 of 94 of the complete genome Drosophila melanogaster mRNA for 15,15 beta carolene cloxygenase (beta-clox gene) Rattus rattus UDP glucuronosyltransferase gene, complete cds
22924 36136 0.96 6.5E-01 T05047.1 23767 37033 1.66 6.5E-01 BF129507.1 12956 25598 4.91 5.4E-01 7657266 13352 25981 1.16 5.4E-01 AF232006.1 13997 26644 3.41 5.4E-01 AF232006.1 13997 26644 3.41 5.4E-01 AF232006.1 14930 27719 1.91 5.4E-01 AF232006.1 1786 30402 0.92 5.4E-01 AF232006.1 18368 31278 0.74 5.4E-01 AF232006.1 18876 31846 0.82 5.4E-01 AF439.1 18920 3293 0.81 5.4E-01 AF842327.1 19920 32994 0.87 5.4E-01 AF842327.1 19920 32994 0.81 5.4E-01 221619.1 19920 32994 0.81 5.4E-01 221619.1 22540 35948 2.09 5.4E-01 </td <td>57266</td> <td>EST02835 Fetal brain, Stratagene (cat#938206) Homo sapiens cDNA clone HFBCQ35 601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3' Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Pseudomonas sylnigae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes Pseudomonas sylnigae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA Chlamydophila pneumonlae AR39, section 74 of 94 of the complete genome Drosophila melanogaster mRNA for 15,15 beta carotene dioxygenase (beta-diox gene) Rattus rattus UDP glucuronosyltransferase gene, complete cds</td>	57266	EST02835 Fetal brain, Stratagene (cat#938206) Homo sapiens cDNA clone HFBCQ35 601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3' Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Pseudomonas sylnigae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes Pseudomonas sylnigae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA Chlamydophila pneumonlae AR39, section 74 of 94 of the complete genome Drosophila melanogaster mRNA for 15,15 beta carotene dioxygenase (beta-diox gene) Rattus rattus UDP glucuronosyltransferase gene, complete cds
23767 37033 1.85 6.5E-01 BF128507.1 12956 25598 4.91 5.4E-01 7657266 13352 25980 1.16 5.4E-01 AF232006.1 13997 26644 3.41 5.4E-01 AF232006.1 14980 27719 1.91 5.4E-01 AF232006.1 17786 30402 0.92 5.4E-01 AF232006.1 18368 31278 0.74 5.4E-01 AW842327.1 18876 0.82 5.4E-01 AW842327.1 19820 32893 0.81 5.4E-01 AW842327.1 19820 32894 0.81 5.4E-01 Z21619.1 19820 32894 0.81 5.4E-01 Z21619.1 22540 35948 0.81 5.4E-01	57266	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3' Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA Chlamydophila pneumonlae AR39, section 74 of 94 of the complete genome Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene) Rattus rattus UDP glucuronosytransferase gene, complete cds
12955 25597 4.91 5.4E-01 7657266 NT 12966 25598 4.91 5.4E-01 7657266 NT 13352 25981 1.16 5.4E-01 AF232006.1 NT 13997 29664 3.41 5.4E-01 AF232006.1 NT 14830 27719 1.91 5.4E-01 AV896087.1 EST 14830 27719 1.91 5.4E-01 AV896087.1 EST 17785 30402 0.82 5.4E-01 AV896087.1 EST 18368 31278 0.74 5.4E-01 AV896087.1 NT 18368 31278 0.82 5.4E-01 AV89439.1 NT 18960 31278 0.81 5.4E-01 AV89059.7 NT 19870 32893 0.81 6.4E-01 Z10919.1 NT 19820 32893 0.81 6.4E-01 Z10919.1 NT 19821 35948 2.09 5.4E-01 Z1019.1	7657266 NT 7657296 NT 32006.1 NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Pseudomonas sylngae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes Pseudomonas sylngae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA Chlamydophila pneumonlae AR39, section 74 of 84 of the complete genome Drosophila melanogaster mRNA for 15,15 beta carolene cloxygenase (beta-clox gene) Rattus rattus UDP glucuronosyltransferase gene, complete cds
12966 25598 4.91 5.4E-01 7657266 NT 13352 25981 1.16 5.4E-01 AF232006.1 NT 13997 26664 3.41 5.4E-01 AF232006.1 NT 13997 26664 3.41 5.4E-01 AF602247.2 NT 14830 27719 1.91 5.4E-01 AF602247.2 NT 17785 30402 0.82 5.4E-01 AF602247.2 NT 17785 30402 0.82 5.4E-01 AF602247.2 NT 18368 31278 0.74 5.4E-01 AW4339.1 NT 18876 31846 0.83 5.4E-01 AW43327.1 EST 19820 32893 0.81 6.4E-01 AW43237.1 NT 19820 32894 0.81 6.4E-01 Z21619.1 NT 19822 32897 0.81 6.4E-01 Z21619.1 NT 22540 36948 2.67 6.4E-01 Z21619.1	7657266 NT 32006.1 NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA Pseudomonas syrlngae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes Pseudomonas syrlngae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA Chlamydophila pneumonlae AR39, section 74 of 84 of the complete genome Drosophila melanogaster mRNA for 15,15* beta carolene dioxygenase (beta-diox gene) Rattus rattus UDP glucuronosytransferase gene, complete cds
13352 25880 1.16 5.4E-01 AF232006.1 NT 13362 25881 1.16 5.4E-01 AF232006.1 NT 13897 26864 3.41 5.4E-01 AF232006.1 NT 14830 27719 3.43 5.4E-01 AF232006.1 NT 1786 30402 3.43 5.4E-01 AF202247.2 NT 1786 30402 0.92 5.4E-01 AF20682.1 NT 18368 31278 0.74 5.4E-01 AF4839.1 NT 18876 31846 0.87 6.4E-01 AF4839.1 NT 18876 32893 0.81 6.4E-01 AF89659.7 EST 19820 32894 0.81 6.4E-01 Z21619.1 NT 19820 32897 1.48 5.4E-01 Z21619.1 NT 22540 2.09 5.4E-01 Z21619.1 NT 23897 1.48 5.4E-01 Z21619.1 NT 2421		Pseudomonas syringae pv. tomato strain DC3000 AvrĒ (avrĒ), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes complete cds; and unknown genes Pseudomonas syringae pv. tomato strain DC3000 AvrĒ (avrĒ), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA Chlamydophila pneumonlae AR39, section 74 of 94 of the complete genome Drosophila melanogaster mRNA for 15,15 beta carotene dioxygenase (beta-diox gene) Rattus rattus UDP glucuronosytransferase gene, complete cds
13362 25981 1.16 5.4E-01 AF232006.1 NT 13997 26664 3.41 5.4E-01 AW896087.1 EST 14830 3.43 5.4E-01 AW896087.1 EST 14980 27719 1.91 6.4E-01 AR002247.2 NT 1785 30402 0.82 5.4E-01 AW842327.1 NT 18368 31278 0.74 5.4E-01 AW842327.1 EST 19820 32893 0.81 6.4E-01 BE96592.2 EST 19820 32893 0.81 6.4E-01 BE96592.2 EST 19820 32893 0.81 6.4E-01 BE96592.2 EST 19820 32894 0.81 6.4E-01 Z21619.1 NT 19820 32897 1.48 5.4E-01 Z21619.1 NT 22540 2.09 5.4E-01 Z21619.1 NT 2387 5.4E-01 AB6272636.1 EST 2387 5.4E-01		Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA Chlamydophila pneumoniae AR39, section 74 of 94 of the complete genome Drosophila melanogaster mRNA for 15,15 beta carotene dioxygenase (beta-diox gene) Rattus rattus UDP glucuronosytransferase gene, complete cds
13897 28664 3.41 5.4E-01 AW896087.1 EST 14830 27719 3.43 5.4E-01 AB02247.2 NT 1786 30402 0.92 5.4E-01 AN7439.1 NT 18368 31278 0.74 5.4E-01 AW842327.1 EST 18876 32710 0.83 5.4E-01 AW842327.1 EST 19820 32893 0.81 6.4E-01 BE966592.2 EST 19820 32893 0.81 6.4E-01 Z21619.1 NT 19820 32894 0.81 6.4E-01 Z21618.1 NT 22540 2.09 6.4E-01 Z21618.1 NT 23887 0.81 6.4E-01 Z21618.1 NT 22540 2.09 6.4E-01 Z21618.1 NT 23887 3.6948 2.87 6.4E-01 Z21618.1 SWIS 24218 37542 3.08 5.4E-01 Q60675 SWIS		OV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA Chlamydophila pneumonlae AR39, section 74 of 94 of the complete genome Drosophila melanogaster mRNA for 15,15 beta carolene dioxygenase (beta-diox gene) Rattus rattus UDP glucuronosytransferase gene, complete ods
14830 3.43 5.4E-01 AE002247.2 NT 14980 27719 1.91 5.4E-01 AJZ76682.1 NT 17785 30402 0.92 5.4E-01 M74439.1 NT 18368 31278 0.74 5.4E-01 AM842327.1 EST 18664 32710 0.87 5.4E-01 AM82327.1 EST 18664 32710 0.87 5.4E-01 AB025017.1 NT 19820 32893 0.81 6.4E-01 BE96659.2 EST 19820 32894 0.81 6.4E-01 Z21619.1 NT 19820 32894 0.81 6.4E-01 Z21619.1 NT 25540 2.09 6.4E-01 BF72536.1 EST 25640 2.09 6.4E-01 BF72536.1 EST 23887 2.6E-01 G6675 SWIS 24218 3.7542 3.08 5.4E-01 G06075 SWIS		Chlamydophila pneumoniae AR39, section 74 of 94 of the complete genome Drosophila melanogaster mRNA for 15,15 beta carolene dioxygenase (beta-diox gene) Rattus rattus UDP glucuronosyttransferase gene, complete ods
14980 27719 1.91 5.4E-01 AJZ76682.1 NT 17785 30402 0.92 5.4E-01 M74439.1 NT 18368 31278 0.74 5.4E-01 AM842327.1 EST 18876 31845 0.83 5.4E-01 AM842327.1 EST 19864 32710 0.87 6.4E-01 AB625017.1 NT 19820 32893 0.81 6.4E-01 BE96692.2 EST 19820 32894 0.81 6.4E-01 Z21619.1 NT 19822 32897 0.81 6.4E-01 Z21619.1 NT 22540 2.09 5.4E-01 Q64428 SWIS 23887 36948 2.87 6.4E-01 G6428 SWIS 24218 37541 3.08 6.4E-01 Q60675 SWIS		Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene) Rattus rattus UDP glucuronosytransferase gene, complete cds
17785 30402 0.92 5.4E-01 M74439-1 NT 18368 31278 0.74 5.4E-01 AW843327.1 EST 18876 31846 0.83 5.4E-01 AB025047.1 NT 19664 32846 0.87 5.4E-01 BE96659.2 EST 19920 32893 0.81 6.4E-01 Z21619.1 NT 19920 32894 0.81 6.4E-01 Z21619.1 NT 22540 2.09 5.4E-01 G04428 SWIS 23887 1.48 5.4E-01 BF672536.1 EST 23887 2.09 5.4E-01 P98858 SWIS 24218 37541 3.08 5.4E-01 G06075 SWIS 24218 37542 3.08 5.4E-01 G06075 SWIS	П	Rettus rattus UDP glucuronosyltransferase gene, complete cds
18368 31278 0.74 6.4E-01 AW842327.1 EST 18876 31845 0.83 5.4E-01 AB025017.1 NT 19864 32710 0.87 5.4E-01 BE96592.2 EST 19920 32893 0.81 6.4E-01 Z21619.1 NT 19922 32894 0.81 5.4E-01 Z21619.1 NT 22540 2.09 5.4E-01 Q64428 SWIS 23867 36948 2.87 6.4E-01 P38858 SWIS 24218 37541 3.08 5.4E-01 Q00075 SWIS 24218 37542 3.08 5.4E-01 Q00075 SWIS		
18876 31845 0.83 5.4E-01 AB025017.1 NT 19864 32710 0.87 5.4E-01 BE96659.2 EST 19920 32993 0.81 6.4E-01 Z21619.1 NT 19920 32994 0.81 6.4E-01 Z21619.1 NT 19922 32997 1.48 5.4E-01 G64428 SWIS 22540 2.09 5.4E-01 BF972536.1 EST 23987 3.694 2.87 6.4E-01 P38858 SWIS 24218 37541 3.08 6.4E-01 G00076 SWIS 24218 37542 3.08 5.4E-01 G00076 SWIS		PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
19920 32710 0.87 5.4E-01 BE96659.2 EST 19920 32893 0.81 6.4E-01 Z21619.1 NT 19920 32894 0.81 6.4E-01 Z21619.1 NT 19922 32897 1.48 5.4E-01 G64428 SWIS 22540 2.09 5.4E-01 G6428 SWIS 23867 36948 2.87 6.4E-01 P38858 SWIS 24218 37541 3.08 5.4E-01 G00075 SWIS 24218 37542 3.08 5.4E-01 G00075 SWIS	Ņ	Rattus norvegicus gene for TIS11, complete cds
19920 32963 0.81 5.4E-01 221619.1 19920 32994 0.81 5.4E-01 221619.1 19922 32997 1.48 5.4E-01 264428 22540 2.09 5.4E-01 P562586.1 23887 36948 2.87 6.4E-01 P36858 24218 37541 3.08 5.4E-01 Q60676		601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
19920 32894 0.81 5.4E-01 221619.1 19822 32897 1.48 5.4E-01 264428 22540 2.09 5.4E-01 264428 23887 36948 2.87 6.4E-01 26858 24218 37541 3.08 5.4E-01 260676 24218 37542 3.08 5.4E-01 260676		S.cerevisiae RIB3 gene encoding DBP synthase
19822 32897 1.48 5.4E-01 O64428 22540 2.09 5.4E-01 D56428 23687 36948 2.87 6.4E-01 P3658 24218 37541 3.08 5.4E-01 Q60676 24218 37542 3.08 5.4E-01 Q60676		S.cerevisiae RIB3 gene encoding DBP synthase
22540 2.09 5.4E-01 8-54E-02 23687 36948 2.87 6.4E-01 P36858 24218 37541 3.08 5.4E-01 Q60676 24218 37542 3.08 5.4E-01 Q60676		MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEUXDEOCEMARY:
23687 36948 2.87 5.4E-01 P36858 24218 37541 3.08 5.4E-01 Q60676 24218 37542 3.08 5.4E-01 Q60676		002076545F1 NIH MGC 62 Homo saniens cDNA clone IMA GE 4248600 F1
24218 37541 3.08 5.4E-01 Q60675 24218 37542 3.08 5.4E-01 Q60675		NITRATE REDUCTASE INADPHI (NR)
24218 37542 3.08 5.4E-01 Q60675		LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN).
	376 SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11944 24499 3.5 5.4E-01 AI858398.1 EST_HI	8398.1 EST_HUMAN	wl37g04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
		Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-
13287 25921 1.54 5.3E-		(Bf), and complement component C2 (C2) genes;>
14866 27596 1.01		Brassica cleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
27597 1.01 6.3E-01 AF11391	3919.1 NT	Brassica deracea var. capitata phospholipase D2 (PLD2) gene, complete cds
15491 28230 6.83	4506328 NT	Homo saplens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF CI	Expression Signal	Most SImilar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2786	Ц	28231		5.3E-01	4506328 NT	ΝΤ	Homo saplens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3237	15999	28649	2.74	5.3E-01	5.3E-01 AF087658.1	LN	Homo saplens secreted C-type lectin precursor (LSLCL) gene, complete cds
4187	16928		1.58	5.3E-01	5.3E-01 U39687.1	IN	Mycoplasma genitalium section 9 of 51 of the complete genome
5371	18172	30860	1.96	5.3E-01	5.3E-01 AI820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5371			1.96		5.3E-01 AI820921.1	EST_HUMAN	zu42h12,y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
2466	18265	31156	0.84	5.3E-01	5.3E-01 AA193672.1	EST_HUMAN	z/42g09.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5
5466	18265	31157	0.84	5.3E-01	5.3E-01 AA193672.1	EST_HUMAN	zz 42g09.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5
5553	18356	31266	1.82	5.3E-01	5.3E-01 BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_Pr28 Homo saplens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5559	18356	31267	1.82	5.3E-01	5.3E-01 BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3288118·3¹ similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
							Roridula gorganias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for
8802	21494		1.8		5.3E-01 L01950.2	NT	chloroplast product
8844	24545	34802	τα σ	F 2E_01	5 3E-01 RE433058 1	HOT HIMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29
3	ı	ı		2.5	100000	NICINIO 1	יייייייייייייייייייייייייייייייייייייי
8854	21545	34693	0.81	5.3E-01	5.3E-01 BF433956.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;
10111	22759	36971	0.62	5.3E-01	5.3E-01 Al954210.1	EST HUMAN	wx84b02.x1 NCI_CGAP_Me15 Homo saplens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20874 CYTOCHROME C_OXIDASE POLYPEPTIDE VA PRECURSOR:
11550			7.3	5.3E-01	5.3E-01 BE566291.1	EST HUMAN	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMACE:3682168 5'
11789	24379	37709	1.72	5.3E-01	5.3E-01 Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
11877	25206		4.03	5.3E-01	AA916053.1	EST_HUMAN	og30e05.s1 NCJ_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);
797	13569	26229	18.35		5.2E-01 1.20770.1	ĻΝ	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1141	13896		8.29	5.2E-0	11 Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFATS) (NF-ATS) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFATS)
1169	13923	26585			5.2E-01 AF224492.1	Ŋ	Homo sapiens phospholipid scramblase 1 gene, complete cds
1879			2.35		5.2E-01 AL163285.2	TN	Homo saplens chromosome 21 segment HS21C085
2142		27605			AB018283.2	IN	Homo saplens mRNA for KIAA0740 protein, partial cds
3117			1.23	5.2E-01	5.2E-01 U65942.1	LN T	Chlamydophila abortus strain S26/3 POMP91A and POMP90A precursor, genes, complete cds
3231	- 1		-		5.2E-01 D73443.1	N	Azotobacter vinelandii icd gene for Isocitrate dehydrogenase, complete cds
3400	- 1				AL116780.1	F	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3437	16193	28843	2.27	5.2E-01	11 AA984165.1	EST_HUMAN	am77g05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'

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		,	-	_	_		-	-	_	_		_		_	-			•	_	~	_		_	•	•	,	_
Top Hit Descriptor	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gldA) genes, complete cds; and termination factor Rho (rho) gene>	Rattus norvegicus lagged protein mRNA, complete cds	Homo saplens mRNA for KIAA1184 protein, partial cots	602132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271939 5'	Arabidopsis thallana DNA chromosome 4, contig fragment No. 49	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds	601823860R1 NIH_MGC_79 Hamo sapiens cDNA clone IMAGE:4043485 3'	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE]; AMYLO-1,6-GLUCOSIDASE (DEXTRIN 8-ALPHA-D-GLUCOSIDASE)	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4ALPHA- GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE	(DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds	Homo sapiens chromosome 21 segment HS21C102	NUCLEAR ENVELOPE PROTEIN CUT11	602076649F1 NIH_MGC_62 Homo saplens cDNA clone IMAGE:4243860 5'	Xenopus laevis mRNA for c-Jun protein, 1978 BP	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds	FIBRILLIN 1 PRECURSOR	Homo sapiens diacytglycerol kinase 3 (DAGK3) gene, exon 10	Homo sapiens diacy/glycerol kinase 3 (DAGK3) gene, exon 10	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE	601874964F1 NIH_MGC_54 Hamo sapiens cDNA clone IMAGE:4102503 5
Top Hit Database Source	Ł	L.	TN	NT	EST_HUMAN	N	TN	N	EST_HUMAN	EST_HUMAN	SWISSPROT		SWISSPROT	EST_HUMAN	NT	NT	SWISSPROT	EST_HUMAN	NT	TN	SWISSPROT	NT	NT	NT	SWISSPROT	SWISSPROT	EST_HUMAN
Top Hit Acession No.	-01 AF008210.1	5.0E-01 AF008210.1	L38483.1	5.0E-01 AB033010.1	5.0E-01 BF576199.1	5.0E-01 AL161549.2	5.0E-01 AL161549.2	5.0E-01 M92304.1	5.0E-01 BF107848.1	-01 BF317212.1	-01 P35573		P35573	5.0E-01 BE869218.1	5.0E-01 AF029215.1	6.0E-01 AL163302.2	013961	4.9E-01 BF571462.1	4.9E-01 AJ243955.1	4.9E-01 U40869.1	Q61554	4.9E-01 AF020931.1	4.9E-01 AF020931.1	4.9E-01 AB040051.1	210606	210606	4.9E-01 BF209791.1
Most Similar (Top) Hit BLAST E Value	5.0E-01	5.0E-01	5.0E-01	5.0E-01	5.0E-01	5.0E-01	5.0E-01	5.0E-01	5.0E-01	5.0E-01	5.0E-01		5.0E-01 P35573	5.0E-01	5.0E-01	6.0E-01	5.0E-01 013961	4.9E-01	4.9E-01	4.9E-01	4.9E-01 Q61554	4.9E-01	4.9E-01	4.9E-01	4.9E-01 Q10606	4.9E-01 Q10606	4.9E-01
Expression Signal	3.19	3.18	1.13	2.75	0.65	0.75	0.75	1.92	0.71	2.74	1.36		1.36	1.12	4	1.86	4.39	2.43	1.54	1.15	0.89	3.05	3.05	1.61	0.84	0.84	1.45
ORF SEQ ID NO:	27601	27602		29241	-	33334	33335		34399	33547	35362		35363					26205	27090	27345	30783	31686	31687	33111	33378	33379	
SEQ ID NO:	14870	14870	16563	16604	19312	20232	20232	21121	21261	20429	22178		22178	22938	24554	24989	24997	13544	14402	14636	18124	18728	18728	20033	20271	20271	21579
Probe SEQ ID NO:	2140	2140	3811	3854	6547	7562	7562	8428	8269	8328	9256		9525	10290	12026	12715	12726	772	1656	1899	5321	5946	5946	7352	7605	7605	8888

WO 01/57275

PCT/US01/00667

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9808	21775	34939	66'0	4.9E-01	4.9E-01 AW339905.1	EST_HUMAN	ho90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266.3' similar to TR:095714 O95714 HERC2.;
9186	25431		1.96	4.9E-01	10946863 NT	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10218	22864	36078	0.84	4.9E-01	4.9E-01 AF053980.1	N	Mus musculus adenylyl cyclase 1 (Adcy1) cDNA, partial cds
10419	L	36286	0.77	4.9E-01	4.9E-01 X90000.1	LN-	H.sapiens DNA for BCL7A gene and BCL7A/IGH locus fussion
11925			1.72	4.9E-01	4.9E-01 AF176912.1	LN	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
12709	25392		6.73	4.9E-01	4.9E-01 AA613562.1	EST_HUMAN	nq22e11.s1 NCI_CGAP_Co10 Homo saplens cDNA clone IMAGE:1144652 3'
4298	17037		22.0	4 RF-04	TN 0284024	FX	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated
	1						Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for meiotic recombination, complete
5420			10.78	4.8E-01		NT	cds
6228		32356	0.79	4.8E-01		TN	Mus musculus slow skeletal muscle troponin T (Tnnt1) gene, complete cds
6289	19352		3.76	4.8E-01	AA659878.1 EST_	EST_HUMAN	nu86f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
7216				4.8E-01	4.8E-01 5031650	LN.	Homo sapiens reproduction 8 (D8S2298E) mRNA
7565	20235		0.78	4.8E-01		LN	Homo sapiens chromosome 21 segment HS21C009
7661	20325		4.05	4.8E-01		IN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7661	20325	33435	4.05	4.8E-01	-01 AL161492.2	NT	Arabidopsis thallana DNA chromosome 4, contig fragment No. 4
7005	00900	PC866	7	A 0 T 0 A	A 1920/244 4	MANUEL TOO	y/77f10 y5 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154795 5 similar to contains element
9144	L		2:10	4.0E-01	-01 AIGZU/44.1	EST HIMAN	MICNO Executive eletition; PM4.HT0350,201209.004.h04.HT0350.Hcmo canians cDNA
10829	L		1 88	4 8F-01		TN	S. cerevisiae ORFs from chromosome X
12217	1		3.04	4.8E-01	7.	LZ	Trypanosoma cruzi transposon VIP II SIRE repeat region
12795	25216		1.66	4.8E-01		FZ	Chlamydomonas reinhardtii cop gene, exons 1-8
6422	19190	32186	8.41	4.7E-01	4.7E-01 BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5
6941			0.94	4.7E-01	.1		qf/2a09.xf Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
7764	20460		0.63	4.7E-01	F11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
7764		33585	0.63	4.7E-01	F11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8974		34816	0.52	4.7E-01	6981501	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
10751			6.11	4.7E-01	3.1	NT	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
11022			2.2	4.7E-01			Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
11252	23914		1.81	4.7E-01			602043889F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4181303 5'
11349		37342		4.7E-01	4.7E-01 AW889448.1		RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12116			1.52	4.7E-01			601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12237	24689		1.51	4.7E-01	-01 AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909198 3'

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Exon SEQ ID NO: 250.56	Most Signal Top Hit Acession (Top) Hit Top Hit Acession Signal Place	1.63 4.7E.01 AP000007.1 NT Pyrococus horikoshii OT3 genomic DNA, 1485001-1738505 nt position (717)	1.38 4.7E-01 6679502 NT Mus musculus proteasome (prosome, macropain) 26S subunit, ATPase 3 (Psmc3), mRNA	1.57 4.6E-01 BF693300.1 EST_HUMAN 602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IVAGE:4245481 5'	1.57 4.6E-01 [BF693300.1 [EST_HUMAN 602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'		1) 4.6E-01 BF313593.1 EST_HUMAN 601900234F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:4129472.5'	3.11 4.6E-01 090643 SWISSPROT INTERFERON REGULATORY FACTOR 3 (IRF-3)	3.11 4.6E-01 090843 SWISSPROT (INTERFERON REGULATORY FACTOR 3 (IRF-3)	1.84 4.6E-01 BE734781.1 EST_HUMAN 801568755F1 NIH_MGC_21 Homo sapiens cDNA clone INAGE:3843637 5'	qh59h02.x1 Soares_fatal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:1849011 3' similar to 2.17 4.6E-01 Al247679.1 EST_HUMAN TR:O15338 O15338 BUTYROPHILIN.;	qh59H02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1846011 3' similar to 2.17 4.6E-01 Al247679.1 EST HUMAN TR:016338 016338 EUTYROPHILIN	4.6E-01 P20050 SWISSPROT	4.6E-01 AF212124,1	0.77 4.6E-01 BE817247.1 EST HUMAN PM0-BN0260-120600-001-F07 BN0260 Homo sepiens cDNA		1.21 4.6E-01 AE000894.1 NT complete genome	3.2 4.6E-01 U62332.1 NT complete cds	. S.2 4.8E-01 U62332.1 NT complete cds	4.6E-01 L07320.1	0.91 4.6E-01 AA493577.1 EST_HUMAN element,contains element L1 repetitive element;	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEIN 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (6K1); CYTOPLASMIC INCLUSION PROTEIN (6K1); CYTOPLASMIC INCLUSION PROTEIN (01); 6 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A 6E-01 090069 SWISSPROT (NI-A) (NI-A)	4.6E-01 BF697399.1 EST HUMAN	SWISSPROT
Exon Sequip DNO: Sigma NO:		4.7E					1 4.6E-0								L	4.6E	4.6E		4.6	4.6E	4.6E		Ŀ	
Exen SEQ ID ORF SEQ ID NO: 08		- 1	1				96							°	°							•		
· 00		755	300												140							25		
1 월 2 G [회[회[전[전[전[전[전]전] 전] 전[전[전]전] 등] 호[호[호[전] 2] 2]	Probe Exo SEQ ID SEQ NO: NO	12813 250	12817 253			i 1			5385 181	5459 182	5472 182	5472 182	Ĺ	L	1		6163 189	6669 195	6669 195		 7629 202	7658 203		L

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9201	21870	35038	11.11	4.6E-01	4.6E-01 P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9876	22526	35720	1.84	4.6E-01	-01 AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
9876		35721	1.64	4.6E-01	4.6E-01 AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10912			2.3	4.6E-01	-01 P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
10922		36850	10.22	4.8E-01	-01 BE185449.1	EST_HUMAN	L5-H10730-100500-075-g05 H10730 Homo saplens cDNA
10922	23602	36851	10.22	4.6E-01	4.6E-01 BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11450	23217	36449	5.32	4.6E-01	4.6E-01 AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11450	23217	36450	5.32	4.6E-01	-01 AF019369.1	Z	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12163	24645		1.77	4.6E-01	4.6E-01 D53316.1	EST HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03 5'
1904	14641	27350	1.43	4.5E-01	4.5E-01 AE001931.1	Z	Delnococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1904	14641	27361	1.43	4.5E-01	-01 AE001831.1	Z	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2873	15840	28284	4.5	4.5E-01	-01 AA677086.1	EST_HUMAN	zj55d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3312	16072	28722	4.58	4.5E-01	-01 Q05793	SWISSPROT	BASEMENT MEMBRANE.SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3372	16131	28787	1.07	4.5E-01	-01 AF126378.1	N	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4007	16753		0.95	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN
4055	16800	29431	0.88	4.5E-01	4.5E-01 AI708908.1	EST_HUMAN	as96e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4155	17887		4.25	4.5E-01	4.5E-01 AW873495.1	EST_HUMAN	ho60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
4890	17817	30236	1.1	4.5E-01	-01 BE963445.2	EST_HUMAN	601657225R1 NIH_MGC_67 Hamo sapiens cDNA clone IMAGE:3868023 3'
5461	18260	31151	1.49	4.5E-01	-01 AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c09 PT0012 Homo saplens cDNA
6510	19275		1.45	4.5E-01 Q00956	Q00956	SWISSPROT	COAT PROTEIN
7312	18995	33073	1.27	4.5E-01	-01 M37036.1	NT	Rat nucleolar proteins B23.1 and B23.2
7509	20180	33273	2.54	4.5E-01	4.5E-01 AI858849.1	EST HUMAN	wi32e02.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426818 3' similar to TR:Q92923 Q92923 SWIISNF COMPLEX 170 KDA SUBUNIT :
7621	1	33396	0.65	4.5E-01		SWISSPROT	DNA PRIMASE
8208	1		0.86	4.5E-01		Z	D.melanogaster Shaw2 protein mRNA, complete cds
8302	20996	34134	3.5	4.5E-01	4.5E-01 AI648596.1	EST_HUMAN	tz56g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
							POLY BETA HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYAI KANOATE) POLYMERASE) (PHB
8457		34292	0.83	4.5E-01	4.5E-01 Q52728	SWISSPROT	POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8680	21372		2.34	4.5E-01	11444786 NT	N	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA

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Probe SEQ ID NO: 0897 10392 10392 10392 10392 10392 10392 10392 12640 12640 12640 12692 13314 6602 5684 66146	Exon SEQ ID NO: 22491 22491 23038 23038 23038 23038 24880 15109 16070 16070 18137 18137 18651 18651 18651	ORF SEQ ID NO: 36254 36256 36299 36290 28719 28720 28720 28720 28720 31309 31591 31591 31594	Signal 0.86 0.86 0.86 0.86 0.86 0.86 0.86 0.86	Most Simi (Top) H (Top) H BLAST I was a 4.5E	It	Top Hit Detabase Source NT NT EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN NT NT EST_HUMAN NT EST_HUMAN	Top Hit Descriptor Escherichia cali K-12 MG1655 section 108 of 400 of the complete genome Bornbyx mori nuclear polyhedrosis vitus, complete genome EST02331 Felab brain, Stratagene (calif936206) Homo saplens cDNA clone HFBCY17 EST02331 Felab brain, Stratagene (calif936206) Homo saplens cDNA clone HFBCY17 EST02331 Felab brain, Stratagene (calif936206) Homo saplens cDNA clone HFBCY17 xo14h01.x1 NCI CGAP_LUS Home Saplens a DNA done IMAGE:2703895 3' similar to SW:INT6_MOUSE G044252 VIRAL INTEGRATION SITE PROTEIN INT-8, [1]; xo14h01.x1 NCI CGAP_Brain Staplens a DNA clone IMAGE:3852991 5' G044262 VIRAL INTEGRATION SITE PROTEIN INT-8, [1]; AV778382 GLC Homo saplens cDNA clone IMAGE:3852991 5' G004262 VIRAL INTEGRATION SITE PROTEIN INT-8, [1]; Homo saplens testle-specific kinase 2 (TESK2), mRNA VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR) Rattus nonregicus SynGAP-b mRNA, complete cds 7/361402.y1 NCI_CGAP_Brit Homo saplens cDNA clone IMAGE:3893795 5' G001237139F7 INI-I MGC 4Homo saplens cDNA clone IMAGE:3803195 5' HISTIDINE-RICH GLYCOPROTEIN PRECURSOR mucin [rats, Sprague-Dawley, suffur-dloxide-treated tracheal epithellum, mRNA Partial, 390 nti] AV774049 GLC Homo saplens cDNA clone GLCCSC12 5' G62711.x1 NCI_CGAP_Brit CAPP CAPP RECURSOR UNKNOWN PROTEIN; G62711.x1 NCI_CGAP_Brit CAPP RECURSOR UNKNOWN PROTEIN; xx27408 GLC Homo saplens cDNA clone IMAGE:1881125 3' similar to TR:C93168 G29168 UNKNOWN PROTEIN; xx27408 CL Homo saplens cDNA clone IMAGE:2885610 3' similar to TR:C085154 O96154 AX27408 CL HOMO SAPLADEHYDE REDUCTSEE: xx27408 XX INCI_CGAP_Brit Homo saplens cDNA clone IMAGE:2886510 3' similar to TR:C085154 O96154 AX27408 XX INCI_CGAP_Brit Homo saplens cDNA clone IMAGE:2886510 3' similar to TR:C085154 O96154 AX27408 XX INCI_CGAP_Brit Homo saplens cDNA clone IMAGE:2886510 3' similar to TR:C085154 O96154 AX27408 XX INCI_CGAP_Brit Homo saplens cDNA clone IMAGE:2886510 3' similar to the character of Homo saplens cDNA clone IMAGE:28865610 3' similar to the charac
6236			1.42		01 AA776132.1	EST_HUMAN	accounties of states of the second of the second second in the second of sec
7297	LL	33056	1.04		-01 AE000571.1	LN 1	Hellcobacter pylori 28895 section 49 of 134 of the complete genome
7740	20436		9.71	4.4E-01	01 AE001188.1 01 Z11679.1	LN LN	Treponema pallidum section 4 of 87 of the complete genome S.tuberosum mRNA for Induced stolon tip protein (partial)
8661		34500	0.84		-01 AA056427.1	EST_HUMAN	zl69a03.s1 Stratagene colon (#937204) Homo saplens cDNA clone IMAGE:509836 3'
9049	21738	34896	0.7	4.4E-01	01 AF112540.1	LN	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds

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			Γ	Γ	Γ		Γ	Γ				Γ	Γ	Γ	Γ		Γ			Γ			Γ		Γ		Γ		Γ	Γ	Γ	Γ	
	Top Hit Descriptor	hh05c08.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2854222 3' similar to SW:NSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6;	ZINC FINGER X-CHROMOSOMAL PROTEIN	qo39f09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR	beta -HKA=H,K-ATPase beta subunit [rats, Genomic, 8983 nt, segment 2 of 2]	beta -HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA	Autographa californica nucleopolyhedrovirus, complete genome	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)	RC2-CT0320-281199-012-c07 CT0320 Homo sapiens cDNA	Callithrix Jacchus MW/LW opsin gene, upstream flanking region	Callithrix Jacchus MW/LW opsin gene, upstream flanking region	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA	MR0-BN0070-270300-008-904 BN0070 Homo sapiens cDNA	Human somatostatin i gene and flanks	Callithrix Jacchus MW/LW opsin gene, upstream flanking region	Callithrix Jacchus MW/LW opsin gene, upstream flanking region	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA	Salmiri sciureus offactory receptor (SSC186) gene, partial cds	Coturnix coturnix Japonica Ifing gene	Equus caballus microsatellite LEX027	DNA GYRASE SUBUNIT B	602023134F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158296 5'	Mus musculus Dix-2 gene, complete cds	Methanococcus voltae flagella-related protein C-I (flaC-flal) genes, complete cds	Erwinia amylovora rcsV gene	hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE: 2968554 5'	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
פון ווסעם פופ	Top Hit Database Source	EST_HUMAN	SWISSPROT	EST_HUMAN	SWISSPROT	SWISSPROT	LΝ	۲	뒫	L	SWISSPROT	EST_HUMAN	Ę	님	EST_HUMAN	EST_HUMAN	F	Ŋ	٦	٦	SWISSPROT	SWISSPROT	EST_HUMAN	NT	LN	1N	SWISSPROT	EST_HUMAN	IN	ĹΝ	LN	EST_HUMAN	EST_HUMAN
5	Top Hit Acession No.	-01 AW612578.1	D62836	4.4E-01 AI268650.1	P28922	-35590	:-01 S76404.1	S76404.1	6677874 NT	9627742 NT	54725	4.4E-01 AW363338.1	4.3E-01 AF155218.1	4.3E-01 AF155218.1	4.3E-01 AW935269.1	4.3E-01 AW 999477.1	100306.1	:-01 AF155218.1	4.3E-01 AF155218.1	4.3E-01 AL161502.2	248634	⁵ 48634	4.3E-01 BE181655.1	4.3E-01 AF179825.1	4.3E-01 AJ001678.1	4.3E-01 AF075629.1	J33367	4.3E-01 BF348001.1	4.3E-01 U51002.1	J97040.1	714604.1	4.3E-01 AW630048.1	4.3E-01 AW630048.1
	Most Similar (Top) Hit BLAST E Value	4.4E-01	4.4E-01 O62836	4.4E-01	4.4E-01 P28922	4.4E-01 P35590	4.4E-01	4.4E-01 S76404.1	4.4E-01	4.4E-01	4.4E-01 P54725	4.4E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01 AF155218	4.3E-01	4.3E-01	4.3E-01 P48634	4.3E-01 P48634	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01 O33367	4.3E-01	4.3E-01	4.3E-01 U97040.1	4.3E-01 Y14604.1	4.3E-01 /	4.3E-01
	Expression Signal	0.57	1.24	2.19	1.88	4.31	1.33	1.33	3.44	3.35	1.91	1.43	2.17	2.17	1.64	0.75	1.29	1.18	1.18	1.19	0.8	0.8	1.59	2.02	4.78	9.0	0.91	1.88	0.61	2.72	96.0	2.18	2.18
	ORF SEQ ID NO:	34834	35025	35709			36132			31000			25835	25836		28466	29501	25835	25836		30742	30743	31515	31534	32384	32646			33260		35053	35468	35469
	Exon SEQ ID NO:	21771	21860	22512	22513	22645	22921	22921	24635	24903	24971	25152	13187	13187	15642	15822	16873	13187	13187	17629	18085	18085	18589	18606	19371	19606	19511	20011	20168	21019	21885	22279	22279
	Probe SEQ ID NO:	9082	9190	9862	9863	2666	10273	10273	12148	12579	12683	12766	402	402	2875	3056	4131	4374	4374	4902	9280	5280	5798	5817	8099	6899	6767	7328	7496	8326	9154	9626	9626

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טווקים באטו גווסספר באטו פאפר ווו סומווו	Top Hit Descriptor	xn63e05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400.3' similar to TR:000189 000189 MU-ADAPTIN-RELATED PROTEIN 2.;	yr45b05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208209 3'	Equus caballus microsatellite LEX027	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA	RG3-BN0034-290200-013-c12 BN0034 Homo saplens cDNA	t264d04.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2293351 3'	Steptomyces coelicolar whiH gene	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR	nz24a09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'	Xylella fastidiosa, section 93 of 229 of the complete genome	ql94b01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:18799453'	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498	SOX-8 PROTEIN	nj69h01.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clona IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);	yf77e01.r1 Soares Infant brain 1NIB Homo saplens cDNA clone IMAGE:28278 5'	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C047	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'	Brca1=breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47	EST369413 MAGE resequences, MAGE Homo sapiens cDNA	EST369413 MAGE resequences, MAGE Homo sapiens cDNA	Homo sapiens cytochrome c oxidase subunit Vic (COX6C), nuclear gene encoding mitochandrial protein, mRNA	295f01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4626493'	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cols	601660352R1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3906085 3'	RC-BT091-210199-142 BT091 Homo sapiens cDNA
שניין ווסאר פונ	Top Hit Database Source	EST_HUMAN	EST_HUMAN	PA FA	EST_HUMAN	EST_HUMAN F	EST_HUMAN t	N FN	П	EST_HUMAN r	NT \	EST_HUMAN o	Г	Г	EST_HUMAN	EST_HUMAN y	Г	L'HUMAN		r_HUMAN	T_HUMAN		NT TN		EST_HUMAN E		EST_HUMAN 2	- L	EST_HUMAN N	NT		EST_HUMAN F
	Top Hit Acesslon No.	-01 AW170559.1	E-01 H65292.1		4.3E-01 AW993658.1	4.3E-01 AW993658.1	4.3E-01 AI874332.1	2.1			,	-01 AI280338.1	V81203.1	:-01 Q04886	-01 AA534093.1	E-01 R13467.1		4.2E-01 AW854162.1	4.2E-01 AL163247.2		2.1			4.2E-01 AW957448.1	4W957448.1	4758039 NT	-01 AA705007.1			П	7	4.1E-01 Al905481.1
	Most Similar (Top) Hit BLAST E Value	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.3E-01	4.2E-01 Q39102	4.2E-01	4.2E-01	4.2E-01	4.2E-01 N81203.1	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.2E-01	4.1E-01
	Expression Signal	0.84	0.5	2.45	1.29	1.29	1.84	2.18	1.64	1.23	4,4	1,41	0.85	0.97	4.88	3.46	0.82	1.63	1.0.1	10.8	10.8	2.15	7	2.21	2.21	0.61	0.94	0.45	1.78	2.69	2.11	1.8
	ORF SEQ ID NO:	35990			37113	37114	37662		26761			29021		29352	30015	30100	31336	31408							33716	33932		35944				26488
	Exon SEQ ID NO:	22776	23055	.,	23833			25025		14676		18381	17886	16713	17383	17463					19552	_ l		20586	20586	20800		22729	23039	23648		13830
	Probe SEQ ID NO:	10128	10409	10849	11166	11166	11745	12770	1337	1941	3596	3628	3698	3964	4649	4731	5626	5693	6112	6852	6852	6911	6993	7891	7891	8106	9870	10081	10393	10972	11370	1072

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats	Porphyra purpurea mitochondrion, complete genome	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds	AV695974 GKC Hamo sapiens cDNA clone GKCBQC11 5'	AV702823 ADB Homo saplens cDNA clone ADBDBE08 5	Homo septens proteoglycan 3 (PRG3) gene, complete cds	HOMEOBOX PROTEIN HLX1	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA	Xylella fastidiosa, section 16 of 229 of the complete genome	Ceanorhabditis briggsae acetylcholinesterase (ace-1) gene, complete cds	Arabidopsis thaliana putative c-myb-like transcription factor (MYB3R-3) mRNA, complete ods	Mus musculus solute carrier family 1, member 6 (Slc1e6), mRNA	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)	Pleuronectes americanus aminopeptidase N (ampN) gene, partial cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2357855 3'	PM0-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA	Mus musculus general transcription factor II I (Gtt2), mRNA	Takitugu rubripes wnt2 (partial), frank1, cftr and frank2 (partial) genes	TRANSCRIPTION FACTOR SOX-10	prion protein [mink, Genomic, 2448 nt]	QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA	la54f11.X1 Soares_total_fatus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE;2047917 3' similar to	contains Alu repetitive element,	Arebidopsis thaliana DNA chromosome 4, contig fragment No. 25	M. musculus gene for kalilkrein-binding protein	Mouse liver receptor handlogous protein (LRH-1) mRNA, complete cds	Homo saplens mRNA for KIAA1631 protein, partial cds	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA	Homo sapiens chromosome 21 segment HS21C079	ye43h06.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element;contains PTR5 repetitive element;
gie Exon Pro	Top Hit Database Source	L'A	NT L	TN	EST_HUMAN	EST_HUMAN	IN	SWISSPROT	LN	IN	IN	ĹΝ	TN	NT	Ę	LN	N	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	SWISSPROT	NT	EST_HUMAN		EST HUMAN	۲	TN.	IN	NT	NT	N	EST_HUMAN
ug	Top Hit Acessian No.	3.9E-01 M19879.1	11465620 NT	D86722.1	3.9E-01 AV695974.1	AV702623.1	AF304354.1	Q61670	11433335 NT	3.8E-01 7019488 NT	AE003870.1	U41846.1	AF214117.1	6678002 NT	3.8E-01 AJ251057.1	AF043383.1	AL161518.2	AI807219.1	AI807219.1	BE154080.1	3.8E-01 6754095 NT	3.8E-01 AJ271361.2			BE072399.1		AI374601.1	3.8E-01 AL161513.2	3.8E-01 X61597.1	M81385.1	AB046851.1	3.8E-01 11441264 NT	AL163279.2	3.8E-01 T95413.1
	Most Similar (Top) Hit BLAST E Value	3.9E-01	3.9E-01	3.9E-01	3.9E-01	3.9E-01	3.9E-01	3.9E-01 Q61670	3.9E-01	3.85-01	3.8E-01	3.8E-01	3.8E-01	3.8E-01	3.8E-01	.3.8E-01	3.8E-01	3.85-01	3.8E-01	3.8E-01	3.85-01	3.8E-01	3.8E-01	3.8E-01	3.8E-01	ļ	3.8E-01	3.8E-01	3.8E-01	3.8E-01	3.8E-01	3.85-01	3.8E-01	3.8E-01
	Expression Signal	3.03	0.58	0.77	1.98	1.47	3.37	2.08	1.44	8.33	1.03	1.29	1.62	3.96	1.14	1.39	7.98	0.79	1.22	1.15	0.97	0.74	1.42	0.74	5.5		4.58	1.25	4.42	0.86	2.04	1.02	1.28	3.55
	ORF SEQ ID NO;	35635		35932		37674		_						28092		28456	28887			29127	29287	29418	31221		32298		32614	32527		34028	34289	34358	34551	
	SEQ ID	22429	22496	22714	23410	24344	25295	24581	24891	12971	14801	15178	15290	15601	15769	15809	16233	16283	16283	16492	16647	16788	18320	19021	19294		19579	19502	20093	20890	21147	,21215	21408	22011
	Probe SEQ (D NO:	9778	9845	10068	10722	11763	11948	12066	12559	156	1863	2460	2576	2638	3003	3043	3477	3527	3541	3738	3897	4043	5522	8247	6528		6662	6840	7416	8186	8455	8523	8716	9461

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Single Exoli Plobes Expleased in Dialii	Top Hit Descriptor	AV755814 BM Homo saplens cDNA clone BMFBCE07 5'	RC0-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA	y/92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'	yf92h11.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'	Borrella burgdorferi (section 10 of 70) of the complete genome	Human p53 (TP53) gene, complete cds	QV3-ET0063-190700-271-e05 ET0063 Homo sapiens cDNA	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds	Mus musculus developmental control protein mRNA, partial cds	Homo sapiens mRNA for KIAA1410 protein, partial cds	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds	ok39c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:1510188 3'	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA	Neisserla meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome	Homo sapiens Interferon-Induced protein p78 (MX1) gene, complete cds	Homo sapiens chromosome 21 segment HS21C078	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds	Mus saxicola haptoglobin mRNA, complete cds	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA	ya50a07.r3 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66324 5'	hd45d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912457 3' similar to contains Alu	Important of management of productions and the second of t	one saprats circulosonia is cheri reading italia + (CIZO); + 1, mixit	Homo sapiens chromosome 12 open reading frame 4 (C12OKF4), mKNA	ok43b11.s1 NCI_CGAP_Lei2 Homo sapiens cDNA clone IMAGE:1516701 3'	Gailus gallus mRNA for beta-carotene 15,15-dioxygenase (bCDO gene)	mouse ig germline alpha membrane exons region	qt48b07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997.31	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)	HUM230A06B Human aorta polyA+ (TFujiwara) Homo sapiens cDNA cione GEN-230A06 5'
III EXOII LIODE	Top Hit Database Source	Г	EST_HUMAN F	EST_HUMAN y			ΤN	EST_HUMAN (J LN		EST_HUMAN N		ΝŢ			IN.		EST_HUMAN \	14074161	NEWDE			T_HUMAN			EST_HUMAN of	NT FN				EST HUMAN
Billo	Top Hit Acession No.	-01 AV755814.1	3.8E-01 BE719219.1			3.8E-01 AE001124.1						3.7E-01 AB037831.1			-01 AW878037.1			2			11525843 NT			3.7E-01 AW0113Z0.1 ES	1450738	6739					3.7E-01 X05958.1				
	Most Similar (Top) Hit BLAST E Value	3.8E-01	3.8E-01	3,8E-01 R42550.1	3.8E-01 F	3.8E-01	3.8E-01	3.8E-01	3.8E-01 (L	3.8E-01	3.8E-01	3.7E-01	3.7E-01 /	3.7E-01	3.7E-01	3.7E-01 /	3.7E-01	3,7E-01	3.7E-01	3.7E-01 L10353.1	3.7E-01	3.7E-01	1	3.7E-01.	9.70	3.7E-01	3.7E-01 /	3.7E-01	3.7E-01 K00691.1	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01	3.7E-01 D79348.1
	Expression Signal	1.67	3.18	2.27	2.27	4.76	2.08	3.39	1.54	1.74	1.51	12.24	9.64	7.39	1.3	2.55	1.15	6.0	99.0	0.72	3.23	9'0		0.50	70.7	2.07	0.65	1.31	9.0	4,12	1.98	2.81	2.81	2.75	1.43
	ORF SEQ ID NO:			37610							99608							31588				33463			aco+c		34096					36882			37593
	Exen SEQ ID NO:	23386	24121	24288	24288		25316	24779	74884		25040			16945	17025		18470	_	19185	19204	19734	20349		\perp				21789	Ш		L	23633		23210	i i
	Probe SEQ ID NO:	10695	11521	11693	11693	12149	12270	12384	12723	12771	12788	2486	3453	4204	4286	4357	5676	5860	6417	6436	7043	7685		BL//	1770	8227	8263	9101	10069	10110	10764	10957	10957	11443	11676

PCT/US01/00667

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Single Exon Propes Expressed in Brain	Most Similar (Top) Hit Acession (Top) Hit Descriptor Signal BLASTE No. Source Source	362 2.87 3.7E-01 6677678 NT Mus musculus retinoblastoma 1 (Rb1), mRNA	2.11	3.09 3.7E-01 AJ243525.1 NT Chlamydophlle psittaci partial omp1 gene for outer membrane protein 1	1.9 3.7E-01 AL121154.1	30995 4.03 3.7E-01 Y18000.1	3062 25701 3.0E-01 AJ009609.1 NT Brassica napus mRNA for MAP4K alpha2 protein	8.22 3.6E-01 U89241.1 NT	26713 3.83 3.6E-01 T80255.1	26714 3.83 3.6E-01 T80255.1 [EST_HUMAN	27356 6.73 3.6E-01 AW 590184.1	27357 6.73 3.6E-01 AW 590184.1 EST_HUMAN	27393 5.7 3.6E-01 AF216207.1	780 1.39 3.6E-01 AF056927.1 INT Rattus norvegious repeat element associated with the Rasgrf1 gene	1.05 3.6E-01 AB002321.1 NT	2.69 3.6E-01 X76725.1 NT	27936 1.23	27937 1.23 3.6E-01[L05435.1 NT		PROTEIN-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE	28090 1.44 3.6E-01 P24206 SWISSPROT	7.16 3.6E-01 AF199485.1	28871 2.16 3.6E-01/X76758.1 NT	28872 2.16 3.6E-01 X76758.1 NT	29745 1.3 3.6E-01 BE707883.1	30285 2.38 3.6E-01 AW339393.1	30762 0.82 3.6E-01 A.1006565.1 (NT	31738 0.85 3.6E-01 P16431 SWISSPROT	32154 1.74 3.6E-01 Y10196.1 NT	3.2	32943 1.9 3.6E-01 AW027174.1	317 33953 0.58 3.6E-01 P98167 SWISSPROT SCO-SPONDIN
	ORF SEQ ID NO:					30995	25701		26713	26714	27356	27357	27393				27936	27937	27950		28090		28871	28872	29745	30285	30762	31738	32154		32943	33953
	SEON NO:	24362	24943	24558		24886		13740	14040		14646	14648	14679				15197	15197	15208		15348	17884	16218	16218	17112	17675	18103			19739	19869	20817
	Probe SEQ ID NO:	11771	11869	12033	12488	12548	25	975	1291	1291	1909	1909	1944	2047	2267	2389	2479	2478	2491		2636	2900	3462	3462	4375	4948	6298	9669	6386	7048	7183	8123

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Probe SEQ ID NO:	Exon SEQ (D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8177	20871	34005	11.45		3.6E-01 AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8900	21591	34731	2.74	3.6E-01	4504956 NT	LN	Homo sapiens lysosomai-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8900	21591	34732	2.74	3.6E-01	4504956 NT	LN	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9091			1.17	3.6E-01	1.2	IN	Homo sapiens chromosome 21 segment HS21C004
6536	21986	35139	1.04	3.6E-01	-01 X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9299	21966		1.04	3.6E-01	01 X17550.1	IN	D. melanogasfer singed gene, exons 3, 4, 5 & 6
9369	21944		0.57	3.6E-01		NT	C.perfringens pic gene for phospholipase C upstream region containing bent DNA fragment
9763	22414			3.6E-01	ପୀ ଭ 53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
9893				3.6E-01		EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
9893	22543	35736	0.51	3.6E-01	01 AW 752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo saplens cDNA
10864	23544			3.6E-01	01 BE902390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
11052		36993	4.12	3.6E-01	01 AB004293.1	N	Arabidopsis thaliana mRNA for SigB, complete cds
							Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete
11421		36419	3.4	3.6E-01	3.1	ΡΉ	делоте
11903			1.83	3.6E-01		뒫	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
11978			1.4	3.6E-01	01 D90901.1	M	Synechocystls sp. PCC6803 complete gename, 3/27, 271600-402289
11987	24528		3.89	3.6E-01	-01 AE000335.1	Z	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12135	L		4	3.6E-01	-01 U66888.1	LN L	Mus musculus Emr1 mRNA, complete cds
12403	24850		2 12	10-38 E	11432508 NT	FZ	Homo sapiens myslold/lymphold or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AE10) mRNA
	L						x60e11.x1 NC) CGAP Pan1 Homo septens cDNA clone IMAGE 2679/16 3' similar to db:K00558 TUBUL IN
12746	25363		2.23	3.6E-01	-01 AW190229.1	EST_HUMAN	ALPHA-1 CHAIN (HUMAN);
204	13017	25657	2.05	3.5E	6678933 NT	N.	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
708	L				7706136 NT	Ň	Homo sapiens GAP-like protein (LOC51306), mRNA
708	L	26132		L	7706136 NT	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
762	13535			3.5E	-01 BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1615		27053	1.1	3.5E-01	-01 BF310688.1	EST_HUMAN	601894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1636	14382	27069	1.96	3.5E	Ψ,	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2281	15006	27747	1.35	3.5E	-01 P06798	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2612	15600	28066	1.76	3.5E	-01 AA223252.1	EST_HUMAN	zr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872.3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3785	16537		98.0	3.5E-	01 AA642138.1	EST_HUMAN	nr60d03.s1 NCi_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4231	16972	29596			3.5E-01 AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
4443	1		0.94		BE146585.1	EST_HUMAN	RC5-HT0218-181099-011-g02 HT0218 Homo sepiens cDNA
4627	17362		1.02		3.5E-01 Y18477.1	NT	Mus musculus Alox12B gene 5' flanking region
4880			4.58	L	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5251		30982	92'0		01 Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5251			92'0	-39.€	01 Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5462		31152	1.13	3.5E-	01 D42045.1	NT	Human mRNA for KIAA0086 gene, complete cds
6143	18921		96'0	3.5E-	01 AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-e11 SN0012 Homo sapiens cDNA
6314	19085	32070	9.0	3.5E-	01 AA431833.1	EST_HUMAN	zw79f03.r1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:782429 5' similar to TR:G1066935 G1066935 F10F2.1;
6369	19129		0.66	3.5E-	01 U37150.1	FN	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
9999	19331	32338	1.08		01 024357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
9269	19438		4.24	3.5E-	01 X98505.1	NT	S.scrofa mRNA for CD31 protein (PECAM-1)
7441	20118	33207			P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7441			0.55	3.5E	-01 P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINETRNA LIGASE) (HISRS)
7970			2.19		11448042 NT	LN	Homo sapiens fumor protein p53-binding protein, 2 (TP53BP2), mRNA
7973		33790		3.5E-	01 BF358871.1	EST_HUMAN	RC4-ET0024-260600-014-407 ET0024 Homo saplens cDNA
8366	21059		69.0	3.5E-	01 AF051561.1	TN	Rattus norvegicus Ne-K-Cl cotransporter (Nkcc1) mRNA, complete cds
8825	21517	34662	1.17		4507610 NT	N	Homo sapiens tyrosine kinase non-receceptor 1 (TNK1), mRNA
9836	22288	35481	1.52	3.5E-	01 002294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-18 SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
9786	1		5.64	3.5E		Ŋ	X.laevis gene for albumin including HP1 enhancer
2986	22517	35713	96.0	3,5E	01 BE174794.1	T_HUMAN	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
10635	23327		2.76	39.€	01 X61084.1	ΙN	C.griseus rhodopsin gene for opsin protein
10946	23625			3.5E-	01 AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
10946	23625	36878	2,39	3.5E-	01 AJ243178.1	M	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11505	24108		1,34	3.5E-	01 U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
11585		37499		3.5E~	01 N77597.1	EST_HUMAN	yz90h12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:290375 5'
11619			1.71	3.5E-01	01 M82885.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
11684	24279	37601	1.51	3.5E-01	01 L05145.1	NT	Human glucokinase (GCK) gane, repeat polymorphism
11776			1.36	3.5E-	01 AI064773.1	EST_HUMAN	HA0542 Human fetal liver cDNA library Homo sapiens cDNA
12063	24578		1.47	3.5E-	01 X64565.1	N	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
12214	- 1		2:32	3.5E-	01 AE001774.1	K	Thermotoga martima section 86 of 136 of the complete genome

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Top Hit Descriptor	Thermotoga maritima section 3 of 136 of the complete genome	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'	Homo sepiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes Isolated from IC4 cervical carcinoma cell line	Pseudomonas fluorescens colR, colS genes, orf222 and partial inaA gene	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)	Synechocystis sp. PCC6803 complete gename, 11/27, 1311235-1430418	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens chromosome 21 segment HS21C010	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418	Canis familiaris rod photorecentor cCAMP ceted channel slubs action in CAND CALL and CAND CALL and CAND CALL CALL CALL CALL CAND CALL CALL CALL CALL CALL CALL CALL CAL	Homo sapiens pulmonary surfactant protein D. promoter region and exon 1	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds	7n94e01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone !MAGE:3572232 3' similar to TR:Q9UJ15 Q9UJ15 DJ1803.1	no/1b10.s1 NCI_CGAP_Phet Home sepiens cDNA clone IMAGE-110n347.31	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA	ql95c05.x1 NCI_CGAP_Kid3 Hamo sapiens cDNA clone IMAGE:1867208.3' similar to contains Alu repetitive element;	Homo sapiens serotonin transporter (hSERT) gene, promoter rection, exons 1B and 2, and partial cds	Arabidopsis thaliana DNA chromosome 4. contic fragment No. 90	zn12d11.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'	Echovirus 22 14B, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D ordelins RNA, complete mature pentities and cds	601571811T1 NIH MGC 55 Homo sapiens cDNA clone IMAGE:3838826 3	UI-H-BI1-aei-e-12-0-UI.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:27195823'	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5	2b53e12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342.3'
Top Hit Database Source	NT	EST_HUMAN	EST_HUMAN	L Z	NT	L	NT	N	N	NT	۱	NT	F	EST HUMAN	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	LN FN	Ϋ́	EST_HUMAN	Į.	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	3.5E-01 AE001691.1	H80814.1	H80814.1	3.4E-01 AJ242956.1	3.4E-01 Y09798.2	3.4E-01 Y00554.1	3.4E-01 D90909.1	3.4E-01 AL163210.2	3.4E-01 AL163210.2	3.4E-01 D90909.1	3.4E-01 IU83905.1	3.4E-01 AF034862.1	3.4E-01 AF106835.1	3.4E-01 BF449010 1	3.4E-01 AA584198,1	AF166341.1	3.4E-01 BE069912.1	-01 A[240973.1	U79746.1	-01 AL161594.2	3.4E-01 AA085313.1	-02971.1	-01 BE748912.1	-01 AW 204505.1	3.4E-01 AL120544.1	195225.1
Most Similar (Top) Hit BLAST E Value	3.5E-01	3.5E-01	3.5E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.45-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01	3.4E-01 L02971.1	3.4E-01	3.4E-01	3.4E-01	3.4E-01
Expression Signal	1.4	3.33	3.33	1.85	7.61	1.72	2.62	0.85	0.85	1.08	6.23	6.0	3.48	97.	238	0.82	1.54	3.23	86.0	2.62	60.9	1.99	0.89	2.43	1.81	1.56
ORF SEQ ID NO:			30724		26386	26725	27858	28416	28416	28555	28568	28749	28933			29823	29963			31304			31681	31759	31889	
Exon SEQ ID NO:	LI		25269	13466	13720		Ì	16767	Ì	15910	16922	(16278	16622	16774	17196	17334	17625	17862	18394	18513	18702	18722	18798	18919	19406
Probe SEQ ID NO:	12402	12793	12793	691	955	1303	2400	3001	3001	3146	3159	3338	3522	3770	4029	4460	4599	4898	5143	5599	5721	5917	5940	6017	6141	6644

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Mark Charles	-0[-0[\ 	
Exon ORF SEQ Expression ('Signal B NO:		§ _ w		Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
19548 32578 1.02			3.4E-01	-01 AI468082.1	EST_HUMAN	tm63g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
32456 0.59	0.59	ı	3.4E-01	BF678702.1	EST_HUMAN	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
0.49			3.4E-01	· 3.4E-01 AE000483.1	NT	Escherichia coli K-12 MG1656 section 383 of 400 of the complete genome
20829 33964 0.6			3.4E-01	3.4E-01 Y14930.1	TN	Homo saplens TCRAV28 gene, allele A4, partial
	2, 0		r,	7 4 400 4 4	144	7n94e01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3672232 3' similar to TR:Q9UJ15
21079 1.51	1.51		3.4E-01	-01 BF449010.1	EST HUMAN	CSUSTO DO 1909.1.1, EST41765 Endometrial tumor Home saplens cDNA 5' end
34296			3.4E-01	3.4E-01 L04690.1	TN	Cricefulus griseus cholesterol 7-aipha-hydroxylase gene, complete cds
21443 34590 1.7			3.4E-01	9633624 NT	N	Bovine enterovírus strain K2577, complete genome
			3.4E-01		SWISSPROT	INTEGRIN BETA-8 PRECURSOR
34965			3.4E-01		SWISSPROT	INTEGRIN BETA-8 PRECURSOR
			3.4E-01	-01 AB017510.1	NT	Ephydatia fluviatilis mRNA for PLC-gammaS, complete cds
33636			3.4E-01	-01 U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
33537	7		3.4E-01	3.4E-01 U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
			3.4E-01	-01 AF193857.1	NT	Dictyostellum discoldeum putative CMF receptor CMFR1 mRNA, complete cds
35433			3.4E-01	-01 U68763.1	NT	Glycine max putative transcription factor SCOF-1 (scof-1) mRNA, complete cds
35648			3.4E-01	-01 AJ225084.1	TN	Homo sapiens FAA gene, exon 16, 17 and 18
23022 0.62	0.62		3.4E-01	-01 AE004096.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
23620 4.72	4.72		3.4E-01	AE000881.1	LN	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (saction 87 of 148) of the complete genome
36912			3.4E-01	-01 P06925	SWISSPROT	PROBABLE E4 PROTEIN
23703 36971 2.17	2.17		3.4E-01	-01 AF045981.1	ž	Rutilus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
			3.4E-01	3.4E-01 M25856.1	TN	Human von Willebrand factor gene, exons 38 and 37
			3.4E-01	M25856.1	· TN	Human von Willebrand factor gene, exons 36 and 37
	1.88		3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-gicerin/MUC18, complete cds
24113 37423 3.65			3.4E-01	-01 AL161515.2	ΙΝ	Arabidopsis thallana DNA chromosome 4, contig fragment No. 27
			3.4E-01	01 BF061948.1	EST_HUMAN	7k69d12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480646 3'
37786			3.4E-01	01 (007000.1	NT ·	Human breakpoint cluster region (BCR) gene, complete cds
24455 1.85	1.85			01 U93604.1	NT	Oltrus variegation virus putative replicase gene, partial cds
24666 11.43	11.43		3.4E-01	01 1.26339.1	NT	Human autoantigen mRNA, complete cds
25192	1.61		3.4E-01	3.4E-01 BE218652.1	EST_HUMAN	hv42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127.3' similar to contains PTR6.t3 PTR5 repetitive element ;
		١				

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	Top Hit Database Source	Beta wilgaris mitochondrion, complete genome		Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-							SWISSPROT PROLINE-RICH PROTEIN LAS17				Mus musculus disintegrin 5 (Dtgn5), mRNA	HUMAN	NT Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds					ISSPROT	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT	DY LOS			Tripozyon negation e Unit syntastes gene, part al cos Rathis nomegicus DMA for roquesiais poste part al cos		POST 12:01 NOT_CONF TO DO DO DO SEPTENS CONA CIONE IMPORTIZZOSAU / 3 SIMILATIO 90:X67522 ANTIGEN EST HUMAN PEPTIDE TRANSPORTER 1 (HUMAN)		EST_HUMAN QV0-DT0047-170200-123-h08 DT0047 Homo sapiens cDNA		
)	Top Hit Acession No.	P838361 NT	-01 AJ297131.1 NT			-01 AF019413.1 NT	-01 X07990.1	-01 X07990.1	-01 AL161545,2 NT	7662485 NT	-01 Q12446 S	-01 BF568880.1 E		-01 U43626.1 NT	6753685 NT	01 AA332734.1 E	01 AF031148.1 N	4507834 NT	01 AJ251805.1	01 AJ007932.2 NT				-01 25002 -01 4757739 NT	8.2	Ī	01 D31662 1 NT		01 A1539114.1	01 D64003.1	01 AW937982.1 E		01 X89819.1
	Most Similar (Top) Hit BLAST E Value	3.4E-01	3.4E-01		į.	3.4E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01	3.3E-01		3.3E-01	3.3E-01	3.3E-01/	3.3E-01	3.35-01	3.3E-01/	3.3E-01/	3.3E-01	3.3E-01	2 200.04	3.35.01	3.3E-01	3.3F-01.4	3.3F-01		3.35-01	3.3E-01 [3.3E-01 ₽	3.3E-01	3.3E-01
	Expression Signal	2.28	2.2			1.82	10.77	4.4	6.0	2.01	2.85	3.76		1.2	1.47	1.02	1.01	4.62	1.87	1.48	1.07	2.1	0.07	103	1.47	1 79	1		1.23	1.22	96.0	2.61	2.61
	ORF SEQ ID NO:		31036						25867	26032	26597	26705			27036				28368	28482	28899	29176	20183	29323	29336	29365	-	-	-	30139		30675	30676
	Exon SEQ ID NO:	26292	_			ı	_[13397		14034		- 1	14347		14757	15125	15715	15817	16243	16541	16551	16682	16697	16731	17073		17375	17517	17865	18047	18047
	Probe SEQ ID NO:	12280	12391			12688	13	103	435	618	1178	1284	000	25	- 193	1731	2022	2404	2949	3051	3486	3789	3790	3932	3947	3983	4334		4641	4786	5146	5241	5241

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Table 4
Single Exon Probes Expressed in Brain

						3	
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top.Hit Database Source	Top Hit Descriptor
5700	18494		0.74	3.3E-4	01 BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
9289			1.9	3.3E-(01 BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo saplens cDNA clone IMAGE:3875753 3'
5856	18643		1.9	3.3E-(11 BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876753 3'
5947		31688	1.18	3.3E-(01 P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
9699	19612		0.71	3.3E-01	01 AB034233.1	NT	Flexibacter litoralls gyrB gene for DNA gyrase B subunit, partial cds
5699			0.71	3.3E-01	01 AB034233.1	NT	Flexibacter litoralis gyrB gene for DNA gyrase B subunit, partial cds
6790	40823	32560	CB 1/		2 3E 04 A IS 28 13 1 4	ECT LIMANI	ty84h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu
80/0		.			1.10.00	בייייייייייייייייייייייייייייייייייייי	heathn vi NCI CGAD Kidit Home seniers of NA Chae IMAGE: 2285809 3' similar to contains Atu
6289	19533	32561	4.82		3.3E-01 AI628131.1	EST_HUMAN	repetitive element; contains element L1 repetitive element;
7682	20346	33458	1.68	3.3E-	01 N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8460		L		3.3E-(01 BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8659		L		3.3E+	01 AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
8659	21351		0.48	3.3E-(21 AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
0700				0	200000	TOGGOOM	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 1 (MAPKIERK KINASE KINASE 1) (MEK KINASE 4) ALEKK 4)
87.69	1	35203	0.0	3.3F-01	11 RER28461 1	EST HIMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sepiens cDNA
0220	22022	L		3 35 04	14 BE 928484 4	EST HIMAN	CM2-FT0041-180500-187-410 ET0041 Homo caniens cDNA
9411				3.35-4	01 N69866.1	EST HUMAN	za67h01.s1 Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:297649 3'
9452				3.3E-(01 BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
9891			2.27	3.3E-01	01 1.41044.1	NT	Homo sapiens high-mobility group phosphoprotain (HMGI-C) gene, exons 1-3, complete cds
10622	23315	36554		3.3E⊣	01 X63953.1	NT	D.mauntiana Adh gene
10622	23315		3.13	3.3E-(01 X63953.1	NT	D.mauntiana Adh gene
10951	23628		1.7)-36.6	01 BF526499.1	EST_HUMAN	602070802F1 NCI_CGAP_Brn64 Homo saplens cDNA clone IMAGE:4213585 5'
11196	23861	37147	11.61	3.3E-01	01 BE219351.1	EST_HUMAN	hv51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
							GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD
11317	24008	37313	3,23			SWISSPROT	
11719				3.3E-	3.3E-01 AA806621.1	EST_HUMAN	ob71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
11741	12840	25453		3.3E-		NT	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene
11977	24621		1.71	3.3E-01	6598319 NT	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12676			3.34	3.3E-(11 AP000002.1	ᅜ	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (277)
444	13230		2.33	3.2E-	01 AF018261.1	전	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds

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Single Exon Probes Expressed in Brain	ORF SEQ Expression (Top) Hit Descriptor Signal BLASTE No. Source Source	1.43	26555 27.53 3.2E-01 AF047013.1 NT	26677 1.36 3.2E-01 Z50202.1 NT	26792 5.42 3.2E-01 Q48624 SWISSPROT	27210 1.25 3.2E-01 Z36041.1 NT	27222) 4.7 3.2E-01 AW957194.1 EST_HUMAN	27223 4.7 3.2E-01 AW957194.1 EST_HUMAN	27286 1.23 3.2E-01/AL111655.1 NT	27621 2.52 3.2E-01 BF203817.1 EST_HUMAN	2.01 3.2E-01 7710079 NT	28159 1.08 3.2E-01 AF060568.1 NT	0.77 3.2E-01[D10872.1 NT	29669 0.91 3.2E-01 4759195 NT	200000	29/30 1.32 3.2E-01 M18818.1 NT	29826 1.21 3.2E-01 Q10268 SWISSPROT	6.7 3.2E-01 BF693617.1 EST_HUMAN	30179 1.17 3.2E-01 Q57081 SWISSPROT	30299 0.74 3.2E-01 BE782748.1 EST HUMAN	30621 3.26 3.2E-01 BE173964.1 EST HUMAN	31596 1.07 3.2E-01 L27221.1 NT	31963 0.9 3.2E-01 AF016494.1 NT	32268 0.64 3.2E-01 AV718037.1 EST HUMAN	1.09 3.2E-01 AB002359.1 NT	33575 0.51 3.2E-01 AJ277661.1 NT	33895 1.48 3.2E-01 M60266.1 NT	33990 0.45 3.2E-01 AJ231001.1 NT	34098 14.41 3.2E-01 X02508.1 NT	34103 13.76 3.2E-01 BF311635.1 EST_HUMAN	1.38 3.2E-01 AL161574.2 NT
			26555	26677	26792	27210	27222	27223	27286	27621		28159		29669	. 80700	28730	29826		30179	30299	30621	31596	31963	32268		33575	33895	33990	34098	34103	
	Exon SEQ ID NO:	13476	13894	14008				ı			15257		16347	17044	77707		_1	17422	17557			18655	18986		ı			20858	20959	1	21054
	Probe SEQ ID NO:	701	1139	1259	1369	1767	1777	1777	1835	2157	2543	2713	3594	4305	4383	202	4464	4688	4826	4965	5190	5868	6211	6501	6634	7755	8072	8164	8265	8268	8361

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									13 Jd	nd 13										r to												
Single Exoli Plones Expressed in plain	Top Hit Descriptor	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'	Delhococcus radiodurans R1 section 152 of 229 of the complete chromosome 1	Oryctolagus cuniculus ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds	Homo saplens chromosome 21 segment HS21C004	Human monocyte antigen CD14 (CD14) mRNA, complete cds	Homo saplens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13	Homo saplens 8-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13	Borrella burgdorfert plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes	hv99f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'	Homo sapiens gene for AF-6, complete cds	EST04702 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDZ21	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds	801507820F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909532 5'	ELONGATION FACTOR TU (EF-TU)	Homo sapiens deoxycytidylate deaminase gene, complete cds	601275480F1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:3616746 5'	ye30h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to pay the promein /Himany.	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA	Homo sepiens KIAA0174 gene product (KIAA0174), mRNA	hi48h08.x1 Sogres_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2975391 3'	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 8	Daucus carota mRNA for transcription factor E2F (E2F gene)	Хуюlla fastidiosa, section 130 of 229 of the complete genome	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1	HYPOTHETICAL PROTEIN HI1236	S.cerevisiae chromosome XV reading frame ORF YOL141w	Mus musculus mRNA for polycystin	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22	yq41f04.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:198387 5'
JIE EXOII PIO	Top Hit Database Source	EST_HUMAN	EST_HUMAN	ΤN	TN	NT	LN	NT	TN	TN	Į.	EST_HUMAN	IN	EST_HUMAN	NT	EST_HUMAN	SWISSPROT	IN	EST_HUMAN	MAN ID FOR	7661971 NT	N-	EST_HUMAN	NT	NT	L	NT	SWISSPROT	NT	Ŋ	Ŋ	EST_HUMAN
3110	Top Hit Acession No.	-01 BF246771.1	-01 BF246771.1	-01 AE002015.1		-01 U51026.1	.2	-01 M86511.1	-01 AF041829.1	-01 AF041829.1			-01 AB011399.1		-01 L07288.1	-01 BE886846.1	-01 083217	-01 L39874.1	6.1	040064.4	-01 7661971	7661971 NT	-01 AW629036.1	-01 AB029069.1	-01 AJ251586.1	-01 AE003984.1	-01 AF176111.1					3.1E-01 R94322.1
	Most Similar (Top) Hit BLAST E Value	3.2E-01	3.25-01	3.2E-01	3.2E-01	3.2€-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	3.2E-01	20 11 20	3.15-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01
	Expression Signal	1.24	1.24	2.65	0.84	0.84	0.51	2.18	0.65	0.65	3.33	0.45	3.41	3.94	3.91	1.44	4.21	2.07	1.75	c	3.39	3.39	1.29	3.35	9.0	0.73	9.73	6.73	0.67	0.88	2.11	0.59
	ORF SEQ ID NO:	34228	34227	34306	34401	34402	34807		34894	34895	35737	35962		36498					30606	2,00	28145	28146			29276	30250	30882	31212	31213		31396	31942
	Exan SEQ (D NO:	21091	21091	21163	21263	21263	21656	21666	21737	21737	22544	22747	22858	23261	25317	25374	24871	24955	25354	}	15532	1	15630	16933	16637	17636	18190	18311	18312	l		25087
	Probe SEQ ID NO:	8388	8338	8471	8571	8571	8965	8976	9048	9048	9894	10099	10210	10566	12010	12392	12524	12655	12712	100	2702	2702	2862	3170	3887	4908	5390	5513	6514	5524	9899	6191

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	Т	Т	Т	T	Т	Т	Т	Т	Т	Т	75	Т	Т	\top	7	7	Г	$\overline{}$		Г	Г	Т	Т	Т	Τ,	T	Т	\top	_	Т
Top Hit Descriptor	RC3-HN0001-310300-011-b04 HN0001 Homo saniens cDNA	q39d01.x1 NCI CGAP Cos Homo septems cDNA clone IMAGE-1874680 31	H.saplens gene for Immunoglobulin kappa light chain variable region A8 and A9	601306121F1 NIH MGC 39 Homo saplens cDNA clone IMAGE:3640420 51	Homo saplens hyaluronan synthase 2 (HAS2) mRNA	V46f01.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE 34620.3	Mus musculus phosphattdvinosital 4-phosphate 5-kinase, two 1 gamma (Pinskin) mRNA	802124743F1 NIH MGC 56 Homo saplens cDNA clone IMAGE 4281611 5	602124743F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4281611 5	qistett.xt NCI_CGAP_Kld3 Homo saplens cDNA clone INAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAAN):	9647h08.st Stratagene fetal spleen (#937205) Homo saplens cDNA clond (#180705) similar to similar t	SOURSESSOR MIN MOD ST HOMO CONTINUED CAMININA-6 CHAINS (HOMAN)	Homo saplens KIAA0764 dene product (KIAA0764) mRNA	Anolis opalinus Isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene	in minor indicates product	Suzzostalion videum 405 noosoma protein 511 mRNA, partial cds	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaphophysin genes,	complete cds; and L-type calcium channel a>	Mus musculus peptidoglycan recognition protein-like (Pglyrpl-pending), mRNA	Mus musculus protein kinase C, epsilon (Pkce), mRNA	Homo sapiens Xq pseudoautosomal region; segment 1/2	xs63f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'	Balaenoptera physalus gene encoding atrial natriuretic peptide	Raftus norvegicus Ca2+/calmodulih-dependent protein kinase II. alpha subunit mRNA 3' untranslatad radion	Corynebacterium sp. ALY-1 alvPG gene for polyculuronate hase, complete cds	PM1-ST0262-261199-001-901 ST0262 Homo sapiens cDNA	Balaenoptera physalus gene encoding atrial natriuretic peptide	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'	Cantadalo orthopoxifus hemacalutinin dene complete cds
Top Hit Database Source	EST HUMAN	EST HUMAN		EST HUMAN	NT	EST HUMAN	NT	EST_HUMAN	EST HUMAN	EST HUMAN	MANIET TOE	EST HIMAN	L	Ė	111		L		L	LN	۲	NT	EST_HUMAN	NT	N	LN	EST_HUMAN	F	T_HUMAN	Į.
Top Hit Acession No.	-01 AW983549.1	-01 AI264458.1	-01 X71887.1	-01 BE737392.1	4885390 NT	-01 R45318.1	6679322 NT	-01 BF696639.1	-01 BF696639.1	-01 AI244001.1	04 755825 4	3F246447 4	-01 7662291 NT	04 4 5 5 0 4 3 0 0 4	04 05204604	T4050504	-U1 AF-195953.1		-01 AF196779.1	10946623 NT	55083		01 AW300400.1	01 AJ006755.1		Γ	3.0E-01 AW817785.1		П	01 AF229247.1
Most Similar (Top) Hit BLAST E Value	3.1E-01,	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.1E-01	3.45-01	3 15-01 F	3.1E-01	3 1E 01	9 4 10 04 /	0.15	3.75-01 /	1	3.15-01	3.1E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01	3.0E-01 △	3.0E-01	3.0E-01	3.0E-01 A	3.0E-01	3.0E-01
Expression Signal	1.34	1.01	3.91	2.41	0.77	1.71	0.54	1.05	1.05	1.74	0 63	1.26	2.56	1 48	303	290	707		3.46	CS.1	2.01	14.52	2.51	5.57	1.	1.18	1,46	1.95	7.22	0.77
ORF SEQ ID NO:	32140	32203						35818		35893		36672				†					25533	25696	26618	26930	27592		29234	29837	30702	30833
SEQ ID NO:	19143	19207	19346			21238			22615	22677	22849	L		24623	1	ı		9000			- 1	- 1	- 1	14244		15969	16597			18152
Probe SEQ ID NO:	6374	6439	6583	6873	7579	8546	9802	9967	9967	10029	10201	10741	11524	12133	12165	12304	12304	000	0007	12038	5	247	1202	1497	2132	3206	3846	4477	5267	5349

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Top Hit Descriptor	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA	tp21a11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE.2188412 3' similar to gb:D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN);contains element L1 repetitive element:	Cavia porcellus mRNA for glutathione s-transferase, complete cds	wr02f10.x1 NCI_CGAP_GC6 Homo saplens cDNA clone IMAGE:2480395 3'	zs57d12.r1 NCI_CGAP_GCB1 Home sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element.	V77e12.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:28291.3'	Suaeda maritima subsp. salsa S-adenosylmethionine sythetase 2 mRNA, complete cds	B subtilis levenase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levenase	B.subtilis levanase operon levD, levE, levF, levF, levG and sacC (partial) genes for fructose phosphotransferase	System polypopulos Filt 10, 10, 20, 50 and events as Miss mileculus Enhanceur A8 (Enhas) mDNA	2/97b12.r1 Soares, NhHMPu, S1 Homo sapiens cDNA clone IMAGE:767711 5'	we27c05.x1 NO_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.t1 L1	Bos tairus mosin I mRNA complete rde	w39408.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE-141615.51	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'	D.discoideum gene for 34 kD actin binding protein	Mus musculus Filih protein (Filih) gene, complete cds; and Ligih protein (Ligih) gene, partial cds	PUTATIVE MULTICOPPER OXIDASE YDR508C	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial ods; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-	galactosy transferase (beta1,3-galactosy tr>	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'	601065830F1 NIH_MGC_10 Homo saplens cDNA clone IMAGE:3452287 5	Bos taurus partial stat5A gene, exons 5-19	Bos taurus partial stat5A gene, exons 5-19	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5	Buchnera aphidicola plasmid pLeu isolate MI 2-isopropyimaliate synthase (feuA) gene, partial cds; 3- isopropyimaliate dehydrogenase (feuB) gene, complete cds; and isopropyimaliate dehydratase subunit (feuC) gene, partial cds
Top Hit Database Source	EST_HUMAN F	EST HUMAN 2	Г	EST_HUMAN w	EST HUMAN	Т	T	N F	E C		THUMAN		T	Т	EST HUMAN	T	NT TN	SWISSPROT	≥ 6	NT TN	HUMAN	EST_HUMAN 6		日	EST_HUMAN 6	R :: 6
Top Hit Acession No.	-01 AW754239.1	-01 AI610836.1	AB016426.1	2.9E-01 AW002902.1	2.9E-01 AA284468.1	R37485.1	2.9E-01 AF321001.1	2.9E-01 X56098.1	2 9F_01 X56008 1	ARTORRO NT	-01 AA418145.1	A 1707128 4	U03420.1	2.9E-01 R69194.1		l	2.1	-01 Q04399		2.9E-01 AF100956.1		2.9E-01 BE540422.1			2.9E-01 BF217743.1	2.9E-01 AF197456.1
Most Similar (Top) Hit BLAST E Value	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2 GE-01	2 9F-01	2.9E-01	2 05-04	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01		2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01	2.9E-01
Expression Signal	2.73	0.72	0.73	0.77	1.1	1.66	0.79	5.19	5.10	6.4	1.47		2.4	0.58	0.58	0.56	1.52	2.95		2.06	1.67	1.67	0.48	0.48	0.94	0.49
ORF SEQ ID NO:	28659	29265	29427		29813		32532	31387	31388	31401	31708	31937	31984	32130	32131		30523	32737	-	32813	33640	33641	33875	33876		
Exon SEQ ID NO:	16008	16627	16797	16809	17188	17986	19507	18471	18471	18482	18747	18964	19007	19135	19135	19383	17966	19688		19750	20515	20515	20743	20743	20756	20931
Probe SEQ ID NO:	3246	3877	4052	4004	4462	5177	5310	5677	5877	5689	5965	6187	6233	6365	6365	6621	6890	9669	-	7059	7820	7820	8049	8049	8062	8237

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Probe E SEQ ID SE NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
	21185	34328	0.84	2.9E-01	-01 AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
	21515	34660	1.02	2.9E-01	-01 AF225908.1	LN	Arabidopsis thaliana sulfonylurea receptor-like protein mRNA, complete cds
8931	21622	34765	0.65	2.9E-01	-01 M22452.1	LN	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
L	21876	35040	0.78	2.9E-01		L	Pyrococcus abyssi complete genome; segment 5/8
9145	21878	35041	0.76	2.9E-01	-01 AJ248287.1	TN	Pyrococcus abyssi complete genome; segment 5/6
10810	23493	36728	1.93	2.9E-01	-01 AF128843.1	FN	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11114	23784	37059	1.75	2.9E-01		NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
L	23784	37060	1.75	2.9E-01	-01 V01394.1	LΝ	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
	24174	37489	1.59	2.9E-01			ny35h02.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.t2 LTR8 repetitive element;
11579	24178	37493	3.55	2.9E-01	E-01 AL139078.2	Į.	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
	24199	37519	1.62	2.9E-01	1	LZ LZ	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
L	24199	37520	1.62	2.9E-01	-01 U35025.1	Z	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12452	24821	31024	4.05	2.9E-01	-01 AF092453.1	LZ	Homo saplens TNF-æ-inducible RNA binding protein (TIRP) gene, complete cds
	25007	30973	1.86	2.95-01	-01 Y08937.1	TN	Chlamydomonas reinhardtil mRNA for nitrite reductase structural locus
12741	25007	30974	1.86	2.9E-01	-01 Y08937.1	N	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
555	13338		1.7	2.8E-01		L	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
	13342		1.01	2.8E-01		NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
	13819	26481	3.69	2.8E-01	-01 AF168050.1	뒫	Guira guira oocyte maturation factor Mos (c-mos) gene, partial cds
1254	14003	26871	1.62	2.8E-01			601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
	14003	26672	1.62	2.8E-01	2.1	T_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
	14017	26684	1.34	2.8⊑-01	-01 D86550.1	L'N	Human mRNA for serine/threonine protein kinase, complete cds
1651	14397	27087	1.11	2.8E-01		NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
1720	14463	27163	2.04	2.8E-01			QV1-CT0364-120200-065-505 CT0364 Homo saplens cDNA
	14742	27467	2.35	2.8E-01	E-01 AL047620.1	EST_HUMAN	DKFZp586l2321_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586l2321
	14858	27588	1.41	2.8E-01		EST_HUMAN	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
	15193	27933	2.04	2.8E-01	-01 AE000494.1	NT.	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2475	15193	27934	2.04	2.8E-01		ᅜ	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
	15264		1.89	2.8E-01		LN.	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
	15380	28118	0.97	2.8E-01		NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
Ш	15736		1.29	2.8E-01	1.1	RT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
	15737	28386	2.04	2.8E-01		Z	B. faurus microsatellite (ETH121)
	15737	28387	2.04	2.8E-01		Z	B. taurus microsatellite (ETH121)
3373	16132	28788	1,13	2.8E-01	-01 AP000004.1	Ę	Pyrococcus harikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)

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						9	
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9788	22439	35647	99'0	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
						!	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b;
9820	22500			2.8E-(01 AF294393.1	L	nuclear gene for mitochondrial product
0986	22608	35813				Z	Homo sapiens hypothetical protein (LOC51319), mRNA
10211	22859		1.47	2.8E-01	9626154	TN	Fujinami sarcoma virus, complete genome
10251	22809	36109	9.0	2.8E-(11 BE959727.2	EST_HUMAN	601654822R1 NIH_MGC_57 Hamo saplens cDNA clone IMAGE:3839765 3'
10644	23335			2.8E-	01 BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Hamo sapiens cDNA clone IMAGE:4109350 5'
10644	23335			2.8E-	01 BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo saplens cDNA clone IMAGE:4109350 5'
10671	23362	38603	3.83	2.8E-(01 BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
10704	22.477) 8E.	A DE 1882 1	TM	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5 flanking region, exons 1 through 7 and complete cds
10/01	1/4000			1000	DE674000 4	Ь	6074 244 PET MILL MCC B2 Home canions of NA close MAACE 4072853 K
11247	23909			7.0	01 81-6/4023.1	ESI HOMAN	OUCLOY410T INIT MOTOLOG TOTAL COURT FINIT CELAZIONUS
11593	24192	37510		2.8E-(01 AL139074.2	N	Campylopacter jejuni NCT C11168 complete genome; segment 1/6
12406	24789		15.41	2.8€-	01 D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12509	24861		4.22	2.8E-	01 BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Hamo sapiens cDNA
12532	24877	31019		2.8E-(01 BE900116.1	EST_HUMAN	601873020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955998 5'
12885	25306	-	2.52		11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
12806	25401		1.49	2.8E-	AW025400.1	EST HUMAN	wu96g05.x1 NCI_CGAP_Kid3 Hamo sapiens cDNA clone IMAGE:2527928 3'
464	13249	26890		2.7E-	Y17324.1	LN TN	Rattus norvegicus CDK104 mRNA
							z39b10.s1 Soares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:788827 3' similar to
289	13377	26007		2.7E-		EST_HUMAN	contains Alu repetitive element;
1238	13987		2.13	-2.7E-	3.1	LN L	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1617	14364		1.58	2.7E-	01 X79815.1	NT	G.lambila SR2 gene
1722	14465	27164	3.5	2.7E-(01 W 58067.1	EST_HUMAN	zd22h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
							GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL
1769	14511	27212		2.7E-		SWISSPROT	PROTEIN P30; NUCLEOPROTEIN P10]
2131	15586		2.25	2.7E-	5.1	ΝΤ	Rettus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2367	15089	27826	10.01	2.7E-	2.7E-01 Y13868.1	INT	Feline Immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial
				1			ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1
2457	15175	27914	4.07		Al310858.1	EST_HUMAN	repelitive element;
2899	15666	28314			01 AF251278.1	NT	Mus musculus serine protease inhibitor 14 (Spl14) mRNA, complete cds
2983	15749		2.63		BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3283	16044				2.7E-01 8393620 NT	۶	Rattus norvegicus Insulin receptor (Insr.), mRNA
3992	16740	29374	1.97		Al928015.1	EST_HUMAN	wc92e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 31

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ongre cyclic topics cyclic in Diali	Top Hit Descriptor	Drosophila buzzatii albha-esterase 6 (aE6) gene. partial cds	Drosophila buzzatii apha-esterase 6 (aE6) gene, partial cds	Homo sabiens DiGeorge syndrome critical region felomenic end	RC1-CT0286-230200-016-e03 CT0286 Homo sariens cDNA	280a01.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gb:X65488 cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U /HIMAN)	290a01.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511846 Similar to ob. X63488 cdst HFTEROGENO IS NIIICI EAB DIRONI IN ECODOMERIA (11 AURAN).	HOMEOBOX PROTEIN HOX.44 (CHOX.14)	Astreopora myriophthalma mitochondrial cyb gene for cytochrome b. partial cds	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN 1 ARCE SI ISI INITIAL	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECLIBAGE	(TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN 1 APGE SLIBINITY	Archaeoglobus fulgidus section 13 of 172 of the complete genome	Archaeoglobus fulgidus section 13 of 172 of the complete penome	FIBRILLIN 1 PRECURSOR	Drosophila melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds	td08h08.x1 NCI CGAP CL1 Homo sapiens cDNA clone IMAGE:2075103.3'	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X	NITROGEN REGULATORY PROTEIN NUT1	NITROGEN REGULATORY PROTEIN NUT1	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and nartial order	Bos faurus micromolar calcium activated neutral protesses 1 (CAPN1) name avone 11.20 and martial calc	EST58740 Infant brain Homo saplens cDNA 5' end similar to similar for mostin-binding marken H	EST58740 Infant brain Homo saplens cDNA 5 end similar to similar to moosin-binding protein H	Oryctolagus cuniculus UDP-clucuronosyltransferase (UGT2813) mRNA, complete cds	ze35b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element,
01 1 1100 018	Top Hit Database Source	۲N	TN	ΤN	EST_HUMAN	EST_HUMAN	EST HUMAN	SWISSPROT	NT	SWISSPROT		SWISSPROT	LN L	Ł	SWISSPROT	LN FN	EST HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	Ŋ	Ę	EST HUMAN	EST HUMAN	NT	EST_HUMAN
5	Top Hit Acessian No.	2.7E-01 AF216214.1	AF216214.1	L77569.1	2.7E-01 AW856131.1	2.7E-01 AA100656.1			2.7E-01 AB033171.1	-01 Q00918				2.7E-01 AE001094.1	Q61554	2.7E-01 U15967.1	AI540070.1	011079	201168	2.7E-01 Q01168	2.7E-01 AF248054.1	2.7E-01 AF248054.1	4A351121.1	Г	2.7E-01 L01081.1	2.7E-01 AA013147.1
	Most Similar (Top) Hit BLAST E Value	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01		2.7E-01 Q00918	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01
	Expression Signal	0.69	0.69	2.12	2.85	2.53	2.53	2.39	0.85	0.66		0.66	0.93	0.93	2.23	0.58	0.79	0.74	0.75	0.75	2.16	2.16	96.0	96.0	0.71	0.68
	ORF SEQ ID NO:	29380				30339		30509		31995		31996	32282	32283	32637	32699		33015	33225	33226	33363	33364	33411	33412	33472	33583
	Exen SEQ ID NO:	ı		16754	17703	17733	17733	17993	18202	19023		19023	19280	19280	19598	19653	19434	19940	20134	20134	20256	20256	20303	20303	20358	20459
	Probe SEQ ID NO:	4005	4002	4008	4980	5011	5011	5185	5402	6249		6249	6515	8515	6681	6916	6952	7256	7461	7461	7588	7588	7638	7638	7694	7763

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						,	
Probe SEQ ID (Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7925	20620		0.53	2.7E-01	01 AF048820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8086	20780	33909	0.51	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:23511 3'
8190	20884	34022	8.0	2.7E-01	AĽ161552.2	NT	Arabidopsis thallana DNA chromosome 4, contig fragment No. 52
8657	21349	34494	65.0	2.7E-01	2.7E-01 Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8925	21616	34760	0.46	2.7E-01	2.7E-01 X03216.1	NT	Staphylococcus aureus transposon Tn554
9232	21911	35084		2.7E-01		SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9232	21911	35085	10.41	2.7E-01		SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINETRNA LIGASE) (THRRS)
9235	21914		2	2.7E-01	2.7E-01 P37928	SWISSPROT	FIMBRIAE W PROTEIN
							Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11,12, 13, 14, 15, 16, 17
9700	22351			2.7E-01	D89660.1	LN	and complete cds
9981	22629		0.74	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10018	22666		3.09	2.7E-01	2.7E-01 AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATca) mRNA, complete cds
10149	22797	36012		2.7E-01	2.7E-01 AF156539.1	LΝ	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10149	22797			2.7E-01	AF156539.1	LΝ	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, Intron 9
10714	23403			2.7E-01	2.7E-01 AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10714	23403			2.7E-01		EST_HUMAN	AV705043 ADB Homo saplens cDNA clone ADBCOD05 5'
10704	23412	36653	3.13	2 75 04	2 7E-04 A (1332)89 1	FIA	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and
11820	24406		1.5	2.7E-01	ŀ	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN C4F8.05C
12482	25190		1.49	2.7E-01	2.7E-01 AB008782.1	LN	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12665	24963		2.83	2.7E-01		LN	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
12811	25054		1.95	2.7E-01		EST_HUMAN	AV742419 CB Homo sapiens cDNA clone CBMAXF02 5'
457	15542	25883		2.6E-01		SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
468	13254		1.38	2.6E-01		LΝ	Bos taurus mRNA for mb-1, complete cds
1372	14120		1.65	2.6E-01	01 BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3912345 5'
1417	14165		1.14	2.6E-01	01 AB013290.1	۲N	Glycine max pseudogene for Bd 30K
1889	14626			2.6E-01	31 AL161472.2	LΝ	Arabidopsis thallana DNA chromosome 4, contig fragment No. 2
1889	14626	27336		2.6E-01	1 AL161472.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04dr10.x1 NIH_MGC_14 Home saplens cDNA clone IMAGE;2968461 3' similar to gb;M36072 60S
2086	14818		10.48		2.6E-01 AW733152.1	EST_HUMAN	ANDUCCOMPLETIVE LINE LINE LINE (TOWNIN), Whim 1900s_cast microse surfact body surfact of protein general (MOUSE);
2148	14878	27613			01 M11844.1	NT	Human prealbumin gene, complete cds
2476	15194		1.62	2.6E-01	01 Y12996.1	NT	B.maritimus rbcL gene

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	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E. Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2548	15263		8.87	2.6E	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890043 5'
3568	16323	28971	8.99	2.6€	-01 M22342.1	F	Bacteriphage T2 DNA (adenine-N6)methyltransferase (dam) gene, complete cds
3634	16387	29028		2.6E	01 AF229118.1	Ę	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A. 2, 3, 4, and 5
4079	16823	29449	96.0	2.6E-	01 AW959510.1	EST HUMAN	EST371580 MAGE resequences, MAGF Homo sapiens cDNA
4134	16876			2.6E-	01 BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo saplens cDNA
4324	17083	29691	1.2			占	Enterococous faeclum strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4459	. 17195	29821	0.8			Į.	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4459	17195	29822	9.0			N L	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4511	17246	29881	1.46		2.6E-01 AA457617.1	EST_HUMAN	aa89d07.r1 Stratagene fetal retina 637202 Homo saplens cDNA clone IMAGE:838477 5'
4601	17336	29962	1.77	2.6E-01	01 U01103.1	N	Arabidopsis thallana PSI type III chlorophyll a/b-binding protein (Lhca3*1) mRNA, complete cds
4667	17401	30035	1.18	2.6E-	01 AF142703.1	· FZ	Ophrestia radicosa maturase-like protein (matk) gene, complete cds; chloroplast gene for chloroplast product
4910	17638	30252	0.95		2.6E-01 AF153350.1	Į.	Mus musculus metalloprotease disintegrin (Adam28) mRNA, complete cds
4914	17642					EST HUMAN	y51e05.r1 Soares placenta Nb2HP Homo saplens cDNA clone IMAGE:152288 5
5257	18063		1.06	2.6E-(_	N F	Paramecium caudatum gene for PAP, complete cds
5484	18283		0.68	2.6E-01	01 AI862398.1	EST_HUMAN	td16a03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element;
0000	0.00	00,10	c c			ļ	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, pim-2 protooncogene homolog plm-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM
2980	25417	00+10	2.35		2.6E-01 AE001811.1	Z	enrancer 3 genes, partial cds; and unknown g> Thermotoga maritima section 123 of 138 of the complete genome
0	0 0 0	200	Č		i d		ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA done IMAGE:2227438 3' similar to SW:NDF1_RAT
9015	8	1000	7.70		Z.OC01 A136Z337.1	ES L'HOMAIN	CO4268 NEUNOCENIC DIPPERENTATION PACIOR 1 COntains element LIR1 repetitive element;
6108	18885	31855	2.26		01 A1582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA done IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element :
6328	19098	32086	0.91			NT	Neisseria meningitidis serogroup A strain 22491 complete genome; segment 6/7
6570	19334	32344	0.73		2.6E-01 BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3836156 5'
6570	19334	32345	0.73			EST_HUMAN	601581754F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3936156 57
6938	19673	32719	0.9		2.6E-01 Al914380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);

PCT/US01/00667

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		_			_	_								_			_													
Top Hit Descriptor	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein mRNA	Startish (P. ochraceus) cytoplasmic actin gene, complete cds	Mus musculus ICR/Swiss abbearaidehnde 3nhochhate dehndrosanses (2. nand 5)	Ureaplasma urealyticum section 57 of 59 of the complete census.	ye11g07.r1 Strakagene lung (#937210) Homo sapiens cDNA clone IMAGE-117468 だ	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	Homo saplens hyperpolarization activated cyclic nucleatide cated nytassium channel 4 JuCh141	PM4-CT0400-310700-005-d08 CT0400 Homo seniens CDNA	PM4-CT0400-310700-005-008 CT0400 Homo capiers CDNA	Adulfex Beolicus section 7 of 109 of the complete persons	2811a12r1 NOI CGAP GCB1 Home satisface CDNA clone IMAGE GRABRO EI	602125525F1 NIH MGC 56 Home saniens cDNA clane IMAGE-0282276 K	EST385464 WAGE resequences. MAGM Homo seniens cDNA	Danio rerio peptide YY precursor gene, complete cds	Arabidopsis thaliana DNA chromosome 4. contia fragment No. 29	wg11c07.x1 Soares NSF F8 9W OT PA P S1 Homo sablens cDNA clone IMAGE 2384780 3	Wg11c07.x1 Sogres NSF F8 9W OT PA P S1 Hrmn seniens CDNA clone IMA DE 236.726.72	RHIB PROTEIN	MOLT-INHIBITING HORMONE PRECURSOR (MIH)	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome	Mus musculus annexin V gene, intron 4 segment containing 5'LTR and gag portion of MuERV-L (murine	SOLATARETANIN MCC 72 Line - Philips	NO 145 1 THE COURSE OF THE TOP OF HEMPERSON AND THE PROPERTY OF THE PROPERTY O	WP:Y71F9A 294.D CE22858:	T3 receptor-associating cofactor-1 fluman, fetal liver, mRNA, 2930 nfl	Homo sapiens KVLQT1 gene	Homo sapiens chromosome 21 segment HS21C007	Homo sapiens partial steerin-1 gene	Rattus norvegicus rabin 3 (RABIN3), mRNA
Top Hit Database Source	F Z	LN LN	L L	N.	EST HUMAN	NT	FZ.	EST HUMAN	EST HUMAN	N	EST HUMAN	EST HUMAN	EST HUMAN	N _T	NT	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	LZ	TN	FN	ECT HIMANI	NUMBER OF THE PROPERTY OF THE	EST HUMAN	N	NT	LN	Į.	Ę
Top Hit Acession No.	4502296 NT	-01 M26501.1	-01 U09964.1	-01 AE002156.1	-01 T89837.1	-01 AL115624.1	4885406 NT	-01 BE696604.1	.01 BE696604.1	-01 AE000675.1	-01 AA251987.1	-01 BF698193.1	01 AW973471.1	01 AF233875.1	-01 AL161517.2	-01 AI741483.1	01 Al741483.1	01 Q03314			01 AE004416.1		-01 RESORTRE 1	1.000	01 AW873588.1	01 S83390.1		01 AL163207.2		8394138 NT
Most Similar (Top) Hit BLAST E Value	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5F-01	2 5F-01		2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01
Expression Signal	2.39	3.32	1.35	1.2	8.42	6.0	4.79	1.58	1.58	16	1.09	0.84	3.04	1.25	7.54	1.53	1.53	26.0	1.25	3.99	2.01	3.7	1 09		0.71	13.48	0.73	86.0	0.95	0.79
ORF SEQ ID NO:	25684		26250		26517	26941		27323	27324					28935	28942	29211	29212			30070	30101	.= -	30135		30315	30678	31598		32299	32442
Exen SEQ ID NO:		13057	13584	13798	13857	14255	14464	15581	15581	15128	15217	16129	16165	16280	16293	16579	16579	17022	17434	17438	17464	17483	17513		17710	18049	18657	18658	19295	19427
Probe SEQ ID NO:	235	248	813	1038	1099	1509	1721	1876	1876	2407	2500	3370	3407	3524	3537	3828	3828	4283	4700	4706	4732	4751	4781		4987	5243	5870	5871	6229	6945

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Single Exun Probes Expressed in Brain	Top Hit Descriptor Source	Feline calicivirus CFI/68 RNA helicase/cystaine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene	Mus musculus SKD1 (Skd1) gene, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18	Homo sapiens chromosome 21 segment HS21C082	HUMAN		HUMAN	ISSPROT E18 PROTEIN, SMALL T-ANTIGEN (E1B 19K)	EST_HUMAN yq84f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'	Mouse testis-specific protain (TPX-1) gene, exan 10	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds	HUMAN RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA		NAW DI	Mouse L1Md LINE DNA	Human mRNA for KIAA0124 gene, partel cds	Homo sapiens sodium/myo-Inositol cotransportar (SLC5A3) gene, complete cds	Litomosoides sigmodontis microfilarial sheath protein SHP1a precursor (shp1a) gene, complete cds	Zea mays cellulose synthese-4 (CesA-4) mRNA, complete cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41	Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt. position (3/7)	Spodoptera frugiperda CALNUC mRNA, complete cds	HUMAN	HUMAN	Homo saplens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	Homo sapiens FL-1 gene, partial	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
ngie n		호	Z	Ę	IN	EST	EST	EST	SWIS	EST	Ł	N.	Ę	Ę	Ä	EST	1	_'î	Ę	Ł	Ā	Z	둗	Ę	Ę	F	EST	l⊢`i	IN	INT	Ϋ́	Ŗ	토
0	Top Hit Acession No.	2.5E-01 U13992.1	2.5E-01 AF134119.1	2.5E-01 AL161506.2	2.5E-01 AL163282.2	BF109040.1	2.5E-01 BE960712.1	BF038595.1	P04492	H53236.1	M88626.1	U89651.2	2.5E-01 U89651.2	2.5E-01 AF085164.1	AF085164.1	2.5E-01 AW581997.1		AW152246.1	2.5E-01 X58491.1	2.5E-01 D50914.1	AF027153.1	1 045315.1	1 AF200528.1	2.5E-01 AL161541.2	2.5E-01 AP000003.1	AF170072.1	2.4E-01 AA936316.1	2.4E-01 BF576124.1	2.4E-01 AJ289880.1	2.4E-01 AJ289880.1	1 Y17293.1	2.4E-01 AF267753.1	2.4E-01 AF251708.1
	Most Similar (Top) Hit BLAST E Value	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	L	7.55-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.5E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01
	Expression Signal	0.88	1.29	0.83	3.6	2.47	0.8	1.87	0.7	3.67	62'0	15.72	15.72	2.06	2.08	1.39	9,0	2.13	1.21	3.43	1.61	1.29	5.12	6.13	1.37	1.37	1.69	3.34	33.63	33.63	1.03	32.88	1.33
	ORF SEQ ID NO:	33011		33259	33303	33564	33574	33955	34128	34368	34613	35265	35266	35253	35254	35858	1,000	36213	36319	36945		37727	37808			30821	25955	26269	26700	26701	26785		27340
	SEQ ID NO:	19936	19962	20167	20206	20440	20450	20819	20990	21226	21466	22094	22094	22081	22081	22846	-0000	7308/	23090	23685	24244	24393	24490	25388	24768	25233	13323	13598	14031	14031	14111	14581	14630
	Probe SEQ ID NO:	7252	7278	7494	7536	7744	7754	8125	8296	8534	8774	9416	9416	9472	9472	8666	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	10441	10444	11013	11647	11803	11932	11960	12365	12412	240	828	1281	1281	1363	1843	1893

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Probe SEQ ID NO:	<u>σ</u>	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2134	14864	27594	1.1	2.4E-01	1 AF111168.2	Z	Homo sapiens serine palmitoy transferase, subunit II gene, complete cds; and unknown genes
2165			1,44	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2258	14985	27725		2.4E-01	2.4E-01 AE000680.1	Z	Aquifex aeolicus section 12 of 109 of the complete genome
2382			1.38	2.4E-01	2.4E-01 BF002171.1	EST HUMAN	7h23d04.x1 NCI_CGAP_Co16 Homo saplens cDNA clone IMAGE:3316807.3' similar to SW:PRSB_XENLA 042586 26S PROTEASE REGULATORY SUBUNIT 6A
2539	1				Γ	N _T	D.dlscoideum (Ax3-K) ponA gene
2765				•	X71783.1	N	S.pombe swi6 gene
2789	15494	28234	2.84	2.4E-01	2.4E-01 AF030154.1	N	Bowne adenovirus 3 complete genome
3129			2.94	2.4E-01	2.4E-01 U72726.1	F	Oryza longistaminata receptor kinase-like protein. family member D. and retrofit (aaa/not) nenee comulaise ade
3145	15909	28554	1.48	2.4E-01	2.4E-01 X74209.1	Z	H.saplens AGT gene, Pstl fragment of Intron 4
3743			62'0	2.4E-01	2.1	N	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4010	16756		0.74	2.4€-01		L	Rattus norvegicus mRNA for alphaB crystallin-ralated protein, complete cds
4883	17610		1.09	2.4E-01	2	N	Arebidoosis theliana DNA chromosome 4. contin fragment No. 85
4989		30317		2.4€-01		NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5375				2.4E-01	Al925707.1	EST HUMAN	wo33d05.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5375			96.0	2.4E-01	A1925707.1	П	wo33d05.x1 NC _CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5397			8.0	2.4E-01	2.4E-01 D50871.1	Г	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5569	18366		8.16	2,4E-01		N	Mus musculus W/m protein (Wrn) gene, camplete cds
5569			8.16	2.4E-01		NT	Mus musculus Wm protein (Wm) gene, complete cds
5597			0.77	2.4E-01	2.4E-01 M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
5799	25076		0.99	2.4E-01		TN	Branchlostoma floridae mRNA for calmodulin 2 (calv2 gene)
		_					7154404.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 :contains element TAR1 TAR1 manefilling element
5805			2.22	2.4E-01	2.4E-01 BF592336.1	EST_HUMAN	
5895	- 1	31627	3	2.4E-01		LN	Drosophila melanogaster p38a MAP kinase gene, complete cds
2999		31741	2.53	2.4E-01	7661801 NT		Homo sapiens HSPC142 protein (HSPC142), mRNA
9050	18830	31793	0.67	2.4E-01		EST_HUMAN	AV733787 cdA Homo sapiens cDNA clone cdAADE11 5'
6441	19209	32206	2.23	2 4E-01		NAM	wc62c11.x1 NCI_CGAP_Par1 Home sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
7243	19928	33004	9.5	2.4E-01	2.4E-01 L43001.1	Т	Bos karrus guandyl cyclase-activating protein 2 (guena?) mRNA complete cyc
7404		33163		2.4E-01		EST HUMAN	1955c11.r1 Soares multiple sclerosis 2NbHMSP Homo sepiens cDNA clane IMAGE: 277460.51
7625	20291	33400	0.91	2.4巨-01		LN	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
8247	20941	34078		2.4E-01		ĻΝ	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2

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Table 4
Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain	Top Hit Descriptor	601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'	602086188F1 NIH_MGC_83 Homo saplens cDNA clone IMA GE:4250372 5'	Campylobacter Jejuni NCTC11168 complete genome; segment 4/6	Campylobacter jejuni NCTC11168 complete genome; segment 4/6	wd43e02xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains MER22 bt TAR1 repetitive element:	Drosophila melanogaster SKPB gene, complete cds	Drosophila melanogaster SKPB gene, complete cds	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6	Mus musculus type 1 sigma receptor gene, complete cds	P.aslatica mosaic virus genomic RNA	601441421T1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3845836 3'	Homo saplens fragile 16D oxido reductase (FOR) gene, exon 6	Arabidopsis thallana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds	Mus musculus mRNA for putative mc7 protein (mc7 gene)	Gallus gallus gene coding for a-actin	601842848F1 NIH_MGC_54 Hamo sapiens cDNA clone IMAGE:4063739 5'	Homo saplens chromosome 21 segment HS21C081	aromatase [Poephlia guttata≂zebra finches, ovary, mRNA, 3188 nt]	Mycoplasma genitalium section 35 of 51 of the complete genome	Methanococcus Jannaschii section 138 of 150 of the complete genome	601142073F1 NIH_MGC_14 Homo saplens cDNA clone IMAGE:3505818 5'	Yersinia pastis HmsH (fmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds	Brassica napus sig gene for S-locus glycoprotein, cultivar T2	Mus musculus cdh5 gene, exon 1, partial	Homo saplens partial intron 3 of the wild type AF-4/FEL gene	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'	Human erythropoletin gene, complete cds	Marinilabilia agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957	no16d06.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repotitive element; contains element ;	yh21b07.s1 Soares placenta Nb2HP Homo saplens cDNA clone IMAGE:130357 3'
gie Exon Pro	Top Hit Database Source	EST_HUMAN	EST_HUMAN	١	١	HST HIMAN	_ 	F	SWISSPROT	LZ LZ	LN	LZ	EST_HUMAN	Ľ	ΙN	LΝ	TN	EST_HUMAN	LN	LΝ	NT	IN	EST HUMAN	LN	Ι	Ľ	Ę	EST_HUMAN	LΝ	LΝ	EST_HUMAN	EST_HUMAN
מוֹאַ	Top Hit Acession No.	01 BF242794.1	01 BF678275.1	01 AL139077.2	01 AL139077.2	01/A/693515 1	01 AF220067.1	2.4E-01 AF220067.1	2.4E-01 Q03692	2.4E-01 AL161494.2	01 AF030199.1	01 Z21647.1	-01 BE617538.1	01 AF217491.1	2.4E-01 AF004213.1	01 AJ278191.1	01 V01507.1	01 BF184542.1	01 AL163281.2	01 S75898.1	01 U39713.1	01 U67596.1	01 BE311893.1	01 U22837.2	AJ245480.1	-01 Y10887.2	-01 AJ235353.1	01 BE297718.1	M11319.1	-01 AB015033.1	01)AA601379.1	01 R21732.1
	Most Similar (Top) Hit BLAST E Value	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2 4F-01		2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01
	Expression Signal	1.02	0.47	0.49	0.49	7 07	0.88	0.88	1.68	4.6	1.39	209	1.32	1.75	2.34	2.74	1.97	2.06	3.66	1.06	5	33.31	4.19	1.12	1.23	2.74	1.51	2.66	1.59	3.38	1.36	7.07
	ORF SEQ ID NO:	34332		34874	34875	35181	35441	35442	36202	36598	36671		37765	37801						25810		56069	26341		27035	27063		27903	28105	26789	28379	
	Exen SEQ ID NO:	21189		i		22013	i	22256	22984	23358	23426	23825	24424	24461	25180		25162	25201	24992	13167	13401	13430	13680	14305	14345	14374	14772	15166	15367	14114	15729	1 1
	Probe SEQ ID NO:	8497	8552	8030	9030	6463	9603	9603	10337	10667	10739	11168	11840	11891	12019	12080	12287	12400	12720	380	622	652	913	1558	1599	1628	2038	2447	2657	2827	2963	3082

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•	Top Hit Descriptor	lipha subunit (tel-alpha alanine version) gene,	spo e	one IMAGE:2591554 3'	s cDNA	i end similar to DnaJ homolog (GB:X63368)	'end similar to DnaJ homolog (GB:X63368)	ibunit delta (Pik3cd), mRNA	ve) gene, complete cds	e IMAGE:2966739 5'	s cDNA	lification system (HinclI methyltransferase (EC	DNA	cDNA	polysaccharide biosynthesis genes		le IMAGE:4102092 3'	NA, complete cds	NA, complete cds	3534 gene)	3534 gene)	s complete genome	15	3 subunit of VLA-3 receptor) (ITGA3), transcript	lete cds and REP+ gene, partial cds	:44 5'	cDNA	NA clone IMAGE:2813773 3' similar to TR:Q9Z175 trains PTR5 by TAR1 repretitive element	e IMAGE:3908689 5'	. INJACE: 1007710 E'
Single Exon Propes Expressed in Brain	Top Hit	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha atanine version) gene, complete cds	Mus musculus prosaposin (psap\SGP-1) gene, complete cds	xc90e06.x1 NCI_CGAP_Brn35 Homo saplens cDNA clone IMAGE:2591554 3	EST376533 MAGE resequences, MAGH Homo sepiens cDNA	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA	Tribolium castaneum transcription factor homolog (Tc-eve) gene, complete cds	┪	1	Haemophilus influenzae genes for Hincil restriction-modification system (Hincil methyltransferase (EC 2.1.1.72) and Hincil endonuclesse (EC 3.1.2.14)	PM2-DT0036-281299-001-f04 DT0036 Homo saplens cDNA	MR0-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes	Murine hepatitis virus strain 2, complete genome	601646155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)	Chlamydophila pneumonlae AR39, section 4 of 94 of the complete genome	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant b, mRNA	Borrella burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds	HCOEST44 HT29M6 Homo sapiens cDNA clone HCoE44 5	PM4-SN0012-030400-001-b06 SN0012 Homo saplens cDNA	xx21d07.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175 Q9Z175 Q9Z175 Q9Z175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2. :contains PTR5.bz TAR4 repetitive element*	601507202F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3908689 5	180214445951 NIH MGC 48 Homo senions CINIA close INACE: 1207710 F
gie Exon Pro	Top Hit Database Source	ĻN.	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N	N.	EST_HUMAN	EST_HUMAN	Ę	EST HUMAN	EST_HUMAN	N	ΡN	EST HUMAN	F	Ę	뉟	ΤN	NT	EST_HUMAN	Į.	Ę	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	FOT HIMAN
lio I	Top Hit Acession No.	11 M68931.1	01 U57999.1	1 AW090541.1	1 AW964460.1	21 AA372164.1	1 AA372164.1	6679318 NT	U77974.1		2.3E-01 AW964460.1	11 X52124.1	13.1			4F201929.1	2.3E-01 BF133577.1	AF004833.1	2.3E-01 AF004833.1	4J250189.1	2.3E-01 AJ250189.1	2.3E-01 AE002167.2	4V709736.1	6006010 NT	U45426.1	T27231.1	AW863940.1	2.3E-01 AW303623.1	2.3E-01 BE882464.1	3E883310 1
	Most Similar (Top) Hit BLAST E Value	2.3E-01	2.3E-01	2.3E-01	2.3E-(2.3E-(2.3E-0					2.3E-01 >	2.3E-01 /	2.3E-01 E	2.3E-01	2.3E-01 /	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01/	2.3E-01 /	2.3E-01	2.3E-01	2.3E-01	2.3E-01 T	2.3E-01 4	2.3E-01/A	2.3E-01 E	2 20 04 0
	Expression Signal	2.16	0.47	0.56	0.45	1.02	1.02	0.62	0.62	0.5	0.59	1.02	0.56	2.45	2.75	0.84	6.11	1.49	1.49	1.77	1.77	3.03	1.75	1,33	4.47	4.88	1.52	2.88	8.63	251
	ORF SEQ ID NO:	33717	34217	34510							35529	35584			35734			36867	36868	37092	37093	37318			-	 -		30711	30613	
	SEQ ID NO:	20587				-	21729					22382	1	l				23617		23811)	- 1	24403	_	I _	L.	24612	25319	25366	24704
	Probe SEQ ID NO:	7892	8391	8671	8786	9039	9039	9480	6096	9628	9682	9731	9767	9834	9892	10340	10351	10937	10937	11144	11144	11324	11815	11855	12004	12088	12120	12173	12206	1225

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	xon ORF SEQ Expression (Top) Hit Top Hit Acession (Top) Hit Top Hit Acession (Top) Hit Descriptor Signal BLASTE No. Signal Alt Descriptor Source	2.35	1.76 2.3E-01 U49645.1 NT	1.55 2.3E-01 AJ006519.1 NT	TO THE POST OF THE	2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	25552 1.63	26993 1.64 2.2E-01 AF187850.1 NT	27547 2.52 2.2E-01 M34640.1 NT	27860 6.3 2.2E-01 BF677538.1 EST_HUMAN	28044 2.02 2.2E-01 BE618258.1 EST_HUMAN	28045 2.02 2.2E-01 BE618258.1 EST_HUMAN	28294 4.36 2.2E-01 BE155625.1 EST_HUMAN	28295 4.36 2.2E-01 BE155625.1 EST_HUMAN	1.57 2.2E-01 AF020503.1 NT	1.97 2.2E-01 AL161562.2 (NT	1.12 2.2E-01 AF155728.1 NT	0.72 2.2E-01 U68174.1 NT	29562 6.45 2.2E-01 AF155142.1 NT	29597 2.11 2.2E-01 AF117340.1	29598 2.11 2.2E-01 AF117340.1 NT	29689 1.21 2.2E-01 U01307.1 NT	29690) 1.21 2.2E-01 U01307.1 NT	1.36 2.2E-01 D50604.1	30133 2.1 2.2E-01/AA211216.1 EST_HUMAN	1.1 2.2E-01 L13299.1 INT	0.93 2.2E-01 S57565.1 NT	30474 2.64 2.2E-01 5835974 NT	31368 2.07	4.5 2.2E-01 D64000.1 NT	31646 0.56	31647
	be Exon SEQ ID SO: O.			12403 24728	24060	7047 7407		1557 14304	2082 14814		2594 15308		2884 15651	884 15651	921 15687	387 16146		4105 16848	4194 16935	4232 16973		4323 17062				4982 17705			- 1	- 1	5910 18694	910 18694
1	Probe SEQ :D NO:	12	12	12	2	4		Ť	Ž	2	લ	લ	ŭ	ন	ধ	ઌ૽	3.	4	4	4,	4.	4	4	4	4	4	ឆ	à	ភ	ភ	ព័	ĭń

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<u> </u>																															
Top Hit Descriptor	Homo sapiens gene for fukutin, complete ods	AV756238 BM Homo saplens cDNA done BMFAHC06 5'	Streptococcus pyogenes phosphotidy/glycerophosphate synthase (pgsA) and ABC transporter ATP-binding profes (staA) names compile cels and unknown genes	Streptococcus pyogenes phosphotidy/glycerophosphate synthase (pgsA) and ABC transporter ATP-binding	protein (stpA) genes, complete cds; and unknown genes	Human glycophorin B gene, exon 4	Human glycophorin B gene, exon 4	Mycoplasma pneumonlae M129 section 45 of 63 of the complete genome	Bacillus halodurans DNA, complete and partial cds, strain:C-125	Mus musculus nm23-M1 gene, promoter region	E.coli sepA and sepB genes	Pan troglodytes McCP2 gene 3'UTR	Thermotoga maritima section 25 of 136 of the complete genome	PMS-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA	2a04f08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291591 5'	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA	Brachydanio rerlo ependymin beta and gamma chains (Epd) gene, complete cds	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG-3)	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds;	nuclear gene for chloropiast product	601869724F1 NIH_MGC_19 Homo sapiens cDNA clane IMAGE:4100189 5	Human herpesvirus 5, complete genome	yb63d08.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:75855 5'	yb63d08.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:75855 5'	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550	precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthests A (pqqA) genes, complete ods; and pyrroloquin>	Mus musculus PHR1 (Phr1) gene, partial cds
Top Hit Database Source	TN	EST_HUMAN	Ŀ		L	Ŋ	NT	IN	TN	TN	LΝ	TN	۲	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	SWISSPROT	۲	LN	TN	TORASSIWS		뉟	EST_HUMAN	N	EST_HUMAN	EST_HUMAN		Z	N
Top Hit Acession No.	2.2E-01 AB038490.1	2.2E-01 AV756238.1	2 2E-01 AE082738 1		.1			.2		2.2E-01 AF155143.1	2.2E-01 Z49933.1		2.2E-01 AE001713.1		8393247 NT	2.2E-01 BF376354.1	W02988.1	2.2E-01 P48634	AJ009839.1	2.2E-01 7657428 NT		090980		197941.1	3F206507.1	9625671 NT	T69472.1	T59472.1		2.2E-01 AF068264.1	
Most Similar (Top) Hit BLAST E Value	2.2E-01	2.2E-01	2 25-04							2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01	2.2E-01 A.	2.2E-01	2.2E-01	2.2E-01 090980		2.2E-01	2.2E-01 BF	2.2E-01	2.2E-01	2.2E-01 T		2.2E-01	2.2E-01
Expression Signal	0.73	10.21	1 28		1.28	1.86	1.86	0.63	99.0	2.04	1.01	0.64	3.53	4.35	1.45	1.04	1.36	13.43	0.69	0.81	3.95	0.58		3.4	1.85	0.95	0.5	0.5		0.58	0.61
ORF SEQ ID NO:	32381	32708	14468		32778	32950	32951	33144	33402		33808	34279	34632		34853	34952	35024	35259	35104	35185	35200	35358		35564	35703	35941	36092	36093		36126	П
Exon SEQ ID NO:	19369	19662	19724		19721	19877	19877	20066	20294	20614	20682	21141	21486	21611	21703	21786	21859	22086	21931	22017	22030	22174	1	22368	i i		ı	22880		22916	22988
Probe SEQ ID NO:	9099	6926	70.29		7029	7191	7191	7386	7628	7919	7887	8449	8794	8920	9013	8088	9189	9207	9252	9263	9276	8521		9715	9853	10076	10232	10232		10268	10341

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						,	
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12758	25019		1.79	2.1E-01	-01 BE672330.1	EST_HUMAN	7a69e02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3223034 3'
195	13008	25650	2.43	2.0E-01	2.0E-01 AB017437.1	IN	Gallus gallus mRNA for avena, complete cds
521	13305		3.11	2.0E-01	7705601 NT	L	Homo sapiens CGI-18 protein (LOC51008), mRNA
683		26103	1.24	2.0E-01	2.0E-01 M77085.1	Z	O.cunniculus germline IgH heavy chain V-H pseudogene, allotype VHa2
792		26225	2.19	2.0E-01	1	NT	Mus musculus Major Histocompatibility Locus class II region
991		26414	1.09	2.0E-01	2.0E-01 D90905.1	LN	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915
1103	13860	26519	2.47	2.0E-01	-01 AL163213.2	N	Homo sapiens chromosome 21 segment HS21C013
1232	13981	26651	1.77	2.0E-01		LV	Homo sapiens rac1 gene
1285	14035	26706	1.63	2.0E-01	2.0E-01 AW384937.1	EST HUMAN	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1443	14190		1.52	2.0E-01		LZ LZ	Plum pox virus strain M, complete genome, isolate PS
1470		26904	14.63	2.0E-01	4503408 NT	Z	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1544	14290	28977	1.97	2.0E-01	2.0E-01 AB007974.1	LN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1550	14296	26983	1.01	2.0E-01	2.0E-01 AF260700.1	Þ	Homo sapiens sodium/iodide symporter mRNA, partial cds
1692	14436	27132	1.4	2.0E-01		LN LN	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1712	14455		1.67	2.0E-01	.3	NT.	Homo sapiens 14q32 Jaggad2 gene, complete cds; and unknown gene
1752			4.33	2.0E-01	2.0E-01 U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1883		27329	1.12	2.0E-01	2.0E-01 BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5
1883			1.12	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
2347	15070		1.63	2.0E-01	2.0E-01 X82877.1	LN	H.sapiens Na+-D-glucose colransport regulator gene
3555	16310		0.71	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element;
3693			0.89	2,0E-01	P34641	SWISSPROT	CED-11 PROTEIN
3822		29206	1.12	2.0E-01	AL163204.2	ΙN	Homo saplens chromosome 21 segment HS21C004
3936	16686		0.76	2.0E-01		N	Sus scrafe
4528	1		8.49	2.0E-01	2.0E-01 BE826165.1	EST_HUMAN	QV4-EN0032-190500-223-e03 EN0032 Homo seplens cDNA
4979	17702	30309	5.26	2.0E-01	8922080 NT	N	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5009	16237	28893	0.8	2.0E-01	2.0E-01 P46607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5359	18161	30845	2.63	2.0E-01	-	L	Rat SOD-2 gene for manganese-containing superoxide dismutase
5655	18450	31363	1.94	2.0E-01	432540	Z	Homo saplens dual oxidase-like domains 2 (DUOX2), mRNA
5750	18542		0.76	2.0E-01		NT	F.rubripes DNA encoding for valyk-tRNA synthetase
5969	1	31712	6,3	2.0E-01		FN	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6081	۱ ا		0.73	2.0E-01		본	Human hepatocyte growth factor gene, exon 1
6192	18968	31943	0.79	2.0E-01	P02467	SWISSPROT	COLLAGEN ALPHA 2(1) CHAIN PRECURSOR

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Single Exon Probes Expressed in brain	Top Hit Descriptor	M.auratus mu class glutathione transferase gene	PM1-CT0247-141099-001-g06 CT0247 Homo saplens cDNA	Mus musculus phosphafructokinase-1 C isozyme (Pfkc) gene, exons 3 through /	GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR	Mouse germ line gene coding for beta-globin (Y2)	Andes virus strain Ol23133 glycoprotein G1 and G2 precursor, gene, partial cds	M.musculus scp2 gene exon 14	601344648F1 NIH_MGC_8 Homo saplens cDNA clone IMAGE:3677794 5	Dictyostelium discoideum random stug cDNA19 protein (rsc19) mKNA, paruai cds	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds	Chlamydla trachomatis section 5 of 87 of the complete genome	DAUGHTERLESS PROTEIN	DAUGHTERLESS PROTEIN	Homo sapiens filamin 2 (FLN2) mRNA, complete cds	Arabidopsis thallana root gravitropism control protein (PIN2) gene, complete cds	Arabidopsis thallana root gravitropism control protein (PIN2) gene, complete cds	Homo sapiens cAMP specific phosphodlesterase (PUE4C) gene, exons z trirougn 1z	Horno sapiens cAMP specific phosphodlesterase (PDE4C) gene, exons 2 through 12	D.melanogaster DNA mobile element (noppel)	R.norvegicus mKNA for NTR2 receptor	Salvelinus pluvius mRNA for transferrin, complete cos	Salvelinus piuvius mKNA tor transferrin, complete cas	Chlorella vulgaris chloropiast, complete genome	Chlorella vulgaris chloropiast, complete genome	Pimephales prometas liver glucose-6-phosphate-1-denydrogenase mxnx, partial cos	Homo saplens ninein-Lm (sororm (rinein) mRNA, complete cas	EST387405 MAGE resequences, MAGN Homo saplens cDNA	ov@0a10.s1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1643810 3	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds	Mus musculus fructosamine 3 kinase (Fn3k), mRNA	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arnt1), mRNA	Mus musculus pale ear (ep) gene, wild type allele, 3 region, parnal cds	Homo sapiens lambda/lota protein kinase C-interacting protein mixivA, complete cus	Homo sapiens lambdaiota protein knase C-interacting protein minyty, complete cus
le Exon Prope	Top Hit Database Source	П	EST_HUMAN		ISSPROT	L			T_HUMAN		NT			/ISSPROT	NT	NT		NT	L	۲	LΝ	LZ	LZ	L'Z	LZ	LΝ	NT	EST_HUMAN	EST_HUMAN	NT	NT	LN	NT	NT	Ł
Builo	Top Hit Acession No.	X61033.1	AW360865.1	AF250371.1	P54422	V00726.1	AF028026.1		7.1	U82511.1	U71122.1	AE001278.1	P11420		AF146692.1			2.0E-01 AF157814.1	2.0E-01 AF157814.1	(78388.1	(97121.1	J89088.1	1 D89088.1	7524759 NT	7524759 NT	2.0E-01 AF206637.2	4F302773.1	2.0E-01 AW975297.1	2.0E-01 AI023592.1	2.0E-01 AF078164.2	11528495 NT	7549743 NT	1.9E-01 AF004353.1	1.9E-01 U32581.2	1.9E-01 U32581.2
	Most Similar (Top) Hit BLASTE	$\overline{}$			2.0E-01	2.0E-01	2.0E-01					2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01 X97121.1	2.0E-01 D89088.1	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	2.0E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01
	Expression Signal	3.2	4.02	1.28	0.68	0.84	5.8	2.95	0.99	0.82	0.68	4.97	0.65	0.65	2.11	1.98	1.98	0.68	0.68	69.0	2.78	1.56	1.56	1.4	1.4	1.51	1.39	1.36	3,58	2.68	1.87	3.9			1.43
	ORF SEQ ID NO:	32094	32200	32954	33102	33452		33925			35129	ŀ	35493			36792		35933										30894			30978			28058	
	Exon SEQ ID NO:	19105			١	1		ì	L	<u> </u>	21957		L	1	l_			L	L				_	L.,	L_	24762	ı	L	١.		L.	L			13420
	Probe SEQ ID NO:	6335	6435	72	7345	7675	7853	8100	8624	9251	9290	9456	9646	9646	9791	9941	9941	10067	10067	10114	10305	10744	10744	11609	11609	12358	12545	12556	12594	12618	12753	108	345	641	641

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31265 31463 31985 32050 32682 32683 32917 33149

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Top Hit Database Source	Marsupial cat bela-globin gene mRNA, partial cds	Marsupial cat beta-globin gene mRNA, partial cds	Г	EST_HUMAN repetitive element;	EST_HUMAN RC5-ET0082-080700-022-A02 ET0082 Homo sapiens cDNA	EST_HUMAN RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA	Arabidopsis thaliana DNA chromosome 4, conttg fragment No. 15	Arabidopsis thaliana DNA chromosome 4, conttg fragment No. 15	Homo saplens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, attematively	recirds.	ol96f02.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537487 3' similar to gb:L21696_cds1 EST_HUMAN PROTHYMOSIN ALPHA (HUMAN);contains element OFR repetitive element;	Г	EST_HUMAN PROTHYMOSIN ALPHA (HUMAN); contains element OFR repetitive element;	Rattus norvegicus sodium channel I mRNA, complete cds	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds	Drosophila melanogaster clathrin light chain mRNA, complete cds	Mus musculus p116Rip mRNA, complete cds	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated	Orzias latibes dene for membrane quantify cyclase OIGC1, complete cds	EST HUMAN wd71f02.xr NCi CGAP Lu24 Homo sepiens cDNA clone IMAGE:2337051 3'	Т	Yersinla pestis plasmid pCD1	Mus musculus guanyate nudeotide binding protein 1 (Gbp1), mRNA	Mus musculus guanyate nucleotide binding protein 1 (Gbp1), mRNA	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA	qg22d10.x5 NCI_CGAP_Kd3 Homo saplens cDNA clone IMAGE:1781811 3' similar to TR:075936 075936 EST_HUMAN GAMMA BUTYROBETAINE HYDROXYLASE;
Top Hit Acession No.	1 M14568.1 NT	1 M14568.1		1 AA912486.1 EST	1 BE830353.1 EST	1 BE830353.1 EST	1.9E-01 AL161503.2 NT	1.9E-01 AL161503.2 NT	F.74	1.9E-01 AFZ3391.1	AA912480.1 EST		1.9E-01 A912480.1	1.9E-01 M22253.1 NT	1.9E-01 AJ243213.1 NT	1.9E-01 L07344.1 NT	1.9E-01 AF287263.1 NT	AF055900.1 NT	1.8E-01 U73200.1 NT	1.8E-01 AB022090.1 NT	4502532 NIT	1.8E-01 AB021490.2 INT	Γ			6753947 NT	6753947 NT	4505036 NT	A1733708.1 EST
Most Similar (Top) Hit BLAST E Value	1.9E-01	1.9E-01		1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	, 10	1.95-1	1.9E-01		1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.9E-01	1.8E-01	1.8E-01	1 RE-04	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01
Expression Signal	1.24	1.24		0.61	0.85	0.85	2.48	2.48	000	Z.03	1.34		1.34	1.53	2.77	1.6	1.3	1.67	2.61	6.0	1 78	101	0.94	1.63	8.26	1.97	1.97	1.2	1.58
ORF SEQ ID NO:	34681	34682		35632	38005	36006	36470	38471	0860		36915		36916	37399	37645	37673	37772			25700	25802								
SEQ ID NO:	21536	21536	L			22790	23237	23237		43340	23661		23661	24088	24320	24343	24431	24785	12858	15539	13150	13503	13728	13828	14015	14239	14239	14577	14597
Probe SEQ ID NO:	8844	8844		9775	10142	10142	10540	10540	1005	0000	10986		10986	11487	11728	11752	11847	12399	30	253	384	729	96	1069	1266	1492	1492	1839	1859

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Mus musculus Scya6, Scya6, Scya16-ps, Scya5 genes for small Inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudocene, small inducible cytokine A5 precursor, scya16 pseudocene.	QV3-DT0018-081299-035-g04 DT0018 Homo sapiens cDNA	Jonopsidium acaule LEAFY protein (LEAFY2) gene. partial cds	xi41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2669756.3	QV0-BN0041-070300-147-004 BN0041 Homo sapiens cDNA	1/45901.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1517043' similar to contains Alu repetitive element;	y/45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1517043' similar to contains Alu repetitive element:	Bowne NB25 mRNA for MHC class II (Bol A-DOB), complete cds	Arabidopsis thallana DNA chromosome 4, contig fragment No. 56	Mus musculus Scya6, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds	S.tuberosum mRNA for alcohol dehydrogenase	MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA	an 28g07, y 5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE: 1700028 5	Mesconicetus auratus Na-taurocholate cofransporting polypeptide mRNA, partial cds	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90	yx38h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:284063 5'	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA	FORKHEAD BOX PROTEIN E3	yy62h02.r1 Soares_multiple_sclerosis_2NbHMSP Homo sepiens cDNA clone IMAGE:278163 5'	Citrulius lanatus mRNA for wsus, complete cds	Citrulius lanatus mRNA for wsus, complete cds	Bacillus halodurans genomic DNA, section 5/14	Human cellular DNA/Human papillomavirus proviral DNA	Bacterlophage Ike, complete genome	nh02a05.s1 NCI_CGAP_Thy/ Homo sepiens cDNA clone IMAGE:943088 similar to contains L1.t3 L1 repetitive element :	AMP NUCLEOSIDASE
JIO EXON Probe	Top Hit Database Source	N E	T HUMAN	Г	EST_HUMAN X	Г	EST HUMAN 10	1	NT		N E	NT	Т	EST HUMAN ar	Т		T HUMAN			г	EST_HUMAN yy	Г	†	1	Ĭ K		EST HUMAN re	П
DIIC	Top Hit Acession No.	01 AB051897.1		01 AF184589.1	01 AW182300.1	01 AW995178.1	1.8E-01 H03369.1	01 H03369.1	1.8E-01 D37954.1	2	01 AB051897.1	01 X92179.1	0.1	11 AI792382.1	01 AF181258.1	01 AL161594.2	11 N28629.1	6678428 NT	6678428 NT			-	-	1.1	1 M73258.1	9626232 NT	1 AA493751.1	
	Most Similar (Top) Hit BLAST E Value	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01 N94853.1	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01
	Expression Signal	1.75	2.36	1.89	1.29	1.76	0.88	0.88	1.43	5.94	2.9	0.94	. 2.03	1.06	4.68	0.82	89.0	1.18	1.18	1.15	2.06	1.18	1.18	0.7	1.23	1.22	0.5	0.94
	ORF SEQ ID NO:	27355			28319		28005	29006		29888	30087	30114	30311	30325	30367	31431	31558	31777	31778	32185		32689	32690	33103	35091	35198		35305
	Exen SEQ ID NO:	14645	15406	15665		15886	16363	16363	17038	17254	17453	17486	17707	17722	17754		18624	18817	18817	19187	19230	19644	19644	20027	21921	22028	22053	22126
	Probe SEQ ID NO:	1908	2697	2898	2904	3121	3610	3610	4289	4519	4721	4754	4984	4999	5035	5718	5835	6037	6037	6419	6463	9069	9069	7346	9242	9274	9391	9473

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					111)		
Probe SEQ ID NO:	Exen SEQ (D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9473	22126	35308	0.94	1.8E-01	1 P15272	SWISSPROT	AMP NUCLEOSIDASE
9514	22167	35348		1.8E-01	1 M26019.1	LΝ	S.commune orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9514	22167	35349	0.91	1.8E-01	1 M26019.1	٦N	S.commune orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9679	22331	35526	0.75	1.8E-0	1 P08123	SWISSPROT	COLLAGEN ALPHA 2(1) CHAIN PRECURSOR
9683	22335	35530	0.77	1.8E-01	1.8E-01 U67548.1	ΤN	Methanococcus Jannaschii section 90 of 150 of the complete genome
10033	22681		87.0	1.8E-01	1.8E-01 AF200252.1	NT	Aquarius amplus cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10266	22914	36124	1.48	1.8E-01	X63440.1	Ŋ	M.musculus mRNA for P19-protein tyrosine phosphatase
10533	23230	36465		1.8E-01	1.8E-01 X77336.1	TN	A.thaliana mRNA for ribonuclectide reductase R2
10577	23272		7.28	1.8E-01	11 U38908.1	L L	Bacterlophage r1t integrase, repressor protein (rro), dUTPase, holin and lysin genes, complete cds
10637	19644		2.61		1 AB018561.1	ΝΤ	Oftrullus lanatus mRNA for wsus, complete cds
10637		32690		1.8E-01	1 AB018561.1	ΙN	Citrulius lanatus mRNA for wsus, complete cds
10638	23329			1.8E-01	1 AF019107.1	LΝ	Dictyostelium discoldeum unknown (DG1041) gene, complete cds
10942	23621	36870		1.8E-01	1 M59257.1	LΝ	Human carcinoembryonic antigen (CEA) gene, exon 4
11439				1.8E-0	X57033.1	IN	B.taurus mRNA for potassium channel
11767	24358	37691	3.45	1.8E-01	8394421 NT	ΙN	Rattus norvegicus Thromboxane receptor (Tbxa2r), mRNA
11967	24514		1.59		TN 1988661 NT	LΝ	Bovine ephemeral fever virus, complete genome
12025	24553	31111	2.04	1.8E-0	1 BF348623.1	EST_HUMAN	602019928F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155318 5'
12476	24839		3.28	1.8E-01		SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12585	24908		1.91	1.8E-01		EST_HUMAN	yh48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12628	24931		2.3			Ā	E.dispar mRNA for hexokinase (hxk1)
12745	25324		1,61	1.8E-01		F	Rattus norvegicus CaBP9k gene
563	13345		1.57	1.7E-01	1.7E-01 BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
181	13559	26221	2:32			NT	P.dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4
941	13708		2.21	1.7E-0		SWISSPROT	NEUROFILAMENT TRIPLET L'PRÔTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1036	13796		1.89	1.7E-0	0.1	ΙN	Lymantria dispar nucleopolyhedrovirus, complete genome
1036	13796	26456	1.89	0-3 <i>1</i> ′1	1 AF081810.1	NT	Lymantria dispar nucleopolyhedrovirus, complete genome
1974	14710		2.6	1.7E-0	1 AF255051.1	TN	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2863	15631	28275	2.29		1.7E-01 AF000716.1	Ļ	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
	1						

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession. No.	Top Hit Database Source	Top Hit Descriptor
2863	15631	28276	2.29	1.7E-01	-01 AF000716.1	LΝ	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2927	15693	28338	1.55	1.7E-01	-01 AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2995	15761	28409	1.33	1.7E-01	-01 AJ238736.1	NT	Naja naja atra obc1 gene, axons 1-3
2995	15761	28410	1.33	1.7E	-01 AJ238736.1	N	Naja naja atra ctv-1 gene, axons 1-3
3103	15868	28508	1.24	1.7E	-01 AF081514.1	ΙΝ	Taxus canadensis gerany/gerany/ diphosphate synthase mRNA, complete cds
3430	18105	28845	1 74	17.	01 A 1289505 1	Ę	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene, adpE
3595	1		1.04	175	-01 AJ224877.1	Ę	Homo sapiens hap1 gene, complete ODS
3616	1		0.92	1.7E-01	5031886 NT	N.	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3018	1888	20300	4 84	77	01 6 1235377 1	- L	Homo sepiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1MIL/HRX gene fused to intron 5 of the AF-4/FFI nema
2010	1		0		A02000 4	F14	Sobietoment also periodities DNA
4077	L		80:1	11/11	-01 Ab2856.1	2	outsecond gragation apria repetitive Dryn. on F7609.X1 Soares fetal liver spleen 1NFLS S1 Homo saplens cDNA clone IMAGE:1848808.3' similar to
4787	17518	30140	1.08	1.7E	-01 AI247635.1	EST_HUMAN	contains OFR.b1 OFR repetitive element;
5054	17773		1.11	1.7E-01	-01 AF072725.1	TN	Zea mays starch branching enzyme IIb (ae) gene, complete cds
5122	17840	30456	0.75	1.7E	-01 D37951.1	N	Rattus norvegicus mRNA for MIBP1 (c-myc Intron binding protein 1), complete cds
5323	18126	30785	2	1.7E-01	-01 AA470686.1	EST_HUMAN	ne13a02.s1 NCL_CGAPCo3 Homo saplens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
	<u> </u>			,			ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S
5506	18304	31205	0.62	1.7E-01	-01 AA470686.1	EG HUMAN	ACIDIO RIBOSOMAL PRO EIN PT (HUMAN); Brudia pahandi mierefilaniai sheath probin SHP3 (shp3) gene, complete cds
6237	1_	31986		1.7E	-01 H72118.1	EST_HUMAN	ys02g06.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:213658 3'
6293	L	32048		1.75	-01 AI370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6293	19066	32049	76.0	1.7E-01	1.7E-01 AI370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:20454923'
6753	17922	30557	0.65	1.7E	-01 BE300286.1	EST_HUMAN	600944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
6780	19524		2.28	1.7E	-01 AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
6902	19640		0.88	1.7E	-01 Z92910.1	NT	Homo sapiens HFE gene
7120			1.1	1.7E	-01 AP000422.1	TN	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7197	L	32957			1.7E-01 BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7380		33139				SWISSPROT	PROBÁBLE PROCESSING AND TRANSPORT PROTEIN ULS6 (HFLF0 PROTEIN)
7396						SWISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
7760	İ		1.32		1.7E-01 AF000573.1	LN	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds	Homo saplens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA	Rat (SHR strain) SX1 gene	Homo sapiens neuroligin 3 Isoform gene, complete cds, alternatively spliced	Homo sapiens neuroligin 3 Isoform gene, complete cds, alternativaly spilced	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'	601116672F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3357184 5'	Bacillus halodurans genomic DNA, section 2/14	EST389564 MAGE resequences, MAGO Homo sapiens cDNA	EST389564 MAGE resequences, MAGO Homo sapiens cDNA	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3	Drosophila melanogaster mRNA for serine protease Inhibitor (serpin-6), (sp6 gene)	Homo saplens chromosome 21 segment HS21C084	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA	nq60e07.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L26081 TRANSFORMING PROTEIN RHOC (HUMAN);	Arabidopsis thallana DNA chromosome 4, contig fragment No. 42	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5	of43a03.s1 NOL CGAP_CNS1 Homo saplens cDNA clone IMAGE:1428924 3'	Mus musculus adenomatosis polyposis coll binding protein Eb1 (Eb1), mRNA	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA		al45f09.s1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:14602973'	AMP NUCLEOSIDASE	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FORN) (NEONATAL FO RECEPTOR) (IGG FO FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)	IGG RECEPTOR FCRN LARGE SUBUNIT PSI PRECURSOR (FCRN) (NEONATAL FC RECEPTOR)	(IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA	Homo saplens chromosome 21 segment HS21C078
le Exon Probes	Top Hit Database Source	NT P			EST_HUMAN R			NT H	EST_HUMAN 60	EST_HUMAN 60			T HUMAN	Ĭ	NT	Η		EST HUMAN TE	\Box	EST_HUMAN 60	EST_HUMAN of				HOMAN	SWISSPROT AN	OII TORNESIMS	Γ	/ISSPROT		NT TA
Suls	Top Hit Acesslon No.	01 AF150669.1	7706426 NT	7706426 NT	1	1.7E-01 D00384.1			1.7E-01 BE253142.1			1.7E-01 AW977455.1	Γ	П	01 AJ251749.1	01 AL163284.2	11427203 NT	01 AA627972.1		01 BE390835.1		7108300 NT	7106300	01 Y08391.1	01 AA883375.1	01 P15272	01 P55899		-01 P55899	1418157	01 AL 163278.2
	Most Similar (Top) Hit BLAST E Value	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01			1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01	1.7E-01		1.7E-01	1.7E-01	1.7E-01
	Expression Signal	0.62	6.19	6.19	0.47	5.09	0.75	0.75	0.48	0.48	7.85	0.51	0.51	3.14	0.63	2.4	1.4	1.72	0.45	8.78	2.65	9.13	9.13	1.62	1.69	1.83	1.62		1.62	2.62	1.95
	ORF SEQ ID NO:	33884	34001	34002	34431	34462	34580	34581	34916	34917	35323	35435	35436	35455	35555		36154	36156		36511	36637	36995	36996	37098	37341		37663		37664	37799	
	SEQ ID NO:	20558	20869	20869	21290	1	H	21435	21755	21755	22143	22250	22250	22268	22359	22781	22940	22942	23147	23274	23398	23725	23725	23813	24038	24307	24337		24337	24453	26320
	Probe SEQ ID NO:	7863	8175	8175	8298	8628	8743	8743	9906	9906	9490	9597	9597	9615	9708	10133	10293	10295	10501	10579	10709	11055	11055	11148	11348	11712	11746		11746	11874	12000

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Probe SEQ ID NO: 12268 12552 14917 1917 1917 1917 1917 1917 1917 191	<u> </u>	ORF SEQ ID NO: 25582 26927 26944 27364 27364 27364 27364 27364 27367 28308 29019 29019 30253 30254 30768	Expression Signal 1.65 1.65 1.65 1.65 1.16 1.16 1.16 1.16	Most Sim (7 op) H (7	Top Hit Acession No. No. No. AIB24404,1 AF27532,1 AF27532,1 AF298117,1 AF298117,1 AF298117,1 AF298117,1 AF298117,1 AF298117,1 AF186589,1 AF18689,1 AF186880,1	Top Hit Detabase Source	Top Hit Descriptor ACID RECEPTOR ALPHA-1 (HUMAN): Human bage globin region on chiromosame 11 Human bage globin september brone-box protein OTX2 gene, complete cds AXONIN-I PRECURSOR (AXONAL CLYCOPROTEIN TAG-1) Crassostrea gloss RNA polymerate complete cds AXONIN-I PRECURSOR (AXONAL CLYCOPROTEIN TAG-1) Crassostrea gloss RNA polymerate largest subunit mRNA, partial cds Homo sapiens mRNA for flowel T-cell activation protein Homo sapiens mRNA for novel T-cell activation protein Homo sapiens and the complete cds AXONIN-I PRECURSOR (AXONAL CLYCA) gene, promoter region Homo sapiens cytochrome P450 344 (CYP34A) gene, promoter region Homo sapiens cytochrome P450 344 (CYP34A) gene, promoter region Populus trichocarpa cv. Trichobel ABI3 gene Populus trichopel ABIA AND GAMAIA 184006 s1 Stratagene codon (#337204) Homo s
5938	18246	31134	2.15	1.6E-01	01 AF034716.1	NT Cot UIMANI	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
9938	١.	31909	0.83	1.6E-01	1.6E-01 BE925803.1 1.6E-01 RF183584.1	EST HUMAN	RC3-BN0034-310800-113-h01 BN0034 Homo saplens cDNA 601800725B4 NIH MGC 18 Homo contract and Alexa MACE And Agent of
6162		31910	0.71	1.6E-01	01 BF183584.1	Г	001009725R1 NIFL_MGC_18 Hamo sapiens cDNA clone IMAGE:4040335 3 601809725R1 NIFL MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3
	1					1	

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Probe SEQ ID S NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6334	19104	32092	2.37	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6334	19104	32093	2.37	1.6E-01	AL161588.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
9685	19602	32641	0.55	1.6E-01	AA398047.1	EST_HUMAN	zt89d04.r1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:729511 5'
6887	17944	30539	5:32	1.6E-01	AW291215.1	EST_HUMAN	UI-H-BIZ-agi-b-06-0-UI.s1 NCI_CGAP_Sub4 Home sapiens cDNA clone IMAGE:27244183'
7676	20340	33453		1.6E-01	AW 246359.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
7703	20366		0.74	1.6E-01	AU136525.1	EST_HUMAN	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004468 5'
7768	20464	33589	1.81		L49349.1	۲	Gorilla gorilla androgen receptor gene, partial exon
7924	20619		0.51	1.6E-01	BE244087.1	EST HUMAN	TCBAP1E0807 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0807
	T						Bacteroides vulgatus beta-lactamase (cfxA) gene, complete cds and mobilization protein (mobA) gene,
8018	20713	33844	0.87	1.6E-01	U38243.1	E	complete cds
8530	21222	34364	0.88	1.6E-01	Z99119.1	F	Bacillus subtilis complete genome (section 16 of 21); from 2997771 to 32/3410
8725	21417	34561	0.63	1.6E-01	R13673.1	EST_HUMAN	yf00h08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:26873 5'
8831	21523		0.59		L36861.1	IN	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
8870	21561	34708	1.72	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
6006	21699		0.83	1.6E-01	AF111167.2	F	Homo saplens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9551	22204		2.09	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041199-011-h01 ST0200 Homo saplens cDNA
9554	22207	35391	1.7	1.6E-01	249501.1	TN	S.cerewislae chromosome X reading frame ORF YJR001w
9589	22242		76.0		BE155664.1	EST_HUMAN	PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA
	23249	36486	3.3	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
10918	23598	36845		1.6E-01	014647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10918	23598	36846	1.59	1.6E-01	014647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10923	23603	36852	1.55	1.6E-01	BE259649.1	EST HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11059	23729		4.28	1.6E-01	AF106064.1	NT	Plasmodium falciparum calclum-dependent protein kinase-3 (odpk3) gene, complete ods
11388	23994	37296	7.28	1.6E-01	6671552 NT	N	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
11706	24301		1.26		BF527237.1	EST_HUMAN	602039465F2 NCI_CGAP_Bm67 Homo saplens cDNA clone IMAGE:4177073 5'
11886	25331		1.64	1.6E-01	6679466	ΓN	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
12002	24538	37273	5.28	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12292	24721	31052	1.72	1.6E-01	L14933.1	NT	Rat convertase PC5 mRNA, 5' end
12321	24740		1.5	1.6E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12418	25149		287.76	1.6E-01	AB045310.1	LN	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
12574	24901		2.4	1.6E-01	AK024496.1	LN.	Homo sapiens mRNA for FLJ00104 protein, partial cds

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Single Excit Floods Expressed in plant	Top Hit Descriptor	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product	Raftus norvegicus chondroitin sulfate protecglycan 5 (neuroglycan C) (Ospg5), mRNA	602152004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293145 5'	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA	L3-HT0619-040700-197-E05 HT0619 Homo saplens cDNA	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'	Homo sapiens chromosome 21 segment HS21C084	Opprinus carpio mRNA for EGGS22 myosin heavy chain, S'UTR	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end	xn39d11.x1 NCI_CGAP_Kid11 Homo caplens cDNA clone IMAGE:2696085 3'	Human gene for dihydrolipoamide succinyliransferase, complete cds (exon 1-15)	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds	UI-H-BI3-akb-b-09-0-UI,s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5	xw56a02.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_na1 THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	oogado5.s1 NCI_CGAP_GC4 Homo sapiens cDNA done IMAGE:1571337 3' similar to gb:M11433 RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);	L.stagnalis mRNA for G protein-coupled receptor	L. stagnalis mRNA for G protein-coupled receptor	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds	Homo sapiens pyruvate dehydrogenase kinasa, Isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein mRNA	hi10f06.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:29814113'	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA	Homo saplens chromosome 21 segment HS21C084	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 57	602083269F1 NIH_MGC_81 Homo saplens cDNA clone IMAGE:4247537 5	S.cerevisiae chromosoma VII reading frame ORF YGL086w
ום בייסוו בוסמם	Top Hit Database Source	L d		EST_HUMAN 6	П	EST_HUMAN L	П	NT TN	OL LN		NT . R	EST_HUMAN x		H		EST_HUMAN [U	EST_HUMAN 6	EST HUMAN T			NT PA	NT IL	\ <u>\</u>		HUMAN	Г			EST_HUMAN 6	
Billo	Top Hit Acession No.	-01 AF287344.1	9506522 NT	-01 BF672698.1	-01 BE710087.1		-01 AV711696.1	-01 AL163284.2	-01 AJ009735.1	(1	-01 L36125.1	-01 AW195516.1		-01 D26535.1	-01 AF117340.1	1	-01 BF695381.1	-01 AW572516.1	Γ		1.5E-01 Z23104.1	-01 Z23104.1	-01 U09964.1	7408358 NT	-01 AW665983.1				1.1	
	Most Similar (Top) Hit BLAST E Value	1.6E-01	1.6E-01	1.6E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1 AE 01	1.5E-01	1.5E-01	1.5E			1.5E-01
	Expression Signal	1.72	1.7	1.52	1.4	1.4	9.31	1.09	1.01	2.76	1.42	0.82	2.96	2.96	1.86	F	1.98	1.15	0.74	5.08	0.82	0.82	2.11	42 O	2.55	1.1	8.35	1.57	1.92	1.55
	ORF SEQ ID NO:		30992									L	26668	26669	26901		28162		28459	28761	28777	28778	29126	20140			29530		28162	
	SEQ ID NO:	24961	24973	25046	13050	13050	15517	13539		13833	13849	13946	14001	14001	14212	14638	15423	15680		16106	16120	16120	16491	18504	1	1_	L.		15423	1
	Probe SEQ ID NO:	12661	12687	12798	241	241	573	786	1070	1075	1091	1194	1252	1252	1465	1901	2716	2914	3048	3347	3361	3361	3738	4750	3848	4028	4161	4676	4703	5132

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Jani	Top Hit Descriptor	Morone saxatilis ganadotropin-releasing hormone type II gene, complete cds	1 PRECURSOR	Caiman crocodilus MHC class II beta chain (hcIlbeta) gene, complete cds	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)	L3-C70219-160200-064-F10 CT0219 Homo sapiens cDNA	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA	Mus musculus genomic fragment, 279 Kb, chromosome 7	601564322F1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:3833981 5'	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA	influenza B virus (BNanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds	Archaeoglobus fulgidus section 68 of 172 of the complete genome	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA	GLUTAMATECYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)		nw30d10.s1 NOT CGAP_GCB0 Homo saplens cDNA clone IMAGE:1241971 3'	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)	EST382376 MAGE resequences, MAGK Homo sapiens cDNA	ob73f02.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element:	Homo saplens HARP (HARP) gene, exon 17 and complete cds	wr52c08.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2491310 3'	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds	UI-HF-BN0-akk-d-05-0-UI.r1 NIH_MGC_50 Homo saplens cDNA clone IMAGE:3077409 5	UI-HF-BN0-akk-d-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5	Saccharomyces cerevisiae weak multicopy suppressor of los1-1 (SOL3) gene, complete cds	MEROZOITE RECEPTOR PK66 PRECURSOR (86 KD PROTECTIVE MINOR SURFACE ANTIGEN)
Single Exon Probes Expressed in brain		Morone saxatilis gonax	THROMBOSPONDIN 1 PRECURSOR	Caiman crocodilus MI-	SEX HORMONE-BIN (SBP) (TESTIS-SPEC	IL3-CT0219-160200-0	Mus musculus transfo	Mus musculus transfo	Mus musculus DNA n	Mus musculus DNA n	Mus musculus genom	601564322F1 NIH_M	Homo sapiens RAD54	Influenza B virus (B/N	Archaeoglobus fulgidu	Homo sapiens chromo	GLUTAMATE-CYST SYNTHETASE) (GAM	AMELOGENIN	nw30d10.s1 NCI_CG	HYPOTHETICAL 61.	EST382376 MAGE re	ob73f02.s1 NCI_CGAP_ LTR2 repetitive element:	Homo sapiens HARP	wr52c08.x1 NCI_CGA	Bos taurus Niemann-F	Bos taurus Niemann-F	UI-HF-BNO-akk-d-05-	UI-HF-BN0-ekk-d-05-	Saccharomyces cerev	MEROZOITE RECEP
gie Exoli Pio	Top Hit Database Source	Z	SWISSPROT	N	SWISSPROT	EST HUMAN	Ę	Į.	NT	LZ LZ	LN	EST HUMAN	M	FZ	Z	뉟	SWISSPROT	SWISSPROT	EST_HUMAN	SWISSPROT	EST_HUMAN	EST HIMAN	LN	EST_HUMAN	۲	LN	EST_HUMAN	EST_HUMAN	TN	SWISSPROT
	Top Hit Acession No.	1 AF056313.1	1 P07996	11 AF256652.1	P15196	1 AW850754.1	1.5E-01 U65016.1	J65016.1	1.5E-01 6753659 NT	6753659 NT	1 AJ276505.1	1.5E-01 BE727658.1	4506396 NT	1.5E-01 AF134907.1	1.5E-01 AE001039.1	11417236 NT		1 Q28462	11 AA714760.1	1 P30143	1.5E-01 AW970295.1	1 5E-01 AA811545 1	1.5E-01 AF210842.1	1.5E-01 AI973157.1	1.6E-01 AF299073.1	AF299073.1	1.5E-01 AW 500611.1	1.5E-01 AW500611.1	1 U48560.1	01 P21303
	Most Similar (Top) Hit BLAST E Value	1.5E-01	1.5E-01	1.5E-01	1.5E-01 P15196	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.6E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01 P48508	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.55-01	1.55-01	1.6E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01
	Expression Signal	1.05	2.16	1.15	6.92	5.08	8.42	8.42	3.09	3.09	1.93	3.1	1.77	2.09	2.21	4.99	J.95	2.35	1.25	1.66	6.82	07.0	2.07	2.98	2.04	2.04	2.04	2.04	0.81	0.96
	ORF SEQ ID NO:	30480	30499	30632		31139	31188	31189	31653	31654	31693	31847		31999	32176			32260	32381	32389	30554			33051		33255		33263		33775
	SEQ ID	17864	17984	18011	18051	1	18291	18291		18700	18734	18880	18929	19025	25089	19205	19216	19259	19348	19375	17958	25102	\mathbf{L}_{-}	i	20162	20162	20171	20171		20652
	Probe SEQ ID NO:	5145	5175	5203	5245	6451	5492	5492	5915	5915	5952	6102	6152	6251	6403	6437	6448	6493	8282	6612	6882	8078	7115	7290	7490	7490	7,499	7499	7640	7987

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Γ	Т	Т	1	Т	т	7	7	7	_	Γ-	T-	T	Т	Т	7	Т	T	т		Т	7	Т	Т	7	T	7	Т	Т	Τ-
Top Hit Descriptor	0085g12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA_clone IMAGE:1673030 3' similar to gb:M26052 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN):	601510523F1 NIH MGC 71 Homo sapiens cDNA clone IMAGE:3912004 5'	C16800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-529H09 5'	Pangaslanodon gigas growth hormone (GH) mRNA, complete cds	Homo saplens mRNA for ASK1, complete cds	WNT-10A PROTEIN PRECURSOR	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA	za59e06.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:296866 3' similar to	PIR:S44443 S44443 RAD23 protein homolog2 - human;	GV0000404 Human Psoriasis Differential Display Homo sapiens cDNA	AV754819 TP Homo sapiens cDNA clone TPAAHB125	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5	Acipenser transmontano vitellogenin mRNA, partial cds	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-deita - 4-deita isomerase gene, complete cds	Aplysia californica carboxypeptidase D mRNA, complete cds	Aplysia californica carboxypeptidase D mRNA, complete cds	P.lenlusculus mRNA for integrin beta subunit	wk53h12.x1 NCI_CGAP_Pr22 Homo sepiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN):	wk53h12.x1 NCI_CGAP_Pr22 Homo saplens_CDNA_clone_IMAGE;2419176.3' similar to gb:M27508_BETA_ GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HLIMAN):	Danio rerio transcription factor Pax8b (Pax9) mRNA, complete cds	Claviceps purpurea ps1 gene	Claviceps purpurea ps1 gene	CM2-BT0688-210300-122-f11 BT0688 Homo saplens cDNA	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C080	Homo sapiens chromosome 21 segment HS21C080	Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1	L6-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA	zw46d02.rf Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773091 5' similar to contains element MER27 repatitive element
Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	N	NT	SWISSPROT	N-		╗		EST_HUMAN	EST_HUMAN	Г	Ļ	¥	١	¥	EST_HUMAN		Τ	LN LN	ĽΣ	EST_HUMAN	EST_HUMAN			¥	EST_HUMAN	H HIMAN
Top Hit Acession No.	-01 AA970317.1	-01 BE884799.1	-01 C16800.1	-01 L27835.1			4501972 NT		01 N74226.1	-01 BF585465.1	-01 AV754819.1	7.1	-01 U00455.1	.01 M77144.1	-01 AF007570.1	-01 AF007570.1		01 AI814046.1		Γ	Γ	Γ		Γ	1.6E-01 AL163280.2				
Most Similar (Top) Hit BLAST E Value	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	į,	1.55-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01	1.6E-01	1.5E-01	1.5E-01	1.5E-01	1.5E-01
Expression Signal	1.13	0.95	11.54	1.6	1.65	0.71	1.16	0	2.88	F	2.3	0.74	7.32	0.53	7.51	7.51	2:92	2.16	2.16	2.01	1.43	1.43	1.62	1.62	7.31	7.31	1.7	1.6	1.95
ORF SEQ ID NO:	33947			34162			34575			34945			33543	35566	35674	35675	35965	36070	36071	36148	36311	36312	36526	36527	36654	36655		36944	36999
Exon SEQ ID NO:	20812	20905	20993	•	1	21204	21429			_	1		20424	22368	22472	Ш	22751	22855	22855	22933					23414	L	23576	23684	23727
Probe SEQ ID NO:	8118	8211	8299	8332	8491	8512	8737	2000	3005	9092	9100	9305	9353	9717	9821	9821	10103	10207	10207	10285	10438	10438	10595	10595	10726	10726	10896	11012	11057

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6490	19257		1.64	1.4E-01	-01 BE266536.1	EST HUMAN	601193523F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3537581 5
6209	19274	32275	2.45	1.4E-01	-01 BF378533.1	EST HUMAN	QV1-UM0036-080300-103-d09 UM0036 Homo saplens cDNA
7026	19718		0.65	1.4E-01	-01 AL118568.1	EST HUMAN	DKFZp761A0910_r1 761 (synonym: hamyZ) Homo sapiens cDNA clone DKFZb761A0910 5
7284	19967		1.51	1.4E-01	-01 AW015373.1	EST HUMAN	UI-H-BI0-aat-c-09-0-UI:s1 NCI_CGAP_Sub1 Homo saplens cDNA clone IMAGE:2710289 3
7521	20192	33283	1.19	1.4E-01	-01 U85645.1	NT	Oryctolagus cuniculus fructose 1,6, bisphosphate aldolase (AldB) gene, complete cds
7653	20317	33427	0.98	1.4E-01	-01 AI305192.1	EST HUMAN	qi90b12.x1 Soares_NhHMPu_S1 Homo saplens cDNA clone IMAGE:1879583.3'
8373	21066		1.23	1.4巨-01	-01 AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
8683	21376		0.57	1.4E-01	-01 A1436093.1	EST HUMAN	th92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2126111 3' similar to TR:002710 002710 GAG POLYPROTFIN
8811	21503	34650	4.18	1.4E-01		EST HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8892	21583	34722	0.59	1.4后-01	L	EST HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5
9021	21711	34864	76.0	1.46-01		EST HUMAN	y10h05.r1 Soares placenta NbZHP Homo sapiens cDNA clone IMAGE:138873 5
9021	21711	34865	0.97	1.4后-01	1.4E-01 R62746.1	EST HUMAN	y10h05.r1 Soares placenta NbZHP Homo sapiens cDNA clone IMAGE:138873.5
9085	21774	34938	8.81	1.4E-01	-01 BF310959.1	EST_HUMAN	601895465F1 NIH_MGC_19 Hamo sapiens cDNA clone IMAGE:4124824 5'
9175	21845	35011	1.24	1.4E-01	-01 W93411.1	EST HUMAN	zd94e04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element:
9246	Į '	35095	0.46	1.4E-01	-01 X73293.1	N	M.vannielii genes rooH, rooB and rooA
9246	21925	35096	0.46	1.4E-01	1.4E-01 X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9258		35111	1.46	1.4E-01	.01 Y10196.1	NT	Homo sapiens PHEX gene
9268	21937	35112	1.46	1.4E-01	-01 Y10196.1	NT	Homo saplens PHEX gene
9350	20421	33541	1.96	1.4E-01	-01 AF121361.1	NT	Drosophila melanogaster signal transducting adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finger protein (DNZ1) genes, complete cds
9704	22355	35551	0.97	1.4E-01	.01 X66092.1	L'N	C.perfringens ORF for putative membrane transport protein
9887	22537	35732	1.26	1.4E-01	-01 AF023813.1	LV.	Macromitrum levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
9988		35846	0.56	1.4E-01	-01 AW021908.1	EST HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
9886		35847	0.56	1.4E-01	1.4E-01 AW021908.1	EST HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5
10157		36022	0.81	1.4E-01	-01 BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10157	22805	36023	0.81	1.4E-01	.01 BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10360	23007		0.57	1.4E-01	01 T84293.1	EST_HUMAN	yd47d03.r1 Soares fetal liver spleen 1NFLS Home sapiens cDNA clone IMAGE:111365 5'
10499	23145	36372	0.62	1.4E-01	-01 Z99117.1	Νī	Bacillus subtilis complete genome (section 14 of 21); from 2599451 to 2812870
10607	23301		1.64	1.4E-01	01 AA811480.1		oa99a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:13203643'
10746	23433	36676	3.24	1.4E-01	-01 R53400.1		y/70c05.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154088 5'
10954	23631	36879	1.31	1.45-01	AW104982.1	EST_HUMAN	xd73e10.x1 Soares_NFL_T_GBC_S1 Home sapiens cDNA clone IMAGE:2603274 3'

PCT/US01/00667

WO 01/57275

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11036		36975	1.3	1.4E-01	-01 T96102.1	EST_HUMAN	ye47g10.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:120930 5'
11036	23707	36976	1.3	1.4E-01	-01 T96102.1	EST_HUMAN	ye47g10.r1 Soares fetal liver spieen 1NFLS Homo saplens cDNA clone IMAGE:120930 5'
11038	23709	36979	2.35	1.4E-01	-01 P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA- F) (VLA-5) (CD49E)
11262	L			1.4E-01	1	LN LN	C.perfringens ORF for putative membrane transport protein
11301	L	L		1.4E-01	-01 AW015373.1	EST_HUMAN	UI-H-BI0-eat-c-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11446	23213	36445	2.37	1.4E-01	1.4E-01 U28760.1	ΤΝ	Borrella burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), trosephosphate isomerase (TPI) genes, complete cds
11612				1.4E-01		NT	M.musculus p16K gene for 16 kDa protein
11743	24335	37661	1.83	1.4E-01	-01 AF146783.2	INT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
11827	24411	37747	1.31	1.4E-01	-01 AW664572.1	EST_HUMAN	hi14h08.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972319 3'
11827	24411	37748	1.31	1.4E-01	1.4E-01 AW664572.1	EST_HUMAN	hi14h08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:29723193'
12213	26172	30904		1.4E-01		TN	Ephydatia fluviatilis mRNA for aldolase, partial cds
12261	24706	31049	2.03	1.4E-01	-01 X74773.1	LN	P.salina plastid gene secY
12276	24714		2.2	1.4E-01	11968117 NT	NT	Rattus norvegicus desmin (Des), mRNA
12318	25383		2.84	1.4E-01	1.4E-01 BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo saplens cDNA clone IMAGE:3634329 5'
12413	24794		1.35	1.4E-01	-01 AF083221.1	LΝ	Fugu rubripes putative neurotransmitter receptore, YDR140w homolog, and glycinamide ribonucleotide transformylase (GART) genes, complete cds
12425	L		2.97	1.4E-01	.1	LN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
12500	l		3.15	1.4E-01 P10447		TORISSIMS	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12708	12222		6.26	1.4E-01		LN	Mus musculus mRNA for prolidase, complete cds
12779	25033		2.37	1.4E-01	1.4E-01 AW377998.1	EST_HUMAN	MR0-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
314	13118		3.12	1.3E-01	4758467 NT	NT	Homo saplens G protein-coupled receptor 50 (GPR50) mRNA
314	13118		3.12	1.3E-01	4758467 NT	IN	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
516	13300	25932	2.8	1.3E-01	AB013139.1	TN	Homo sapiens gene for NBS1, complete cds
621	13400	26035	1.05	1.3Ē-01	-01 AJ277606.1.	NT	Human calicivirus HU/NLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
621	13400	26036	1.05	1.3E-01	-01 AJ277606.1	칟	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
824	13594	26264	0.92	1.3E-01		NT	P.dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4
874	ı		1.8	1.3E-01	1.3E-01 AF139518.1	ΝŢ	Rattus norveglous A-kinase anchor protein mRNA, complete cds
1005	13765	28425	1.31	1.3E-01		N L	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

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	Top Hit Descriptor	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deanwatten	AV712467 DCA Homo saplens cDNA clone DCAAFF05.5'	Homo sapiens adapter protein CMS mRNA, complete cds	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA	Botrytis cinerea strain T4 oDNA library under conditions of nitrogen deprivation	Rhodopseudomonas acidophila pucB5, pucA5, pucB6, pucA6, pucA7, pucA8, pucA8 and pucC cenes and ORF151	RC4-ST0173-191099-032-d12-ST0173 Homo sepiens cDNA	Archaeoglobus fulgidus section 91 of 172 of the complete genome	Carassius auratus keratin type I mRNA, complete cds	Homo saplens chromosome 21 segment HS21C007	Boyine branched chain alpha-keto acid dihydrollooy transacylase mRNA complete cde	Arabidopsis thallana DNA chromosome 4, contia fragment No. 77	Bacterlophage SPBc2 complete genome	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA	Schistosoma mansoni fructose bisphosphate aldolase mRNA, complete cds	xx23f10.x1 Soares NFL T GBC S1 Homo sablens cDNA clone IMAGE:2813995.31	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'	Homo sapiens chromosome 21 segment HS21C080	Bovine branched chain alpha-keto acid dihydrolipovi transacylase mRNA, complete cds	601126096F1 NIH_MGC 9 Homo sapiens cDNA clane IMAGE:2990063 5	RC4-TN0077-180900-012-c05 TN0077 Homo saplens cDNA	ha07b06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA done IMAGE:2872979 3' similar to contains L1.b1 L1	L1 repetitive element;	CVV-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA	Emericella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA done IMAGE:4177233 5'	602039337F2 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4177233 5	Schizosaccharomyces pombe gene for Alp41, complete cds	Cjacchus Intron 4 of visual pigment gene (red allele)	26f3 Human retina cDNA randomly primed sublibrary Homo saplens cDNA
and Thomas and	Top Hit Database Source	N _T	EST HUMAN	Г			LN	L HUMAN			LN	IN		LN	EST_HUMAN		EST_HUMAN	EST_HUMAN	Г			EST_HUMAN	EST_HUMAN		П	HOMAN			EST_HUMAN (EST_HUMAN 6	Г		-	EST_HUMAN
5	Top Hit Acession No.	-01 AL115285.1	1.3E-01 AV712467.1	1.3E-01 AF146277.1	6680957 NT	1.3E-01 AL117078.1	1.3E-01 AJ243578.1	-01 AW812104.1	1.3E-01 AE001016.1	1.3E-01 M86918.1	-01 AL163207.2	1.3E-01 M21572.1	1.3E-01 AL161581.2	-01 AF020713.1	1.3E-01 AW364341.1	AF026805.1	-01 AW273741.1	-01 AV752279.1	-01 AV752279.1	-01 AL163280.2	-01 M21572.1	-01 BE272339.1	-01 BF091980.1	, 2000						1.3E-01 BF527281.1	-01 BF527281.1	-01 AB031326.1	-01 X88891.1	-01 W26367.1
	Most Similar (Top) Hit BLAST E Value	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.35-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01 /	1.3E-01	1.3E-01	1.3E-01	1.3E-01 /	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	L	1.35-01	1.0-30.1	1.3E-01	1.3E-01	1.3E-01 E	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01
	Expression Signal	2.6	1.13	1.18	76.0	2.18	1,22	1.2	3.34	4.76	1.01	0.98	1.43	1.27	4.24	2.03	18.62	0.99	66.0	12.76	0.77	2.68	0.74	6	3 8	2.23	0.77	0.75	0.97	0.57	0.57	15.12	1.95	0.75
	ORF SEQ ID NO:		26609		27303	27400			-	28042	28474	28849				29518	29532	29627	29628		29806	29863		11000	77000	80/00	+		31346	31628	31629	32162	32241	
	Exon SEQ ID NO;		13945		14588	14687	14896	15013	15101	15306	15831	16139			16879	16887	16903	16998	16998	17018	17181	17233	17688	07.00	200	3 3	18213	18295	18433	18681	18681	19161	19241	19608
	Probe SEQ ID NO:	1105	1193	1425	1850	1952	2167	2288	2379	2592	3065	3443	3969	4117	4137	4145	4163	4257	4257	4279	4445	4497	4963	0,70	5070	3510	2414	5497	2838	2896	5896	6392	6474	6691

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Top Hit Acession Database	01 BF529560.1 EST_HUMAN	21 H48664.1 EST_HUMAN	01 BE272339.1 EST_HUMAN	01 11423294 NT	M BF690522.1 [EST_HUMAN	11 BE562528.1 EST_HUMAN	11421556 NT	01 Z74102.1 NT	01 8923919 NT	01 BF690522.1 EST_HUMAN	01 R11172.1 EST_HUMAN		11068003	01 11068003 NT	01 AF023129.1 NT	1 N86348.1 EST_HUMAN	01 8393940 NT	01 AW851599.1 EST_HUMAN	01 AL 163246.2 NT	01 AU121237.1 EST_HUMAN	01 AW247836.1 EST_HUMAN	01 BF330999.1 EST_HUMAN	01 H01883.1 EST_HUMAN	01 AF119117.1 NT	01 6671745 NT	01 BF677328.1 (EST_HUMAN	01 BF677328.1 EST_HUMAN	01 BE279449.1 EST_HUMAN	01 BE619364.1 EST HUMAN	01 BF683555.1 EST_HUMAN	-01 BE618346.1
	BF5295	H48664.	BE2723		BF6905.	BE5625		Z74102.		BF6905	R11172	R11172			AF0231	N86348		AW851	AL1632	AU1212	AW247	BF3308	H01883	AF1191		I BF6773	I BF6773	I BE2794	1 BE6193	1 BF6835	BEATA
Most Similar (Top) Hit BLAST E Value	1,3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.3E-	1.3E-	1.3E-	1.3E-01	1.3E-	1.3E-	1.3E.	1.3E.	1.3E-01	1.3E		1.3E-	1.35	1.3E-01	1.3		1.3E-	1.3E	1.3E.	1.3E-	1 30
Expression Signal	66.0	1.96	0.88	1.34	1.17	0.51	0.64	4.47	4.44	1.02	0.58	0.58	0.61	0.61	3.71	0.56	66.0	0.85	1.1	0.64	0.52	2.93	1.56	1.33	3.28	1.42	1.42	4.26	1.94	1.44	1 37
ORF SEQ ID NO:				33694	33727		33998			34258										_	36347		36701	36980		37263		37504			24000
SEQ ID NO:	19651	19849	20554	20568	20597	20830	20866	20937	20979	21119	21538	21538	21807	21807	21947	22323	22599	22678	25128	23069	23117	23225	23458	23710	23879	23963	23963	24188	24317	i I	20070
Probe SEQ ID NO:	6914	7162	7859	7873	7802	8136	8172	8243	8285	8426	8847	8847	9119	9119	9372	9671	9951	10030	10291	10423	10471	10528	10775	11039	11216	11304	11304	11589	11723	11755	12444

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Single Exon Propes Expressed in Brain	Top Hit Descriptor	Gallus gallus scyc1 gene for lymphotactin, exons 1-3	R.norvegicus crp2 gene for cystatin related protein 2	Ephydatta fluviatilis mRNA for sALK-6, complete cds	wu24d09xf Soares, Dieckgraefe, colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:060287 KIAA0539 PROTEIN.;	#39b02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_ma1 ANNEXIN V (HUMAN);	Dictyostelium discoldeum ORF DG1016 gene, partial cds	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'	AU149146 NT2RM4 Hamo sapiens cDNA clone NT2RM4001691 3'	AV735249 cdA Home sapiens cDNA clone cdAAJB11 5'	al48e09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR.Q16671 Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR.	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATCA) (NF-ATCA)	at6909.x1 NCI CGAP Eso2 Homo sabiens cDNA clone IMAGE-1960553 3/	H.sapiens DNA for endogenous retroviral like element	UI-H-Bi3-aki-e-10-0-UI,s1 NCI_CGAP_Sub5 Homo saplens cDNA clone IMAGE:2734554 3/	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'	Homo sapiens chromosome 21 segment HS21C013	QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA	ts18g07.x1 NGL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] ;contains element PTR5 repetitive element :	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN):	Human creatine kinase-B mRNA, complete cds	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	QV1-BT0259-261099-021-d05 BT0259 Homo sapiens cDNA	Methanococcus jannaschii section 142 of 150 of the complets genome	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
gie Exon Prop	Top Hit Database Source	NT	Z F	F	EST_HUMAN	EST HUMAN	Z	N.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		T	Τ	EST HUMAN	Г	П	EST_HUMAN	EST HUMAN	Т	EST HUMAN	Į.	N	EST_HUMAN	П		NT
uio	Top Hit Acession No.	1.3E-01 AJ242790.1	1.3E-01 Z13994.1	1.3E-01 AB026829.1	-01 AW001114.1	1.2E-01 Al421744.1	-01 U66912.1	-01 AF039442.1	1.2E-01 AU149146.1	1.2E-01 AU149146.1	AV735249.1	-01 AA897474.1	-01 014934	1.2E-01 AI285402.1	1.2E-01 X89211.1	1.2E-01 AW449368.1	1.2E-01 BF248490.1	AL163213.2	AW996556.1	1.2E-01 AI623388.1	U18018.1	1.2E-01 A1720470.1	1.2E-01 M16364.1	X56882.1	1.2E-01 AW370668.1	J67600.1	1.2E-01 Z99118.1	X56882.1
	Most Similar (Top) Hit BLAST E Value	1.3E-01	1.3E-01	1.3E-01	1.3E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.26-04	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01	1.2E-01 U18018.1	1.2E-01	1.2E-01	1.2E-01 X56882.1	1.2E-01	1.2E-01	1.2E-01	1.2E-01
	Expression Signal	4.43	1.51	1.43	2.26	8.42	1.05	4.33	3.22	3.22	4.36	1.23	1.28	2.81	20.17	1.03	1.75	1.2	1.49	1.12	1.3	2.5	2:92	0.97	1.59	1.12	0.8	0.82
	ORF SEQ ID NO:					25844			26778	26779			27082	27082			27642	27748	28047	28176	28262	28318	28350	28418	28641			28921
	SEQ ID NO:	24695	24713	24915	24936	13199	12826	13317	14103	14103	14110	14243	14373	14392	14504	14650	14910	15009	15311	15438	15615	15659	15701	16770	15987	16014	16228	16267
	Probe SEQ ID NO:	12247	12274	12606	12636	374	416	534	1355	1355	1362	1496	1627	1646	1762	1913	2181	2284	2597	2731	2847	2903	2935	3004	3224	3252	3472	3511

PCT/US01/00667

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3511	16267	28922	0.82	1.2E-01	01 X56882.1	LN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3592	16228		1.46	1.2E-01	01 299118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
4160	16900	29528	1.97	1.2E-01	01 254255.1	TN	P.clarkii mRNA; repeat region (ID 2MRT7)
4160	16900	29529	1.97	1.2E-01	01 Z54255.1	N-	P.darkii mRNA; repeat region (iD 2MRT7)
4672	17406	30041	1.1	1.2E-01	01 Z48183.1	NT	L.esculentum mRNA for glyoxalase-I
4739	17471		0.92	1.2F-01	01 AF221633.1	LΝ	Rana ridibunda pitultary adenylate cyclase activating polypeptide variant 2 precursor, mRNA, complete cds, afternatively soliced
5170	L.	30492	0.81	1.2E-01	01 AA744369.1	EST HUMAN	ny63c04.s1 NCL_CGAP_GCB1 Home sapiens cDNA clone IMAGE:1282950 3'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively
5217	18025	30649	٢		01 AF223391.1	NT	spliced
5227	18034	30659	2.59	1.2E-01	-01 W33035.1	EST_HUMAN	zc08d02.r1 Soares_perathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5284			2.3	1.2E-01	01 298266.1	NT	Homo saplens gene encoding plakophilin (exons 1-13)
5418			0.68	1.2E-01	1.2E-01 Z48234.1	NT	M.domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6107	18884	31853	1.93	1.2E-01	1.2E-01 BE620945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6163	18930	31898	1.36	1.2E-01	01 P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
9029	18981	31960	2.35	1.2E-01	01 AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6270	19043	32020	1.54	1.2E-01	01 M26925.1	NT	Mouse galactosytransferase mRNA, complete cds
6337	19107	32097	0.57	1.2E-01	01 AA747535.1	EST_HUMAN	nx85c01.s1 NCI_CGAP_GCB1 Homo caplens cDNA clone IMAGE:1289024 3'
0999	19315	32321	1.14	1.2E-01	01 BF347985.1	EST_HUMAN.	602023112F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4158386 5'
8700	19616	32658	0.59	1.2E-01	01 AF295739.1	LN	JC virus agnoprotein, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
7793	20488		1.4	1.2E-01	01 BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA
7862	20557	33683	4.36	1.2E-01	01 Al913753.1	EST_HUMAN	wc99g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II;
7908	1		79'0	1.2E-01	1.2E-01 Q02369	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX 1-822) (CI-B22)
8208	20902		0.73	1.2E-01	01 AI832681.1	EST_HUMAN	at71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377438 3'
8296	20989		10.29	1.2E-01	01 AW083652.1	EST_HUMAN	xc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
							Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional
8315	21008		3.34	1.2E-01	01 AF053772.1	NT	regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8354	21047	34184		1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8354	1	34185		1.2E-01	1.2E-01 J03956.1	LN	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8499			1.09	1.2E-01	01 AJ271736.1	ΝΤ	Homo sapiens Xq pseudoautosomal region; segment 2/2
8589	21281		1.49	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome

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בייפור בי	ORF SEQ Expression (Top) Hit Acession ID NO: Signal BLAST E No. Source Source		35252 2.93 1.2E-01 X77961.1 NT		36543 1.38 1.3	2.17 1.2E-01 D26184.1 NT	3.18 1.2E-01 BE962324.2 EST_HUMAN	1.58 1.2E-01 BF314481.1 EST_HUMAN	37168 2.61 1.2E-01 AF190493.1 NT	37238 1.65 1.2E-01/R40249.1 EST_HUMAN	1.67 1.2E-01 M65109.1 NT	2.53 1.2E-01 AV658033.1 EST_HUMAN	3.52 1.2E-01/AJ271736.1 NT	30605 2.87 1.2E-01 Q04912 SWISSPROT	A CONTRACTOR OF THE CONTRACTOR	6.10 1.ZE-01/AF18889Z.1 N.	3.19 1.2E-01 AF039442.1 NI	2.11 1.2E-01 X53981.1 NT	30611 1.44 1.2E-01 BE061418.1	31007 5.86 1.2E-01/AI299903.1 EST_HUMAN	2.83 1.2E-01 L10187.1 NT	7.95 1.2E-01 096433 SWISSPROT	30989 1.39 1.2E-01 AE004428.1 NT	1.81 1.2E-01 Z99118.1	30614 1.38 1.2E-01 9845282 NT	25964 0.8 1.1E-01/AI561003.1 EST_HUMAN	26010 1.65 1.1E-01 AA569006.1 EST_HUMAN	26452 2.03 1.1E-01 BF697308.1		26552 4.62 1.1E-01/AW 972158.1 EST_HUMAN EST384142 MAGE resequences, MAGL Homo sepiens cDNA	26648 3.01 1.1E-01 D64004.1 NT	26943 2.52 1.1E-01 AU140363.1 EST_HUMAN	1.85 1.1E-01 6755215 NT (Mus musculus pre T-cell antigen receptor alpha (Picra), mRNA
			35252	35750	36543				37168	37238				30605		1			30611	31007			30989		30614	25964	26010	26452		26552	26648	26943	
<u> </u>	Exen SEQ ID NO:	3 21315		Ш		Щ				3 23944	2 24093		24683	5 25351		7,0047		_]			- 1			j		13334	13379	13792	13821			14257	_
	Probe SEO ID NO:	8623	947	066	10611	10801	10999	11094	11220	11283	11492	11892	12230	12305	1001	12417	124 18	12525	12586	12610	12632	1263	12663	12800	12812	551	601	1032	1083	1136	1227	1511	2312

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2540	15530		1	1.1E-01	E978676 NT	F	Raftus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2572	15286		1.17	1.1E-01	-01 AW821909.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Homo saplens cDNA
3030	15798	28442	0.82	1.1E-01	01 F03265.1	EST_HUMAN	HSC1RF022 normalized Infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3336	16096		1.78	1.1E-01	6753231 NT	L	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3415				1.1E-01	01 BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3627066 5'
3444	16200	28850	1.21	1.1E-01	-01 X62135.1	TN	C.reinhardtii nuclear gene on linkage group XIX
3570	16325	28972	22.0	1.1E-01	-01 Y07695.1	NT	A.immersus gene for transposase
3688	16441		0.74	1.1E-01	1.1E-01 P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3696	16450	29089	1.47	1.1E-01	.01 X52708.1	L	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4090	16833		1.28	1.1E-01	01 AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4090	16833		1.28	1.1E-01	-01 AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-507 ST0290 Homo saplens cDNA
4226	16967		8.78	1.1E-01	01 AF157068.1	TN	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4224	16995	29624	0.77	1.1E-01	-01 AW802056.1	EST_HUMAN	L5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
							Tapa-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1
4594		23958	0	1.1E-01	01 S44957.1	NT	of 7]
4780	17512	30134	1.2	1.1E-01	-01 Y07695.1	LN	A.immersus gene for transposase
							Mus musculus major histocompatibility locus class III region;butyrophilin-like protein gene, partial cds;
				7			Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2),
4957	16839		0.85	1.1E-01	01 AF030001.1	NT	CREB-RP, and tenascin X (TNX) genes, comple>
5077	17796	30412	1	1.1E-01	-01 P70281	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 3 (SCP-3 PROTEIN)
							nx76a03.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Atu repetitive
5584	18381		1.4	1.1E-01	01 AA747218.1	EST_HUMAN	element; contains element MER35 repetitive element ;
5653	18448	31361	1.23	1.1E-01	-01 AF020927.1	LΝ	6 Homo sapiens diacyiglycerol kinase 3 (DAGK3) gene, exon 6
5687	18480	31399	0.58	1.1E-01	01 AL110985.1	LN⊤	Botrytts cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5745	18537	31459	1.81	1.1E-01	-01 X68851.1	LN	S.pombe ste8 gene encoding protein kinase
5781	18572	31200	5.31	1.1E-01	-01 M86533.1	NT	Providencia rettgeri penicillin G amidase gene
2936	18718	31676	1.67	1.1E-01	-01 AJ007973.1	۲N	Homa sapiens LGMD2B gene
2955	18737	31696	1.75	1.1E-01	-01 BE769152.1		PM3-FT0024-130800-004-f12 FT0024 Homo saplens cDNA
5975				1.1E-01	01 AW853699.1	EST_HUMAN	RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA
6330	19100	32088	0.67	1.1E-01	-01 AL 163282.2	LN	Homo sapiens chromosome 21 segment HS21C082
6338	19108	32098	1.25	1,1E-01	.01 AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6381	19150	.		1.1E-01	7.1	EST_HUMAN	qg76d06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6512	ŀ	32278		1.1E-01		SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6604	19367		3.03	1.1E-01	-01 AF032922.1	۲	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2699			2.81	1.1E-01	11432372 NT	NT	Homo sapiens phosphatidylinositol givean class B (PIGB) mRNA
6948			2.0	1.1E-01	-01 AE002155.1	N.	Ureaplasma urealyticum section 56 of 59 of the complete genome
6948	19430	32446	2.0	1.1E-01	01 AE002155.1	F	Ureaplasma urealyticum section 56 of 59 of the complete genome
2802			0.89	1.1E-01	-01 BF382758.1	EST HUMAN	801816524F1 NIH MGC 56 Homo sapiens cDNA clone IMAGE 4050653 5
7203			0.84	1.1E-01	01 AP000006.1	Ľ	Pyrococcus harikoshii OT3 aenamic DNA 1166001-1485000 nt postiina (6/7)
7435	L.	33199		1.1E-01	01 BF684628.1	EST HUMAN	602140976F1 NIH MGC 46 Homo sapiens cDNA clone IMAGE:4302019 5'
7435			7.16	1.1E-01	01 BF684628.1	EST_HUMAN	602140976F1 NIH MGC 46 Homo sapiens cDNA clone IMAGE 4302019 5'
7555	20225	33329	1.93	1.1E-01	01 P41067	SWISSPROT	TRAB PROTEIN
7595	20263		3.35	1.1E-01	01 AA788784.1	EST HUMAN	ah31b06.s1 Soares, parathyroid, tumor NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb;J03483 CHROMOGRANIN A PRECURSOR (HUMAN):
7868	20563		0.5	1.1E-01	01 U67492.1	L	Methanococcus jannaschii section 34 of 150 of the complete cenome
8107	20801		1.7	1.1E-01	7.	EST HUMAN	nh04g10.s1 NCI_CGAP_Thyr Homo saplens cDNA clone IMAGE 943362
8107	20801		1.7	1.1E-01		EST HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8153	20847	33979	1.15	1.1E-01	01 X91233.1	F	H.saplens IL15 gene
8193	20887		1.14	1.1E-01	01 AW817918.1	EST_HUMAN	PM1-ST0270-080200-001-109 ST0270 Homo saplens cDNA
8249	20943	34081	1.45	1.1E-01	01 AL134349.1	EST_HUMAN	DKFZp547P194_H 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547P194 5
8717	21409	34552	80.0	1 15.01	01 03482 1	F	Pediococcus acidilactici H plasmid pSMB74 pediocin AcH production (pap) gene cluster papA, papB, papC
		İ					and paper genes, complete cos
8810	21602	34649	0.86	1.1E-01	01 Ai807474.1	EST HUMAN	w/48c01.x/ Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alurepetitive element;
8906	21597		0.47	1.1E-01	01 AF050081.1	FZ.	Homo saplens C16orf3 large protein mRNA, complete cds
8941	21632			1.1E-01	01 AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743.5'
8941	21632	Ì	2.04	1.1E-01	3.1	EST_HUMAN	293b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
8033	21723	34877	0.74	1.1E-01	01 112727.1	NT	P. furiosus partial dph5 gene and argF gene
9063	21752	34912	2.04	1.1E-01	1,172675.1	EST HUMAN	yd19h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to db://db:1181.80DIUMPOTASSIUM-TRANSPORTING ATPASE RETA.2 (HIIMAN):
0606	21779		9.0	1.1E-01	01 BE893260.1	Т	601436972F1 NIH MGC 72 Home sapiens cDNA clone IMAGE:3922048 5
9322	21989		0.88	1.1E-01		Г	CM3-HT0142-271099-026-g11 HT0142 Homo saplens cDNA
9396	22058		2	1.1E-01	01 BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
9810	22461		0.5	1.1E-01/	01 AL161543.2	Γ-	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10017	22665		0.45	1.1E-01	9.1		601140231F1 NIH_MGC_9 Hamo sapiens cDNA clone IMAGE:3049543 5'
10106	22754		1.67	1.1E-01		EST_HUMAN	y96a09.s1 Soares placenta Nb2HP Homo saplens cDNA clone IMAGE:1470643'
10235	22883	36096	1.26	1.1E-01	1.1E-01 U60529.1		Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10708	15796	28442	2.05	1.1E-01		EST HUMAN	HSC1RF022 normalized Infant brain cDNA Homo saplens cDNA clone c-1r102 3'

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					1115	באבון ווופעד בופוווס	
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	- Top Hit Descriptor
10840	23522		2.75	1.1E-01	1 AF169032.1	TN	Carassius auratus activin beta A precursor, mRNA, complete cds
		L					yn35f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu
10974	23650	36903	`	1.1E-01	1.1E-01 R23708.1	EST_HUMAN	repellive element, contains TAKT repellive element;
10983	23658			1.1E-01	6981351 NT	LV	Rattus norvegicus Phosphofructbklnase, Ilver, B-type (Pfk), mRNA
11002	18480	31399	1.31	1.1E-01	1 AL110985.1	L	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11134	23802	37079	1.58	1.1E-01	1.1E-01 X70058.1	NT	M.musculus cytokine gene
11169			3.21	1.1E-01	1 Z11910.1	NT	Z.mobilis tot and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11169	_			1.1E-01	1 Z11910.1	NT	Z.mobilis tgt and iig genes encoding tRNA guanine transglycosylase and DNA ligase
11277	L		2.81	1.1E-01	1 P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11674	24269		1.65	1.1E-01)1 AL161511.2	ΙN	Arabidopsis thallana DNA chromosome 4, contig fragment No. 23
11990	24629		1.36	1.1E-01		EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
12096	24598		3.92	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120800-014-f03 NT0112 Homo sapiens cDNA
12341	l		1.97	Ξ	BE974556.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
12750	25012	30977	3.15	1.1E-0	1 BF239753.1	EST_HUMAN	601906350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1179	13932		2,74	1.0E-01	1.0E-01 O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
	L						ws08d01.x1 NC_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.t3
1249				1.0E-01	11 AI985499.1	EST_HUMAN	MEK7 repetitive element ;
1371				1.0E-01	1 AL161504.2	본	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2493	15210		1.11	1.0三-01	M 451365.1		UI-H-Bi3-alc-d-07-0-UI.s1 NCI_CGAP_Sub5 Homo saplens cDNA clone IMAGE:2736420 3
3503	16259	28913	1.19	1.0E-01	1 BF033991.1	EST_HUMAN	601456301F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859849 5'
3708	16461	29100	1.03	1.0E-01	1 BF239818.1	EST_HUMAN	801906489F1 NIH_MGC_54 Homo sapiens oDNA clone IMAGE:4134071 5
3817	16569			1.0E-01	01 AF297061.1	NT	Escherichia coll enterotoxin EspC (espC) gene, complete cds; and unknown genes
3817	16569	L		1.0E-01	1 AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3935	ļ	29326	2.53	1.0E-01	01 BF365703.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo saplens cDNA
4518	17253			1.0E-01	1 AI792349.1	EST HUMAN	an32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4664		30032	1.19		1.0E-01 U50450.1	LN	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
4866	17594	30217	2.35	1.0E.(1 AW952344.1	EST_HUMAN	EST364414 MAGE resequences, MAGB Homo sapiens cDNA
5238	18044	L	9.73	1.0E-01	1.0E-01 W86490.1	EST_HUMAN	zh62h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416895 3'
5789	18580		1.21		11 AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
5934	18717	31675	14.15	1.0E-(01 AF274875.1	INT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6243	19017	31991	66.0		1.0E-01 AA481879.1	EST HUMAN	zv41g10.s1 Soares ovary tumor NbHOT Homo saplens cDNA clone IMAGE:756258 3' similar to contains L1.t3 L1 repetitive element ;
6256	1				01 AA406039.1	EST HUMAN	zu67c12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'
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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6924	- 1		1.81	1.0E-01	01 R23821.1	EST_HUMAN	//////////////////////////////////////
7635	- 1		2.67	1.0E-01	01 Y12488.1	FN	M.musculus whn gene
6022		33486		1.0E-01	01 AJ011400.1	IN	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7709	20373		99.0	1.0E-01	01 AJ011400.1	LN	Bos taurus mRNA for b17.2 subunit of NADH:ublquinons oxidoreductase complex (complex (
7834	20529	33656	99'0	1.0E-01	01 AA861091.1	EST_HUMAN	ak32g01.s1 Soares, testis, NHT Homo sapiens oDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP- DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8066	20760		0.5	1.0E-01	4758365 NT	L	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8390	21083		96'0	1.0E-01		EST_HUMAN	x09b01.x1 NCI_CGAP_Ut4 Homo saptens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN);contains TAR1.t3 TAR1 repetitive element;
9084	21773		1.04	1.0E-01	5.2	Z	Rattus norvegicus synaptic SAPAP-interacting protein Synamon mRNA, complete cds
9395	22057	35228		1.0E-01	01 R44993.1	EST_HUMAN	yg33h04.s1 Soares infant brain 1NiB Homo sapiens cDNA clone IMAGE:34549 3'
9407	22069		1.6	1.0E-01	01 M76729.1	TN	Human pro-alpha-1 (V) collagen mRNA, completa cds
9450	22000		3.02	1.0E-01	01 AE001501.1	۲Z	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9464	22074		0.75	1.0E-01		EST HUMAN	zc66c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:327282.3'
9721	22372		1.67	1.0E-01		EST HUMAN	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5
9835	22486		8.12	1.0E-01	01 AB046799.1	L	Homo sapiens mRNA for KIAA1579 protein, partial cds
9835	22486	35688	8.12	1.0E-01	01 AB046799.1	LN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10043	22691		0.97	1.0E-01	01 AW957425.1	EST_HUMAN	EST369615 MAGE resequences, MAGE Homo sapiens cDNA
10048	22696	35912	0.51	1.0E-01	01 T51952.1	EST HUMAN	yb29a06.s1 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72562.3' similar to contains Alu repetitive element
10229				1.0E-01	01 BE792750.1	EST HUMAN	601584604F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3939096 5'
10554	1 1		1.95	1.0E-01		EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
10958	23634		2.35	1.0E-01		EST_HUMAN	601877703F1 NIH_MGC_55 Homo saplens cDNA clone IMAGE:4106089 5'
10958	23634		2.35	1.0E-01		EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5
11376	23983	37283		1.0E-01	01 BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3836734 5'
11510	24110		1.52	1.0E-01	01 AP000400.1	Ę	Escherichia coli O157:H7 genomic DNA, prophage (Sakal-VT1) Inserted region. substrain:RIMD 0509952
11594	24193			1.0E-01	01 Z71446.1	N L	A.thaliana mRNA for CLC-b chloride channel protein
11594	24193			1.0E-	01 Z71446.1	TN	A.thaliana mRNA for CLC-b chloride channel protein
11832	24416			1.0E-	01 AV649035.1	EST_HUMAN	AV649035 GLC Homo saplens cDNA clone GLCBPG01 3'
11832	24416	37756		1.0E-		EST_HUMAN	AV649035 GLC Homo saplens cDNA clone GLCBPG01 3'
12083	24921		4.32	1.0E-	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo saplens cDNA clone IMAGE:3451933 5'
12300	24725		1.71	1.0E-01	7662165	Z	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA

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	Top Hit Descriptor	Drosophila melanogaster fiz gene	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds	Bacillus halodurans genomic DNA, section 1/14	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA,	complete cas	601070219F1 NIH_MGC_12 Homo sapiens cDNA cione IMAGE:3456365 5	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'	Homo sapiens neurexin III-alpha gene, partial cds	2u45c03.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740932 3	7477c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3'	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element contains element MIR MIR repetitive element:	M443-00 of NCI CGAD Over Home senions of the IMACE-2508528 2 similar to contains Alu	repositive element; contains element MIR MIR repetitive element;	Mus musculus phospholipid transfer protein (PItp), mRNA	O.saftva RAmy3C gene for alpha-amylase	Homo sapiens I factor (complement) (IF) mRNA	Daucus carota leucoanthocyanidin dloxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds	Leptosphaeria maculans beta-tubulin mRNA, complete cds	Leptosphaeria maculans beta-tubulin mRNA, complete cds	Human HPTP delta mRNA for protein tyrosine phosphatase delta	Human laminin B1 chain gene, exon 26	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA	Alce arborescens mRNA for NADP-malic enzyme, complete cds	Homo sapiens fibroblast growth factor receptor 3 (achondroplasta, thanatophoric dwarfism) (FGFR3) mRNA	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)	Caulobacter crescentus thymydilate kinase (trik) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
	Top Hit Database Source	노	EST_HUMAN	뉟	LN TN	Ŀ	N	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	N.	EST HUMAN		EST_HUMAN	Z	N	IN	Ŋ	Ŋ	INT	TN	TN	EST_HUMAN	LN L	NT .	LN.	EST HUMAN	SWISSPROT	TV.
	Top Hit Acession No.	-01 X00854:1	-01 BE537719.1	-01 U66834.1	-01 AP001507.1	7 0007 101	-02 AF2/4008.1	-02 BE545554.1	-02 BE545554.1	-02 AF099810.1	-02 Al821637.1	-02 BE674249.1	-02 D83710.1	-02 AW103088.1		-02 AW103088.1	6755111 NT	-02 X56338.1	4504578 NT	-02 AF184274.1	E-02 AF257329.1		-02 X54133.1		-02 BF037421.1	8393751 NT	-02 AB005808.1	4503710 NT	-02 BE168660.1	-02 099795	-02 AF099189.1
	Most Similar (Top) Hit BLAST E Value	1.0E-01	1.0E-01	1.0E-01	1.0E-01	200	9.9E-02	9.9E-02	9.9E-02	9.9E-02	9.9E-02	9.9E-02	9.9E-02	9.9E-02		9.9E-02	9.9E-02	9.8E-02	9.8E-02	9.8E-02	9.8E-02	9.8E-02	9.8E-02	9.8E-02	9.8E-02	9.8E-02	9.7E-02	9.7E-02.	9.7E-02	9.7E-02	9.7E-02
	Expression Signal	2.22	2.74	5.03	9.6	, 9	1.27	1.53	1.53	1.32	0.75	0.93	9.17	0.93		0.93	0.98	1.43	6.0	3.64	6.24	6.24	0.77	1.18	2.05	1.78	1.31	1.49	2.08	3.48	0.94
	ORF SEQ ID NO:						1		28236		29324		30547			33635	35055					29595			36436		26752		27724		30695
	Exon SEQ ID NO:	24738	24921		25002		-1	ı			16683		17951	20510	ì	20510	21887	13333	15865	15906	16939			21884	23204	24570	14077	14326	1	18714	18067
	Probe SEQ ID NO:	12317	12614	12677	12733	2010	19/7	2790	2790	3260	3933	4632	6875	7815		7815	9156	920	3100	3142	4198	4198	7381	9153	11437	12052	1328	1580	2257	3962	5261

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Caulobacter crescentus thymydliate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes,	EST386546 MAGE resequences, MAGC Homo saplens cDNA	Bacillus subtilis complete genome (section 16 of 21); from 2997771 to 3213410	yw41c03.s1 Weizmann Olfactory Epithelium Homo saplens cDNA clone IMAGE;254788 3'	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapians cDNA clone IMAGE:254788 3'	wx78b08.x1 NCI_CGAP_0v38 Homo sepiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_ma1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);	Mus musculus ligatin (Lgtn) mRNA, partial cds	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:16784853'	Proteus mirabilis fimbrial operon, strain H14320	EST378303 MAGE resequences, MAGI Homo sapiens cDNA	601498088F1 NIH_MGC_70 Homo sepiens cDNA clone IMAGE:3900165 5'	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55	602086769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250969 5'	Antirthinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)	Antirhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162	ym19h03.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:48653 3'	CM2-BN0023-050200-087-f12 BN0023 Homo saplens cDNA	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)	ac68a09.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:867736 3'	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds	Arabidopsis thallana DNA chromosome 4, contig fragment No. 38	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'	601453642F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3857243 5'	601453642F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3857243 5'
gie Exon Probe	Top Hit Database Source	L Z	T HUMAN		Г	EST_HUMAN	EST_HUMAN F	Г	EST_HUMAN	EST_HUMAN	±N	EST_HUMAN E	1		HUMAN	EST_HUMAN 6	TN		EST_HUMAN 6		П	SWISSPROT			EST_HUMAN (EST_HUMAN 8					1	EST_HUMAN 6
uio	Top Hit Acession No.	9 7E-02 AE099189 1	9.7E-02 AW954476.1	9.7E-02 Z99119.1		9.7E-02 N22798.1	9.7E-02 Al953984.1	9.7E-02 U58337.1	9.6E-02 A1080721.1	9.6E-02 Al080721.1	9.6E-02 Z32686.2	-02 AW966230.1	:-02 BE910039.1	9.6E-02 AU137084.1	9.6E-02 AV687898.1	:-02 BE894895.1	9.6E-02 AJ243211.1	AJ243211.1	-02 BF677270.1	9.6E-02 AB013985.1	85.1			-02 H14599.1	-02 AW992395.1	-02 P51854	:-02 AA780728.1	9.5E-02 AB003473.1	9.5E-02 AL161538.2	:-02 P51854	:-02 BF035861.1	BF035861.1	9.5E-02 BF035861.1
	Most Similar (Top) Hit BLAST E Value	9 7F-02	9.7E-02	9.7E-02	9.7E-02	9.7E-02	9.7E-02	9.7E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.6E-02	9.5E-02	9.5E-02	9.5E-02	9.5E-02	9.5E-02	9.5E-02	9.5E-02	9.5E-02	9.6E-02
	Expression Signal	0.94	1.43	3.24	1.28	1.28	1.49	2.84	1.11	1.11	5.8	0.99	3.13	9.0	1.31	1.12	1.29	1.29	9.0	1.54	1.54	3.35	7.22	3.34	2.1	0.85	0.55	4.72	7.68	0.84	1.83	1.83	2.36
	ORF SEQ ID NO:	96908	_			33708	34587		27470	27471	29675	30276			35300		35790	35791	35884	35915		١	36572		29452	31289	32729	32963	33234	31289			36509
	Exon SEQ ID NO:	18087	1	1	1	20577	21440	23819	14744	14744	17050	17668	18795	20968	22121	22423	22587	22587	22668	22699	22699	22806	23334	- 1	1		19681	19888	20141	18376	20475	20475	23273
	Probe SEQ ID NO:	5261	5924	7198	7882	7882	8748	11152	2009	2009	4311	4940	6014	8274	9444	9772	9939	9939	10020	10051	10051	10158	10643	12652	4081	5579	6988	7202	7467	7597	7780	7780	10578

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Probe SEQ ID NO: 10578 1827 1867 1867 1867 1287 1287 1287 1288 3251 4885 576 8146 8146 8146 9810 10091 12550			Signes			Top Hit Database Source Source EST HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	Top Hit Descriptor Top Hit Descriptor Source International Source Source NIT Meabricolum DNA' for CONTIG MOX73 NIT Actinetobacter sp. cysD., cobD., sodd, lysS, rubb, rubb, estB, ormplete cds NIT Adhers non-vegicus calcium channel alpha-1C subunit (ROBS) mRNA, complete cds NIT Adhers non-vegicus calcium channel alpha-1C subunit (ROBS) mRNA, complete cds NIT Adhers non-vegicus calcium channel alpha-1C subunit (ROBS) mRNA, partial cds NIT Adhers non-vegicus calcium channel alpha-1C subunit (ROBS) mRNA, partial cds NIT Homo saplers naeophenynges alphelium specific protein (NESG1), mRNA Source Sourc
222	13034		8.37	9.2E-02	J60315.1 J60315.1	ZZ	Molluscum contagiosum virus subtype 1, complete genome Molluscum contagiosum virus subtype 1, complete genome
222 2224 3175	1111			9.2E-02 9.2E-02 9.2E-02	9.2E-02 U60315.1 9.2E-02 R54156.1 9.2E-02 Q28631	NT EST_HUMAN SWISSPROT	Molluscum contagiosum virus subtype 1, complete genome yg98f07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 5' MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3289	16061	28709	0.85	9.2E-02	02 AA534354.1	EST_HUMAN	nf79e01.s1 NCI_CGAP_Co3 Homo seplens cDNA clone IMAGE:926136 3'

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		_				_		_							_	_	_							_						
Top Hit Descriptor	Mus musculus pre T-cell antigen receptor alpha (Ptora), mRNA	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2900176 5'	ya99c09.r1 Stratagene placenta (#897225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb.X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S). ALPHA SUBUNIT (HUMAN)	H.vulgare xylose isomerase gene	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds	Podospora anserina milochondrion, complete genome	O. cuniculus k12 keratin gene	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54	Homo sapiens WSH55 gene partial cds: and CLICA DDAH. Gân Gân Gân Gân Gân Gân Gân	CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'	Aeropyrum penix genomic DNA, section 4/7	Mus musculus thymopoletin zeta mRNA, complete cds	Homo sapiens gamma adducin gene, exon 9	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end	Tg616≂Cyl actin [Tripneustes gratilla≃sea urchins, embryos, Genomic, 5275 nt]	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes	zp38h12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMACE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA:	Rattus norvegicus cell cycle protein p55CDC gene, complete cds	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE	RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTICEN MOVAR (KB) CELLS FED.)	AN LIGEN MOV 19) (ND CELLS FBF)	h/39g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu	repetitive element;	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial ods	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds	Dictycstellum discoldeum spore coat structural protein SP65 (cotE) gene, complete cds	Plasmodium faiciparum P-type ATPase 3 gene
Top Hit Database Source	LΝ	L'N	EST_HUMAN	EST HUMAN	LN	N	LN	LZ	NT		뉟	EST_HUMAN	Z	N	Ν	EST_HUMAN	LN	NT	EST_HUMAN	Ę	NT		TOGGGGIVIO	ON ISSUED		EST_HUMAN	NT	NT	TN	TN
Top Hit Acession No.	6755215 NT	J92048.1	9.2E-02 BE299722.1	149920.1	E-02 X95256.1	-02 AF026552.3	11466872 NT	(77665.1	-02 AL161554.2		-02 AF129756.1	-02 AW160658.1	-02 AP000061.1	-02 U39073.1	-02 Y14379.1	-02 T02984.1	-02 S74059.1	-02 Y11187.1	-02 AA179901.1	9.1E-02 AF052695.1	1,7291390.1		02 546338	13320					۲.	-02 X65740.2
Most Similar (Top) Hit BLAST E Value	9.2E-02	9.2E-02	9.2E-02	9.2E-02	9.2E-02	9.2E-02 /	9.2E-02	9.1E-02	9.1E-02		9.1E-02	9.1E-02	9.1E-02	9.1E-02	9.1E-02	9.1E-02	9.1E-02	9.1E-02	9.1E-02	9.1E-02	9.1E-02		100 B	9.05-02	ļ	9.0E-02	9.0E-02	9.0E-02 /	9.0E-02 /	9.0E-02
Expression Signal	1.28	66.0	0.76	1.98	2.2	1.27	1.4	4.19	1.33		1.44	14.94	0.79	0.72	0.88	1.37	1.25	1.19	1.4	2.12	1.93		7	?		5.28	6.45	. 6.45	0.84	3.27
ORF SEQ ID NO:				33732	33889				29812					33383	34659		36218						28145	3	-	27064	28252	28253	28744	29989
Exon SEQ ID NO:	16328	16954	17013	20902	20770	24290	25412	12825	17187		18438	19968	20244	20275	21514	22974	23001	23029	25348	24653	25204		13501	3	,	14377	15511	15511	16091	17354
Probe SEQ ID NO:	3573	4213	4274	7907	8076	11695	12736	414	4451		5643	7285	7575	7609	8822	10327	10354	10383	12110	12181	12637		727	13,	į	1631	580g 780g	2806	3331	4619

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Top Hit Descriptor	za68a12.r1 Soares_fetal_lung_NbHL19W Homo saplens cDNA clone IMAGE:297684 6' sImilar to PIR:S52171 S52171 small G protein - human ;	7h63d03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element:	y11b08.s1 Scares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'	Escherichia coli strain E2348/69 pathogenicity Island, rOrf1 (rorf1), rOrf2 (rorf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN	(esch), SepQ (sepQ), Tir (tir), OrtU (ortU), >	SUZIZACSUFZ NIH_MGC_30 Home sapiens cunA cigne invAcE:4263831 3	OVZIZBUJUTZINIT MIGC. 30 FIORD SEPTIONS CLINA CIONE IMAGE: 4203831 3	TMU-TILUSOS-COTTOS-UOS-DUI TILUSOS FIGURO SEPRETS CONA Artichim garrietatim Atranfino protein (Atranfino) gana partial ode	U-H-Bi3-eio-f-08-0-U1:s1 NCI CGAP Sub5 Home sapiens cDNA clone IMAGE:3068294 3/	UI-H-Bi3-alo-f-08-0-UI.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'	Homo saplens similar to endoglycan (H. saplens) (LOC63107), mRNA	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE]	H. sapiens flow-sorted chromosome 6 Hindlil fragment, SC6pA20F8	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'	EST180187 Liver, hepatocellular carcinoma Homo saplens cDNA 5' end	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element ;	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1	MER10 repetitive element;	EST4454 Fetal brain I Homo sapiens cDNA 5' end	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)	MYOSIN-2 ISOFORM	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMACE:4286180 5'	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])	EST11595 Uterus Homo saplens cDNA 5' end
Top Hit Database Source	EST_HUMAN	EST HUMAN	EST HUMAN		LN L	ESI_HUMAN	EST HUMAN	EST HOMAN	EST HIMAN	EST HUMAN	Z L	SWISSPROT	LN	SWISSPROT	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN		EST HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN	NT	SWISSPROT	EST HUMAN
Top Hit Acession No.	W56037.1	BF062651.1	R62805.1		AF022236.1		BF701593.1	DE1535/2.1	AV 452122 1		11433478 NT	P47259	Z79021.1	P29475	BF701665.1	BF701665.1	AA309319.1	AI285627.1		AI285627.1	AA339356.1	P30143	P19524	BF696918.1	U29895.1	Q27474	AA299128.1
Most Similar (Top) Hit BLAST E Value	9.0E-02	9.05-02	9.0E-02		9.0E-02	8.9E-02	8.95-02	8.9E-02	8.9E-02	8.9E-02	8.9E-02	8.9E-02		_	8.9E-02	8.9E-02	8.9E-02	8.9E-02		8.9E-02	8.9E-02	8.9E-02	8.9E-02		8.9E-02		8.8E-02
Expression Signal	5.21	1.14	0.72		2.01	1.99	1.99	1.22	3.22	3.22	3.39	1.64	2.06	1.08	0.72	0.72	4.72	8.0		0.8	0.76	1.49	1.48	3.05	1.61	1.59	1.03
ORF SEQ ID NO:	31640		32619		-		26850		31474			32848	L	33768	33858		34331	35356			35477						29272
Exon SEQ ID NO:	18691	19381		}	- 1	14166	14156	15107	18552	18552	18567	19782	20132	20644		ļ	21188	22173		22173	22284	25173	25207	24591	24716	14100	16833
Probe SEQ ID NO:	5906	6819	9999		12486	1418	1418	23,72	5760	5760	5776	7093	7458	7949	8030	8030	8496	9520		9520	9632	11882	11940	12085	12284	1352	3883

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SEQ ION SE						֓֞֜֜֜֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	
	SEQ ID	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	Database Source	Top Hit Descriptor
4014	16760		3.55	8.8E-02	-02 000268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130)
	16955		66.0	8.8E-02	4502804 NT	N	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4269 1	17009		1.27	8.8E-02	4580423 NT	LΝ	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
	20120		0.57	8.8E-02	-02 D17520.1	۲N	Sheep mRNA for angiotensinogen, complete cds
	21577	34719	1.07	8.8E-02	-02 AA151872.1	EST_HUMAN	zn99a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
	23732	37003	2.7	8.8E-02	-02 BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
	23732	37004	2.7	8.8E-02	-02 BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
	23891	37178	6.92	8.8E-02	-02 AL040129.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
	24395	37729	1.49	8.8E-02	-02 P97803	SWISSPROT	CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN 3 (PROTEIN EF-10)
12155 2	24641	31098	2.66	8.8E-02	-02 Z71561.1	Z	S.cerevisiae chromosome XIV reading frame ORF YNL285w
	14388	27077	1.15	8.7E-02	-02 AI167281.1	EST_HUMAN	ox65b01.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:16611613'
3681	16434	29077	3.66	8 7E-02	-02 1082695.2	LΝ	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes. complete cds: and bissma membrane calcitim ATP-asa isoform 3 (PMCA3) and bissma membrane calcitim ATP-asa isoform 3 (PMCA3) and bissma membrane calcitim ATP-asa isoform 3 (PMCA3) and bissma membrane calcitim ATP-asa isoform 3 (PMCA3).
L	1						
	16434	29078	3.66	8.7E-02	-02 U82695.2	Ā	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and bigiycan (BGN) genes, complete ods; and plasma membrane calcium ATPase Isoform 3 (PMCA3) cene, partial ods
L	17392	30027	1.19	8.7E-02		L	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5231 1	18037	30663	5.88	8.7E-02		EST_HUMAN	2255g08.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:701438 3'
	18037	30664	5.88	8.7E-02		EST_HUMAN	zs55g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA cione IMAGE:701438 3'
	19578	32612	0.77	8.7E-02		LN	Mus musculus partial Konq1 gene for potassium channel protein, exons 10-14
	19578	32613	0.77	8.7E-02		TN	Mus musculus partial Konq1 gene for potassium channel protein, exons 10-14
4	19425	32440	0.71	8.7E-02		NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
	20457		0.45	8.7E-02	-02 AA284532.1	EST_HUMAN	z/20e03.s1 Soares overy tumor NbHOT Homo sapiens cDNA clone IMAGE:713692.3'
8413 2	21106	34246	6.0	8.7E-02		NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
	21106	34246	6.0	8.7E-02	3-02 AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
	23304		2.46	8.7E-02		LN	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
	23943	37237	2.55		-02 AJ007763.1	IN	Gluconobacter oxydans tRNA-lle and tRNA-Ala genes
	24633		2.1	8.7E-02		NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
	24750		1.75	8.7E-02	6679057 NT	NT	Mus musculus nidogen 2 (Nid2), mRNA
	13979	26649	7.02	8.6E-02		NT	Homo saplens Xq pseudoautosomal region; segment 2/2
2240 1	14968	27706	1.82	8.6E-02	8,6E-02 BE408667.1	EST HUMAN	601304016F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3638643 5'
	15946	28596	4.57	8.6E-02		NT	Trichomonas vaginalis bela-tubulin (btub1) gene, complete cds

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						שום באטוו רוטג	Single Exoli Probes Expressed in Brain
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3635	16388		3.77	8.6E-02	AF153362.1	Z-	Dictyostelium discoideum adenytyl cyclase (acrA) gene, complete cds
5134	17852		0.86	8.6E-02	8.6E-02 BF570296.1	EST_HUMAN	602185716T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310259 3'
6003			4.75	8.6E-02	8.6E-02 Y10826.1	LN	Homo sapiens LON1b gene
6281		32033	1.56	8.6E-02	8.6E-02 J00440.1	LN	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6281			1.56	8.6E-02	8.6E-02 J00440.1	LN	Mouse germline IgM chain gene, D region; D-q62, mu switch region (part a)
7481			1.34	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
7831			1.25	8.6E-02	TN 9900675	۲N	Homo saplens Snf2-related CBP activator protein (SRCAP) mRNA
7831			1.25	8.6E-02	5730066 NT	ĮŅ.	Homo saplens Snt2-related CBP activator protein (SRCAP) mRNA
7969			0.62	8.6E-02	11427428 NT	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8031	20726		0.81		U60168.1	LΖ	Dictyostalium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9637	22289	35482	1.76		8.6E-02 AF111170.3	LZ LZ	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9673			0.58		8.6E-02 AW662153.1	EST HUMAN	hi20c08.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972846 3'
10053	22701	35918	0.81	8.6E-02	8.6E-02 AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
10865	23545	36792	8.	8.6E-02	8.6E-02 AF206551.1	FZ	Lacerta media cytochrome c oxidase subunit 1 gene, partial ods; mitochondrial gene for mitochondrial product
10865	23545	36793	. 8.	8.6E-02	8.6E-02 AF206551.1	FZ	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11214	ı		4.64	8.6E-02	8.6E-02 BF305606.1	EST HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA cione IMAGE:4139216 5'
11214	23877		4.64	8.6E-02	8.6E-02 BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11417	ı		5.97	8.6E-02	8.6E-02 AE001073.1	NT TN	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11568	24167	37481	2.11	8.6E-02	AF283660.1	Ę	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete ods
2395	ı		3.3	8.5E-02	8.5E-02 AE000652.1	N	Heirobacter pylori 28695 section 130 of 134 of the complete genome
5583	18380	31292	0.75	8.5E-02	8.5E-02 AA985491.1	EST HUMAN	og83b07.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592917.3' similar to gb:K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5621	18417		1.29	8.5E-02 P08089	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
5921			6.95	8.5E-02	AF233885.1	Ę	Mus musculus phospholipase C-like protein mRNA, partial cds
8504	21196		1.65	8.5E-02	8.5E-02 6754779 NT	F	Mus musculus myosin XV (Myo15), mRNA
9736			2.81	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo saplens cDNA
9736	L	35592	2.81	8.5E-02	8.5E-02 BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo saplens cDNA
10261		36119	0.54	8.5E-02	8.5E-02 X76731.1	NT	V. smmodytes gene for ammodytoxin C
10382	23028		0.87	8.5E-02	11418108 NT	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11105			8.87	8.5E-02	8.5E-02 AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11125	23794	37070	4.43	8.5E-02	AB001562.1	TN	Streptococcus mutans gene for glucose-1-phosphate uridylylitransferase, complete cds

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-		Т	Т	T	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	Т	1	Т	Т	Т	Т	Ţ.	7	_		Т	Т	Т	Т	Т	Т	Г
	Top Hit Descriptor	EST72736 Ovary II Homo sapiens cDNA 5' end	zd44e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5	wf10f11.x1 Sogres_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2350221.3' similar to contains element MSR1 renefitive element	Cavia porcellus giycoprotein alpha-subunit mRNA, complete cds	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds	Homo sapiens mRNA, similar to rat myomegalin, complete cds	601190436F1 NIH_MGC_7 Hamo sapiens cDNA clone IMAGE:3534393 5'	Homo sapiens mRNA for FLJ00050 protein, partial cds	CM3-BT0790-260400-162-405 BT0790 Homo sapiens cDNA	Homo sapiens attractin precursor (ATRN) gene, exon 2	as88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335642.3' similar to TR:088312 088312 GOR4.	vi83112.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE 145895 51	kodes hexagonus mitochondrion, complete genome	kodes hexagonus mitochondrion, complete genome	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210.37	wo79f11x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'	Homo sapiens protocadherin 43 gene, exon 1	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drp2) mRNA, complete cds	og88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA done IMAGE:1455422 3' similar to contains L1.11 L1 L1	repenate element;	ode1710,ST NCI_CGAP_Kide Homo sapiens cDNA clone IMAGE:1592779 3	ia05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE I IKF	Arabidopsis thallana DNA chromosome 4, contig fragment No. 91	Dictyostellum discoideum DocA (docA) mRNA, complete cds	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929993 5'	Gallus gallus mRNA for for OBCAM protein gamma isoform	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C006	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
101111111111111111111111111111111111111	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST HUMAN	Z	Z	LN	EST_HUMAN	LN	EST HUMAN	NT	FST HIMAN	EST HUMAN	NT	NT	SWISSPROT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	MALE	TOT HOMEN	EST HOMAN	EST HUMAN	NT	LN	EST HUMAN	LN L	NT	TN	NT
	Top Hit Acession No.	4A362934.1	8.4E-02 W69330.1		8.4E-02 AF257213.1		8.4E-02 AB042555.1	-02 BE267153.1	8.4E-02 AK024458.1	8.4E-02 BE095074.1	-02 AF218890.1	-02 A1735184 1	-02 R79408.1	5835680 NT	5835680 NT	-02 P75334	8.3E-02 AI436797.1			-02 AF052683.1	-02 AF195787.1				-02 AW683503.1		-02 AF020409.1	-02 BE958458.1	-02 Y08170.2	-02 AF167077.2		-02 AL161498.2
	Most Similar (Top) Hit BLAST E Value	8.5E-02	8.4E-02	8.4E-02	8.4E-02	8.4E-02	8.4E-02	8.4E-02	8.4E-02	8.4E-02	8.4E-02	8.4E-02	8.4E-02 F	8.3E-02	8.3E-02	8.3E-02	8.3E-02	8.3E-02	8.3E-02/	8.3E-02	8.3E-02 A	, 00 L0 0	0.35-02/	0.3E-02	8.3E-02	8.3E-02	8.3E-02	8.3E-02 E	8.2E-02	8.2E-02	8.2E-02 A	8.2E-02
	Expression Signal	3.8	3.73	-	1.07	1.07	4.97	9.84	1.72	7.18	1.01	1.83	1.68	0.92	0.92	6.91	0.83	0.83	1.05	3.05	2.98	97	01.0	1.32	1.41	1.88	0.49	1.67	7.15	1.98	2.07	1.35
	ORF SEQ ID NO:		28121	29184	29685	29686	30472	30661	32366	33751	34578	36118	31122	27465	27466	28980	29001	29002	31914	32023	33702				35291					26914		
	Exon SEQ ID NO:		15602	16553	17060	17060	17855		19353	20623	21433	22908	1	l '	1			16360		19046	20575	2000	0000	70007	22116	22001	22888	25353	14105	14228	15837	16536
	Probe SEQ ID NO:	12700	2672	3801	4321	4321	5137	5229	0690	7928	8741	10260	12070	2005	2005	3580	3607	3607	6166	6273	7880	7044	1010	020	9438	9451	10240	12158	1357	1481	3071	3784

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Single Exoli Flobes Explessed il Dialil	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C006	LEUCOCYTE ANTIGEN CD97 PRECURSOR	LEUCOCYTE ANTIGEN CD97 PRECURSOR	LEUCOCYTE ANTIGEN CD97 PRECURSOR	Mus musculus zinc transporter (ZnT-3) gene, complete cds	.inflatum transposon Restless DNA	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds	AV743341 CB Homo saplens cDNA clone CBLANF07 5'	RC2-PT0004-031299-011-d05 PT0004 Homo saplens cDNA	Beet necrotic yellow veln virus RNA-2	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356696 6'	Chlamydophila pneumoniae AR39, section 73 of 94 of the complete genome	Mus musculus epidermal growth factor receptor (Egfr) yene, exons 5 through 28, and complete cds,	alternatively spiced	Xylella fastidiosa, section 152 of 229 of the complete genome	A1484F Heart Homo saplens cDNA clone A1484	Homo saplens chromosome 21 segment HS21C079	wd86f08.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:2338503 3'	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds	Homo sapiens chromosome 21 segment HS21C002	EST366723 MAGE resequences, MAGC Homo sepiens cDNA	Molluscum contagiosum virus subtype 1, complete genome	Human gene for dihydrolipoamide succinyliransferase, complete cds (exon 1-15)	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2287259	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'	Diotyoselium discoideum cyclic nucleotide phosphodiesterase gene, complete cds	Thermoplasma acidophilum complete genome; segment 5/5	EST378191 MAGE resequences, MAGI Homo saplens cDNA
e exoli Flobe	Top Hit Database Source	NT H	SWISSPROT LE	SWISSPROT LE	SWISSPROT LE		NT T.	EST_HUMAN 60		П	THUMAN	Г	EST_HUMAN 60	Τ		NT		EST_HUMAN A1)H	EST_HUMAN WC)H		T_HUMAN				EST_HUMAN PI	NT S		EST_HUMAN 60			EST_HUMAN ES
Billo	Top Hit Acesslon No.	06.2							8.2E-02 AF309555.1					8.2E-02 AE002246.2			6.1			8.1E-02 AI692681.1	26974	11426974 NT			3.1				8.0E-02 BE067219.1			8.0E-02 BF246744.1		8.0E-02 AL445067.1	
	Most Similar (Top) Hit BLAST E Value	8.2E-02	8.2E-02 P48960	8.2E-02 P48960	8.2E-02 P48960	8.2E-02 U76009.1	8.2E-02.2	8.2E-02	8.2E-02/	8.2E-02 /	8.2E-02	8.2E-02 X04197.1	8.2E-02	8.2E-02/		8.2E-02	8.1E-02/	8.1E-02 T11532.1	8.1E-02	8.1E-02/	8.1E-02	8.1E-02	8.1E-02/	8.1E-02	8.0E-02	8.0E-02 U60315.1	8.0E-02	8.0E-02 D26535.1	8.0E-02	8.0E-02	8.0E-02 D90915.1	8.0E-02	8.0E-02 M23449.1	8.0E-02	8.0E-02/
	Expression Signal	1.07	4.97	4.97	4.97	2.44	2.39	1.49	3.09	0.57	2.95	5.36	2.24	4.03		3.65	0.79	1.19	99.0	1.25	0.61	0.61	1.64	2.08	5.03	0.79	9.85	9.85	3.27	1.09	1.09	4.2	86'0 .	1.45	1.01
}	ORF SEQ ID NO:	29371	29617	29618	29619	30354		30687	32707		34509	35332	35512	31102			31378	32040			34067	34068	-	37395	25447	26344	27134	27135	27343	27835	27836		26486	28315	29182
	Exon SEQ ID NO:	16737	16992	16992			l_		19861	20298	21362	22152	22315	24646		25138	18463	19059	19786	1	20932	20832	1	1	16534	13682	15576	15576	14633	15096	15096	15191	13827	15867	16549
	Probe SEQ ID NO:	3989	4251	4251	4251	5022	5070	5252	6925	7632	8670	9499	9663	12164		12554	2668	6286	1607	7482	8238	8238	9812	11482	5	916	1694	1694	1896	2374	2374	2473	2823	2901	3797

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Single Exol Modes Explessed III Diani	Top Hit Descriptor	ti31g02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:21321143'	M.musculus gene for gelatinase B	UI-H-BI1-afd-f-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721547 3'	Homo sapiens ABCA1 (ABCA1) gene, complete cds	Homo sapiens ABCA1 (ABCA1) gene, complete cds	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	H,sapiens AGT gene, intron 4	H.saplens AGT gene, Intron 4	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds	Drosophila orena hunchback region	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA	600943191F1 NIH_MGC_15 Hamo sapiens cDNA clone IMAGE:2959510 5'	ar98c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173649 3' similar to gb;226876 60S RIBOSOMAL PROTEIN L38 (HUMAN);	Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (og8),	CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG9 (cg9), CG1 (cg1), CG6 (cg6), CG2 (cg2), and CG7 (cg7) genes, complete cds	Mus musculus colony stimulating factor 1 receptor (Osf1r), mRNA	Mus musculus colony stimulating factor 1 receptor (Csf11), mRNA	602019770F1 NCI_CGAP_Bm67 Homo sapiens aDNA clone IMAGE:4155401 5'	Arabidopsis thaliana RXW24L mRNA, partial cds	Human bone statoprotein (BNSP) gene, exons 2, 3 and 4	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611;	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611;	oo59d02,y5 NCL CGAP_Lu5 Homo saplens cDNA clone IMAGE:1570467 5' similar to contains L1.t3 L1 repetitive element;	oo59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.เ3 L1 repetitive element ;
ום בייחו גוסמב	Top Hit Database Source	EST_HUMAN #	N-	EST_HUMAN L	NT TN		NT	IN TN	TN	TN	T. O	TN		HUMAN	EST_HUMAN 6		<u> </u>			EST_HUMAN 6		TN	EST HUMAN F	П	EST_HUMAN C	EST_HUMAN C	EST_HUMAN	
giilo	Top Hit Acession No.	8.0E-02 AI434202.1					3.1			8.0E-02 AL163209.2			4503034 NT	7.9E-02 BE250008.1			7.9E-02 AF0306942	1044	6681044 NT	7.9E-02 BF348454.1			E-02 BF368016.1	E-02 U27832.1	E-02 A1081644.1	7.9E-02 A1081644.1		
	Most Similar (Top) Hit BLAST E Value	8.0E-02	8.0E-02	8.0E-02	8.0E-02 ₽	8.0E-02 A	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	8.0E-02	7.9E-02	7.9E-02		7.9E-02	7.9E-02	7.9E-02	7.9E-02	7.9E-02	7.9E-02 L24757.1	7.9E-02	7.9E-02 L	7.9E-02	7.9E-02	7.8E-02	7.8E-02 AI793275.1
	Expression Signal	1.43	6.33	0.87	3.15	1.82	3.79	1.12	1.12	0.55	2.27	6.39	2.21	3.52	7.25		0.97	5.01	5.01	0.99	1.31	1.02	1.16	2.79	4.21	4.21	1.77	1.77
	ORF SEQ ID NO:	20083			31516				35128		36623	31070		27634	28392		29168	29217	29218			30204		33754	35773	35774	26604	26605
	Exon SEQ ID NO:	17457	17496				20722		21956	22706	23383	24665	17903	14900	15744		16529	16583				17581	19360	20626	22575	22575	13940	13940
	Probe SEO ID NO:	4725	4764	5108	5801	7080	8027	9289	9289	10058	10692	12195	12748	2171	2978		3777	3832	3832	4645	4760	4851	6597	7931	9927	9927	1188	1188

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					5	מה בייהיים הוא	Ourgo Event topo Expressed III Drain
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5027	16484		2.47	7.8E-02	02 BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
6976	19457	32479	0.88	7.8E-	-02 U82695.2	NT	Homo saplens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
6976	19457	32480	98'0	7.8E	-02 082695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8684	21376				7.8E-02 BE897947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5
8779	21471	34618		7.8E	-02 X78344.1	LN.	S.cerevísiae CAT8 gene
8951	21642	34789	0.79	7.8E	-02 AF233437.1	FN	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8951	21642	34790	0.79	7.8E	-02 AF233437.1	Ę	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete eds
9261	22015	35183		7.8E		EST HUMAN	nc68b06.r1 NCI_CGAP_Pr1 Homo saplens cDNA clone IMAGE:771731
9701	22352	35547	0.62	7.8E-02	-02 299124.1	Z	Bacillus subtilis complete genome (section 21 of 21); from 3999281 to 4214814
10562	23258	36494	4.58	7.8E	-02 U32323.1	N	Human interleukin-11 receptor alpha chain gene, complete cds
12754			3.92	-38.7	-02 AF096349.1	LN	HIV-1 strain 97USNG30 from USA, envelope glycoprotein (env) gene, partial cds
1378	15568	26800	1.25	7.7E-02	02 AF181897.1	LN	Homo sapiens WRN (WRN) gene, complete cds
3574	16329		1.97	7.7E-02	-02 AJ238093.1	LN	Homo saplens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5456	18255	31145	69.0	7.7E-02	-02 AF062636.1	ΝT	Galfus galfus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
7809	20504	33825	5.37	7.7E-02	-02 AA402949.1	EST HUMAN	zu53d11.r1 Soares ovary tumor NbHOT Homo saplens cDNA clone IMAGE:741717 5' sImilar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.;
9735	1	35590		7.7E-02	-02 P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10031	ļ	35895		7.7E.	-02 Al318662.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo saplens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S_RIBOSOMAL PROTEIN L38 (HUMAN);
							ta80b08.x1 NCI_CGAP_HSC2 Homo saplens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S
10031	22679	35896		7.7E	Al31866	EST_HUMAN	RIBOSOMAL PROTEIN L38 (HUMAN);
10933		36863	4.51	7.7E-02		LZ	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
12389			2.68	7.7E-02	11436859 NT	N	Homo saplens interferon regulatory factor 7 (IRF7), mRNA
3382	16141	28798	1.97	7.6E-02	-02 BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo saplens cDNA clone IMAGE:3634903 5'
3403	16161	28812	1.14	7.6E-02	-02 AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3547	16302		0.71	7.6E-02	-02 AJ400877.1	LΖ	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
9009	1			7.6E-02		T HUMAN	an25g02.x1 Gessler Wilms tumor Homo saplens cDNA clone IMAGE:1699730 3'
]	1				, i i i i i i i i i i i i i i i i i i i	ı	

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	Top Hit Descriptor	4 Homo sapiens cDNA clone IMAGE:3608401 5	sno	11168 complete genome; seament 5/6	106 HT0545 Homo sapiens cDNA	77 Homo saplens cDNA clone IMAGE:3839810 3'	se phosphate translocator	se phosphate translocator	904 BN0046 Homo saplens cDNA	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA	Homo saplens solute carrier family 6 (neurotransmitter transporter, alvoine) member 9 (S) CRAO) mDNA	ir interleukin-18, intron 1 and exon 2	d11 Homo saplens cDNA clone IMAGE:2472257 3'	w/52b02xf NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA		sapiens cDNA clone HEMBA1000264 5'	7061c05.x1 NCL_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:3578504 3' similar to contains element MER27 repetitive element;	9 Homo sapiens cDNA clone IMAGE:4100449 6'	A	109 LT0054 Homo saplens cDNA	NS80567, complete genome	omeodomain transcription factor 1 (PItx1), mRNA	GBC_S1 Homo saplens cDNA clone IMAGE:2358385 3'	rrier protein (ANT-2) gene, complete cds	ceptor like kinase 1 (Acvir1), mRNA	erminal hydrolase related polypeptide (Uchrp), mRNA	ain 1NIB Homo sapiens cDNA clone IMAGE:32339 5'	9 Homo sapiens cDNA clone IMAGE:3895264 5'	protein 2 (PWP2) gene, exons 15 to 21, and complete cds	hh67d11.71 NCI_CGAP_GU1 Homo septens cDNA clone IMAGE:2967861 6' similar to SW:SCA2_HUMAN 015127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.
	Top Hit Descriptor	601236402F1 NIH_MGC 44 Hamo sapiens cDNA clone IMAGE:3608401 5	Homo sapiens SCL gene locus	Campylobacter jejuni NCTC11168 complete genome; segment 5/6	RC1-HT0545-020800-017-d06 HT0545 Homo sapiens cDNA	601654915R1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:3839810 3'	L.esculentum mRNA for triose phosphate translocator	Lesculentum mRNA for triose phosphate translocator	QV3-BN0046-150400-151-e04 BN0048 Homo sapiens cDNA	mo sapiens solute carrier family 6 (neurotransmitter transporter	mo sapiens solute carrier family 6 (neurotransmitter transporter	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2	wq24h09.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2472257 3	wi52b02x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE	טראסוני (הטואסוי),	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'	7o61c05.x1 NCL_CGAP_Pr28 Homo sepiens cDNA clone IMAGE MER27 repetitive element;	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5	C.flmi DSM 20113 16S rDNA	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA	Equine herpesvirus 4 strain NS80567, complete genome	Mus musculus paired-like homeodomain transcription factor 1 (PIX1), mRNA	wf43h01,x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2358385 3	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds	Rattus norvegicus Activin receptor like kinase 1 (Acvr11), mRNA	Mus musculus ubiquintin c-terminal hydrolase related polypeptide (Uchrp), mRNA	yg14g06.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:32339 5	601493368F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895284 5	Human periodic tryptophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds	hh67d11.71 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 6' 015127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.
	Top Hit Database Source	EST_HUMAN 60	Γ	NT	EST_HUMAN RC	Ţ	Γ	NT L.e	EST_HUMAN Q\				T_HUMAN		T	EST_HUMAN AU	EST_HUMAN ME	EST_HUMAN 60	NT C.f	EST_HUMAN RC			T_HUMAN				1	EST_HUMAN 60		hhe EST_HUMAN 01
}	Top Hit Acession No.	.02 BE379328.1	-02 AJ131016.1	7.6E-02 AL139078.2		3.2	7.6E-02 X92656.1	-02 X92656.1	-02 AW996645.1	5902093 NT	5902093 NT	7.5E-02 AB015961.1		00 00000		02 AU116913.1		02 BF206809.1 E	02 X79460.1	1	7.4E-02 AF030027.1	6755069 NT	.1	02 L78810.1	6978442 NT	6678492 NT		02 BE880112.1 E	02 ∪56089.1	02 AW629605.1
	Most Similar (Top) Hit BLAST E Value	7.6E-02	7.6E-02	7.6E-02	7.6E-02	7.6E-02	7.6E-02	7.6E-02	7.6E-02	7.5E-02	7.5E-02)	7.5E-02	7.5E-02	7 55 00	1.00-02/	/.5E-02 /	7.5E-02	7.5E-02	7.5E-02	7.4E-02 /	7.4E-02 /	7.4E-02	7.4E-02/	7.4E-02 L	7.4E-02	7.4E-02	7.4E-02 R17477.1	7.4E-02	7.4E-02	7.4E-02
	Expression Signal	0.92	1.47	1.63	0.49	0.75	0.71	0.71	2.45	1.44	1.44	1.17	0.91	1 05	3 !	1.17	0.54	0.7	0.72	1.46	0.92	1.32	0.86	2.03	2.94	2.1	2.18	1.52	1.03	1.12
	ORF SEQ ID NO:				35979			36360	37595	26199	26200	29833	31477	34066	200	34234		36252	36361	25891			28981	30024	30108	30235		33618	34228	34913
	Exon SEQ ID NO:	1	22024	22448		22895	23133	23133	24273	13540	13540	17207	18553	20030	Т	20017	22580	23036	23134	- 1	Į		16336	17390	17473	17616	19172	20496	21092	21753
	Probe SEQ ID NO:	6263	9270	9797	10119	10247	10487	10487	11678	767	787	4472	5762	8236	200	8403	9932	10390	10488	465	1445	2585	3581	4656	4741	4889	6403	7801	8399	9064

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						יהיי ווייאם סופ	סיישור ו מסיס באלי מידים ו
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9064	21753	34914	1.12	7.4E-02	2 AW629605.1	EST_HUMAN	hh67d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW :SCA2_HUMAN O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2;
9339	20410			7.4E-02	7.4E-02 A1672939.1	EST_HUMAN	we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9339	20410		0.52	7.4E-02	7.4E-02 AI672939.1	EST_HUMAN	we74d02.x1 Soares_Dieckgraafe_colon_NHCD Homo saplens cDNA clone IMAGE:2346819 3'
9714	22365		1.03		7.4E-02 U62293.1	LN	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
9841	22492	35692	0.52		7.4E-02 BF512678.1	EST_HUMAN	UI-H-BW 1-amg-g-06-0-UI,s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3'
10939	23619	36869			AA059167.1	EST_HUMAN	zf64e01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381720 5'
12126	24618		1.53		11525893 NT	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12381			2.21		7.4E-02 AW379431.1	EST_HUMAN	CM4-HT0243-081199-037-411 HT0243 Homo sapiens cDNA
456	13242	25881	1.5		7.3E-02 BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
456	L		1.5			EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
699	13445	26085	3.9			NT	Thermotoga maritima section 101 of 138 of the complete genome
1464	15570	26900	3.62	7.3E-02		EST_HUMAN	CMO-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1837	L		12.41	7.3E-02		F	Homo sapiens chromosome 21 segment HS21C102
6361	19131	32126			7.3E-02 AA779977.1	EST HUMAN	z/24802.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:451178 3' similar to db:102428 26S PROTEASE SUBUNIT 4 (HUMAN);
7368	L	L			7.3E-02 P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7368		33129		L	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8068	L	L		L	7662107 NT	N-	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
9110			1.14			F	Homo sapiens mRNA for KIAA0518 protein, partial cds
	L						724a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:451178.3' similar to
11179	19131	32126	•		7.3E-02 AA779977.1	EST HUMAN	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
11844	24428		5.07		11560138 NT	뒫	Raftus norvegicus caspase recruitment domain protein 9 (LOC64171), mRNA
							Methanobacterium thermoautotrophicym from bases 1029155 to 1039934 (section 88 of 148) of the complete
117	12937	25577	-	7.2E-02	7.2E-02 AE000882.1	된	genome
							Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the completa
117	12937	25578	-	7.2E-02	7.2E-02 AE000882.1	LN L	genome
1458	14205				AL163301.2	TN	Homo saplens chromosome 21 segment HS21C101
1458	14205	26891	2.72		7.2E-02 AL163301.2	LN	Homo sapiens chromosome 21 segment HS21C101
							Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial
2852	15267		2.83		7.2E-02 U14794.1	Ā	cds
3865			96'0		7.2E-02 AW 298322.1	EST_HUMAN	UFH-BW0-aji-a-05-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
4312			4		BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo saplens cDNA clone IMAGE:4251950 5
4644	17378	30010	0.7		11466563 NT	Ę	Rhodomonas salina mitochondrion, complete genome

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Top Hit Descriptor	Methanococcus jannaschii section 73 of 150 of the complete genome	CALMODULIN	601883558F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE;4095710 5	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative	And the manage (Anipo) genes, complete cas	Strongylocentrolus purpuratus mitochondrion, complete genome	PROLINE-RICH PROTEIN MP-3	PROLINE-RICH PROTEIN MP-3	Lactococcus lactis cspE gene	Human gene for sex hormone-binding globulin (SHBG)	AV712452 DCA Homo sapiens cDNA clone DCAAUG01 5'	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products,	601763523F1 NIH MGC 20 Homo sabiens cDNA close IMAGE 4028438 5	hq2411.x1 NCI_CGAP_Adr1 Homo saplens cDNA clone IMAGE:3120333 3' similar to TR:Q92340 Q92340	086207.51 NCI CGAP GCB1 Home saniens cDNA clone IMAGE-1346844.3	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calclum ATPase isoform 3 (PMCA3) cane, partial cds	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 57	zj28h05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:4516413'	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds	Homo sapiens putative transmembrane protein dectin-1 mRNA, complete cds	af81a04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone (MAGE:1048398 5)	AJ230796 Homo saplens library (Seranski P) Homo saplens cDNA clone PS13D5 3'	Homo sapiens ataxia telangiectasta (ATM) gene, complete cds	CM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA	Homo saplens ATP-citrate lyase gene, intron 3	Historian interest modes from the part (TO) and the following the second of the second	601872281F1 NIH MGC 53 Homo sabiens cDNA clone IMAGE:4092981 5'	qd92a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922.3'
Top Hit Database Source	뉟	SWISSPROT	EST_HUMAN	H	E L	Z	SWISSPROT	SWISSPROT	TN	N	EST_HUMAN	FZ	EST HUMAN	ĺ	1	ĻΝ	EST HUMAN	EST_HUMAN	EST_HUMAN	L	LN	EST_HUMAN	EST_HUMAN	IN	EST_HUMAN	N.	Ŀ	T HUMAN	П
Top Hit Acession No.	E-02 U67531.1	P11120	7.2E-02 BF216086.1	A E004406 4	7.2E-02.01 E03.007 NT	- 1	P05143	E-02 P05143	E-02 Y17217.1	X16349.1	7.2E-02 AV712452.1	145611	7.2E-02 BF125399.1	7 2E 02 AMO72407 4	7.2E-02 AA768204.1	7.2E-02 U82695.2	E-02 BE565003.1	E-02 BE539214.1	E-02 AA706897.1	E-02 AF049874.1	E-02 AY009090.1	7.2E-02 AA773696.1	7.2E-02 AJ230796.1	J82828.1	4W900962.1	7.2E-02 AF020439.1	00000	7.1E-02 BF208802.1	7.1E-02 Al125264.1
Most Similar (Top) Hit BLAST E Value	7.2E-02	7.2E-02 P11120	7.2E-02	7 25 02	7 25 02	/.ZE-02	7.2E-02 P05143	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7 2F-02 14561 1	7.2E-02	7 25 02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02	7.2E-02/	7.2E-02	7.2E-02 U82828.1	7.2E-02	7.2E-02/	7 15 02 02300 1	7.1E-02	7.1E-02
Expression Signal	2.88	10.1	1.58	0.64	100	6.1	8.0	0.8	0.61	0.49	2.32	60 67	0.93	63.0	0.62	1.93	5.54	. 3.68	0.48	3.3	1.34	1.57	4.45	1.73	8.19	3.62	2.04	5.07	0.77
ORF SEQ ID NO:			32824	37840			33910				35346	35509	35867	35747	35955	36108	36234			36753	37775	31113					27344	27751	33622
Exen SEQ ID NO:				19775			[20781	21653	22127	22164	22311	1	22442	22740	22898	_ ;			23512	24433	24560	24583	24654		25362	14634	15015	20502
Probe SEQ ID NO:	5205	5206	7068	7085	7100	5017	1808	8087	8962	9474	9511	9659	9814	000	10092	10250	10372	10395	10509	10830	11849	12035	12069	12182	12196	12599	1897	2290	7807

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11922	24483		6.41	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
515	13299	25931	1	7.0E-02	7.0E-02 Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1486	14233		1.27	7.0E-02	7.0E-02 X96677.1	٦	Martellia Mtcut-1 gene
1758	14498		1.08		AA056343.1	EST_HUMAN	z166f04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:609599 37
3027	<u> </u>	28440			7.0E-02 AW138152.1	EST_HUMAN	UI-H-BI1-acy-c-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
	_						al65a12.s1 Sogree_testis_NHT Homo saplens cDNA clone 1375678 3' similar to gb;K03002 60S
3878		29266				EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN)
4119	16861		1.28			EST_HUMAN	CM0-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4189	16930	29560	1.06		7.0E-02 AF077821.1	NT	Canis familiaris Inducible nitric oxide synthase mRNA, complete cds
4877	17604	30227			BF381987.1	EST_HUMAN	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
5293	18098		29.0		7.0E-02 Y09143.2	LN	Lumbricus rubellus mRNA for cyclophilln B
7300	19983	93055			7.0E-02 AV689285.1	EST_HUMAN	AV689285 GKC Homo sapiens cDNA clone GKCCAE06 5'
7506		33271	0.84		7.0E-02 Y19187.1	LN	Gallus gallus mRNA for parttal aczonin, XL spliced variant (acz gene)
8996	21686				9628113 NT	Ę	African swine fever virus, complete genome
9497		35331			7.0E-02 K02901.1	N	Rat ig germline epsilon H-chain gene C-region, 3' end
9852	L	35702			7.0E-02 U27266.1	۲	Human myosin binding protein H (МуВР-Н) gene, complete cds
11345	24035	37338	4.98	7.0E-0	2 AA724295.1	EST_HUMAN	ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837 IGHT JUNCTION PROTEIN ZO-1 (HUMAN);
594	13285				AL163210.2	Ā	Homo sapiens chromosome 21 segment HS21C010
501		25918		6.9E-02	6.9E-02 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1310	14058		1.2	6.9E-02	4507968 NT	F	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3773	1					SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3773	16525	29164	1.41	6.9E-02 Q06364	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
							Enterococcus faecium cystetne aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BgIB (bgIB), beta-glucoside specific transport protein (bgIS), transcription antiterminator (bgIR), enterocin B
5113	17831	30448			6.9E-02 AF121254.1	Ä	precursor (enfB), enterocin B immunity profe>
5127	17845	30462	1.25		6.9E-02 BE264605.1	EST_HUMAN	601192383F1 NIH_MGC_7 Hamo saplens cDNA clone IMAGE:3536253 5'
7516	20187		0.61		6.9E-02 AF164967.1	TN	Canine distemper virus strain A75/17, complete genome
7951	Ш		1.12		6.9E-02 U12022.1	TN	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
8451	21143		1.01	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8451		34283	1.01	6.9E-02	6.9E-02 BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9018				j	6.9E-02 U22967.1	N	Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
12065	24580		1.82		X74315.1	N	X laevis XFD2 mRNA for fork head protein

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Table 4
Single Exon Probes Expressed in Brain

		T	Ī	32	22												T		T												Γ		
Oligio Exoli Flobes Expressed il Bialli	Top Hit Descriptor	PROTEIN TRANSPORT PROTEIN HOFC HOMOLOG	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone INACE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN):	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone INAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN):	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds	al75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 13766263'	al75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'	al75a06.s1 Soares_tests_NHT Homo sapiens cDNA clone 1376626 3'	MR0-HT0069-071099-001-c05 HT0069 Homo saplens cDNA	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR	RC1-BT0254-090300-017-d09 BT0254 Homo sapiens cDNA	Homo saplens chromosome 21 segment HS21C068	Dictyostellum discoldeum myosin heavy chain kinase A (MHCK A) mRNA, complete cds	Pyrococcus abyssi complete genome; segment 5/6	Pyrococcus abyssi complete genome; segment 5/6	FB4A8 Fetal brain, Stratagene Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1	ah67705.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'	EST387948 MAGE resequences, MAGN Homo sapiens cDNA	Mus musculus latent TGF beta binding protein (Tgfb), mRNA	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, oomplete cds	qg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:18414063'	HOMEOBOX PROTEIN HOX-D4 (CHOX-A)	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)	xb61c11.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2580788 3'	UI-H-BI1-acr-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 31	UI-H-BI1-acrg-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3	Drosophila melanogaster cactin mRNA, complete cds	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcipts	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1395793'	Homo saplens mesothelin (MSLN), transcript variant 1, mRNA	Homo saplens mesothelin (MSLN), transcript variant 1, mRNA
פום באסוו ביוס	Top Hit Database Source	SWISSPROT	LN	EST_HUMAN	EST HUMAN	LΖ	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	R	FZ	L/S	K	EST_HUMAN	EST_HUMAN	EST_HUMAN	LΝ	NT	EST_HUMAN	SWISSPROT	LN	ΤN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	ΤN	EST_HUMAN	NT	LN
5	Top Hit Acession No.	-02 P44621	6.9E-02 AF195953.1	6.8E-02 AA496759.1	6.8E-02 AA496759.1	-02 AF156673.1	-02 AA781996.1	6.8E-02 AA781996.1	6.8E-02 AA781996.1	6.8E-02 BE141076.1	>20792	90.1		J16856.1	6.8E-02 AJ248287.1	1,7248287.1	T03214.1	VA758014.1	6.8E-02 AW975839.1	9910585 NT	-02 AF115536.1	5.1	-02 P17278			-02 AW082688.1	-02 AW137359.1			.1	-02 R64306.1	7108357 NT	7108357 NT
	Most Similar (Top) Hit BLAST E Value	6.9E-02	6.9E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02 /	6.8E-02	6.8E-02 P20792	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02	6.8E-02 T03214.1	6.8E-02	6.8E-02	6.8E-02	6.7E-02	6.7E-02	6.7E-02 F	6.7E-02	6.7E-02	6.7E-02	6.7E-02	6.7E-02	6.6E-02	6.6E-02	6.6E-02 F	6.6E-02	6.6E-02
	Expression Signal	1.69	1.46	1.56	1.56	3.77	1.19	1.19	1.19	0.86	0.6	1.09	8.73	0.63	5.01	5.01	2.3	2.85	1.65	3.06	1.93	2.27	4.52	0.55	0.55	0.47	0.69	0.69	1.07	3.31	10.57	2.59	2.59
	ORF SEQ ID NO:			27321	27322	27346	28503	28504	28505				32939	33358	34017	34018						27333	29097	33567	33568	34167	35333	35334	26771	27641	28865	28881	28882
	Exon SEQ ID NO:		24817	14613	14613	14637	15862	15862			19291				20880	20880	25379	24537	24888	24920	14266	14623	16459	20445	20445	21030	22153	22153	14096	14909	16212	16227	16227
	Probe SEQ ID NO:	12232	12447	1875	1875	1900	3097	3097	3097	4516	6525	6239	7180	7584	8186	8186	11873	12001	12551	12613	1519	1886	3706	7749	7749	8337	9200	9500	1348	2180	3456	3471	3471

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Single Exon Plobes Expressed in Drain	Top Hit Descriptor	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)	P.vulgaris mRNA for chalcone synthase	MATERNAL EFFECT PROTEIN STAUFEN	MATERNAL EFFECT PROTEIN STAUFEN	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds	Dictyostellum discoldeum darlin (darA) gene, complete cds	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)	Human respiratory syncyfial virus, complete genome	Human respiratory syncytial virus, complete genome	ij97g06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149498 3'	Homo sapiens EWS, gar22, rrp22 and bam22 genes	Homo sapiens vinculin (VCL), mRNA	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA	Homo saplens chemokine receptor CXCR4 gene, promoter region and complete cds	Mus musculus DIPB gene (Dipb), mRNA	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'	Homo sapiens E2F-like protein (LOC51270), mRNA	Xenopus laevis alpha(E)-catenin mRNA, complete cds	Aquifex aeolicus section 96 of 109 of the complete genome	zv46h12.s1 Soares overy tumor NbHOT Homo saplens cDNA clone IMAGE:756743 3' stmilar to gb:M26038 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);	Azotobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial ods	601656817R1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:3865637 3	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'	zr32g05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'	Rabbit microsomal epoxide hydrolase	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds	A.carterae precursor of peridinin-chlorophylla-protein (POP) gene	Mus musculus histone deacet//ase 5 (Hdac5), mRNA	Mus musculus histone deacetylase 5 (Hdac5), mRNA
le Exon Propes	Top Hit Database Source	NT FN	SWISSPROT IN	SWISSPROT IN		SWISSPROT M		NT TN	NT TN	/ISSPROT			EST_HUMAN #9	OH IN		T_HUMAN				EST_HUMAN 60		NT Xe	NT	EST HUMAN HL		EST_HUMAN 60	EST_HUMAN 60	HUMAN	EST_HUMAN 213		NT IN			
Builo	Top Hit Acession No.	25.1	02 Q61703	02 Q61703	02 X06411.1			-02 AF052572.1	55.1	-02 060673	9629198 NT	9629198 NT		-02 Y07848.1	11430559 NT	02 BF374248.1		9937991 NT		02 BF027639.1	7706068 NT		-02 AE000764.1		-02 U22661.1		Γ		.1	.02 M21496.1	3.1	02 X94549.1	6996923 NT	6996923 NT
	Most Similar (Top) Hit BLAST E Value	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02 P25159	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	6.6E-02	8.6E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	8.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.5E-02	6.4E-02	6.4E-02	6.4E-02
	Expression Signal	1.29	7.03	7.03	3.44	0.56	0.56	1.81	0.84	0.53	0.58	0.58	0.65	1.66	0.63	6.88	1.46	2.66	1.38	2.49	1.32	3.08	1.77	2.03	0.95	0.55	0.55	0.48	5.56	3.73	4.68	2.09	0.96	1.18
	ORF SEQ ID NO:	29436	30261	30262	32258	32286	32287	33670	34206		34654	34655	35701	35845		36811	37793			25977	26398	26793	27169	31162	30549	35693	35694	36225	36466			25970	28429	28429
	SEQ ID NO:	16805	17649	17649	19256	19283	19283	20542	21085	21370	21511				22670	23563	24451	24812	25006	13349	13732	14118	14470	18270	17953	22493	22493	23010	23232	24463	24691	13343	15780	15780
	Probe SEQ ID NO:	4060	4921	4921	6489	6701	6701	7847	8372	8678	8819	8819	9851	8887	10022	10883	11867	12442	12740	568	996	1370	1728	5471	6877	9842	9842	10363	10535	11894	12240	561	3014	4839

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5363	18165	30850	1.67	6.4E-02	-02 AI191956.1	EST_HUMAN	qe07b01.x1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element ;
5791	18582	31509	0.65	6.4E-02	7305186 NT	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6022				6.4E-02	02 AF052733.1	LN	Heterodera glydnes beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6022	18802	31764	4.21	6.4E-02	02 AF062733.1	NT	Heterodera glycines beta-1, 4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
8308				6.4E-02		EST_HUMAN	we73g12.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 31
6719	19634		5.43	6.4E-02	02 BE974448.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo saplens cDNA clone IMAGE:3950503 3
7360		33119		6.4E-02	02 AL162757.2	LN L	Nelsseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
8234			2.91	6.4E-02	53323	ΤN	Mus musculus chaperonin subunit 6a (zeta) (Cot6a), mRNA
8563		34392		6.4E-02	02 AA093305.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9025	21715			6.4E-	02 AF150195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9486			0.55	6.4E-	02 BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-g06 OT0083 Hamo saplens cDNA
9617				6.4E-	02 AB011126.1	LN	Homo sapiens mRNA for KIAA0554 protein, partial cds
10161	52809	36027	69'0	6.4E-	02 AF087150.1	LN LN	Homo sapiens DNA topolsomerase II beta (TOP2B) gene, exons 16, 17, and 18
10161	22809	36028		6.4E-	02 AF087150.1	TN	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
11709	24304	37629	1.47	6.4E-02	02 (091328.1	FZ	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) oene. RoRat cane, and sodium phosphate transporter (NPT3) nane, complete and
11709	24304	37630	1.47	6.4E-02	6.4E-02 U91328.1	Ľ.	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12141			2.7	6.4E-02	1.1	IN	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12188	24659	31065	2.47	6.4E-02		NT.	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1749	14491	27191	2 87	я С.		F	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23,
3590	İ		2.38	6.3E-02	6.3E-02 P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6046	18825	31786		6.3E-02	-	EST HUMAN	601873316F1 NIH MGC_54 Hamo sapiens cDNA clone IMAGE:4097499 5'
7142	19829		0.82	6.3E-02	6.3E-02 X97869.1	Z	H. sapiens gene encoding La autoantigen
9191		35026		6.3E-02	1	LN	Drosophila melanogaster Domina gene, exons 1-3
9913				6.3E-02		LN	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain; CMR-152
10171	- 1		0.85	6.3E-02		EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10615		31786		6.3E-02		EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
4224	16965		2.81	6.2E-02	02/AL161572.2	Z	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68

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	r .	Γ-		_					_		r		_	_		_	_				_			_				_	т-
Top Hit Descriptor	Rattus norvegicus differentation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)	Spirulina platensis DNA for adenylate cyclase, complete cds	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds	Porcine group C rotavirus (strain Cowden) outer membrane protein (VPT) mRNA, complete cds	af20a06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds	Metarhizium anisopliae mRNA for Chymotrypsin (chy1 gene)	Rattus norvegious UDP-glucose glycoprotein:glucosytransferase precursor (Uggt) mRNA, complete cds	Aquifex aeolicus section 82 of 109 of the complete genome	7/37h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3623815 3' similar to TR:Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1] ;	Human mRNA, Xq terminal portion	Arabidopsis thallana K+ inward rectifying channel protein (AtKC1) gene, complete cds	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA	H.sapiens mRNA for B-HLH DNA binding protein	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'	IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA	Eptatretus burgeri mRNA for RNA polymerase III largest subunit, partial cds	S.japonicum mRNA for serine-enzyme	Homo saplens chromosome 21 segment HS21C007	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo saplens cDNA clone IMAGE:826310 5'	Thermotoga maritima section 89 of 136 of the complete genome	EST380924 MAGE resequences, MAGJ Homo saplens cDNA	Mesocestoldes corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gin, tRNA-Phe, tRNA-Met,	zo 78c04.11 Strategene Hel a cell s3 937216 Homo sepiens cDNA clone IMAGE:626310 67	2078c04,r1 Stratagene HeLa cell s3 937216 Homo sapiens oDNA clone IMAGE:026310 5
Top Hit Database Source	Z F	SWISSPROT	TN	FZ	NT	EST_HUMAN	LN.	TN	LN	Ę	뉟	EST HUMAN	LZ	NT	Į.	LZ LZ	EST_HUMAN	EST_HUMAN	EST_HUMAN	L	IN		EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	±4	FST HUMAN	
Top Hit Acession No.	1					6.2E-02 AA778450.1	TN 86877898				6.2E-02 AE000750.1				4507070 NT	2 X99268.1				6.1E-02 AB025333.1			6.0E-02 AA188730.1		6.0E-02 AE001777.1		000000000000000000000000000000000000000	T	
Most Similar (Top) Hit BLAST E Value	6.2E-02	6.2E-02	6.2E-02	6.2E-02		П								6.1E-02		6.1E-0			6.1E-02	6.1E-02	6.1E-02	6.1E-02					00 00		\
Expression Signal	1.02	6.31	0.65	1.03	9.0	0.52	1.65	1.56		1.74	13.39	2.5	5.59	2.29	4.1	3.75	0.57	0.57	4.91	1.27	2.27	5.61	0.76	0.76	1.54	1.09	700	90	0.9
ORF SEQ ID NO:			32656	33292					37315	37791		31037				33986	34388	34389	36560				25559		26855	28130			25560
SEQ ID NO:	17043	17277	19615	1		1			24011		25405	24782	l.,	16721	l	20855	21251					. !	12922			15391	00727	ı	1
Probe SEQ ID NO:	4304	4542	8698	7527	8846	9243	9380	11095	11320	11865	11989	12394	249	3972	6023	8161	8559	8559	10630	11862	11945	12633	96	98	1239	2682	0416	2027	2937

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	_	_	•	_	_		-	_	-	_	-,-		-			_	_											
Top Hit Descriptor	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	EST84266 Colon adenocardinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'	Rattus norvegicus testis specific protein mRNA, complete cds	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains	Homo sarians efimilated trans-arthra factor (EQ UDA) (STAREO) TONA	Homo sapiens affairteath transaction fector (50 to 70	601815274F2 NIH MGC 56 Home saniens cDNA clane IMA GE-4040926 81	qf98b08.x1 Soares testis NHT Homo saplens cDNA clone IMAGE:1754199.31	Reclinamonas americana mitochondrion, complete genome	ts78a06.x1 NCI CGAP GC6 Homo sepiens cDNA clone IMAGE:2237362.3/	ts78a06.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2237362 3'	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, excus 1-2	Aclbenser baeri partial (GLV gene for Immunoglobulin light chain variable region, exons 1-2	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa- like	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-	like	zn87c08.r1 Stratagene lung carchoma 997218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:X69181 60S RIBOSOMAL PROTEIN L31 (HUMAN);	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA	wf99h03.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2360885 3' similar to TR:O60298 CO2098 KIAA0551 PROTFIN	RC1-DT0001-290100-012-e10 DT0001 Home seniens cDNA	Mus musculus p53 tumor suppressor gene, exon 10 and 11 partial cds. alternatively enlined	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds	w/34602.x1 NCI_CGAP_Ov/8 Homo sapiens cDNA clone IMAGE:2631450 3' similar to TR:065386 065386 F12F1.20 PROTEIN.	w/34e02.x1 NC]_CGAP_Ov/8 Homo saplens cDNA clone IMAGE:2531450 3' similar to TR:065386 065386 F19F1 20 PROTEIN	Mus musculus iroquois related homeobox 5 (Drosophila) (irx5), mRNA	601877609F1 NIH_MGC_55 Homo saplens cDNA clone IMAGE:4105994 5'
Top Hit Database Source	EST_HUMAN	EST HUMAN	EST_HUMAN	NT	EST_HUMAN	PAPA LINAMI	LON LON	₽N	EST HUMAN		۲	EST HUMAN	EST HUMAN	LN	TN	EST_HUMAN		EST HUMAN	THUMAN		HUMAN	Т	Γ		EST HUMAN			THUMAN
Top Hit Acession No.	-02 AA372376.1	AA372376.1			6.0E-02 AW370211.1	A (R07537 1	6.0F-02 5474698 NT	5174698INT	6.0E-02 BF382349.1	AI204275.1	11466495 NT	6.0E-02 A1623167.1			-02 AJ245365.1	-02 AA309797.1		-02 AA309797.1	6.0E-02 AA128386.1	11431702 NT	-02 A1809273.1	_	Π		-02 AW028748.1		5249	5.9E-02 BF242748.1
Most Similar (Top) Hit BLAST E Value	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	0-=0-	6.0F-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02	6.0E-02		6.0E-02	6.0E-02	6.0E-02	6.0E-02	5.9E-02	5.9E-02	5.9E-02	5.9E-02	5.95-02/	5.9E-02	5.9E-02
Expression Signal	1.48	1.48	0.72	0.69	0.94	0.77	3.07	3.07	2.33	2.13	0.54	1.17	1.17	1.66	1.66	0.5		0.5	1.69	2.19	2.31	3.87	2.89	1	0.73	0.73	1.68	0.8
	28639			30370		31868	30524	30525	32842	33355		35007	35008	35147	35148	35659		35660	-	31064		25671	28396	30173	30457	30458	34350	
ທ	15986			17756	18117	18900	17967	1		20249	21014	21842	21842	21973	21973	22456		22456	23965	24658	24894	13035	15748	17548	17841	17841	21207	20422
Probe SEQ ID NO:	3223	3223	3625	5037	5313	6122	6891	6891	7088	7580	8321	9172	9172	9306	9306	9805		9805	11306	12187	12564	223	2982	4817	5123	5123	8515	9351

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10685	23376		3.2	5.9E-02	TN 028789	Į.	Mus musculus follistatin-iika (Fetl), mRNA
10944		36872		5.9E-02	11433356 NT	N L	Homo sapiens ninein (LOC51199), mRNA
11544	24144		1.59	5.9E-02	5.9E-02 AJ240733.1	LN L	Gallus gallus HKC9 telomere junction
912	13679		5.18	5.8E-02	5.8E-02 D90110.1	LN L	Thiobacillus ferrooxidans merC, merA genes and URF-1
2864	15632		96'0	5.8E-02	5.8E-02 AJ223621.1	N	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
4322	17061	29687	4.9	5.8E-02	5.8E-02 AW051927.1	EST HUMAN	wx24c02.x1 NCI_CGAP_Kld11 Homo saplens cDNA clone IMAGE:25445783'
4322	19021	29688	6.4	5.8E-02	5.8E-02 AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4510	17245	29879	4.95	5.8E-02	5.8E-02 AI247505.1	EST_HUMAN	qh56f01.xf Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4510	17245	29880	4.95	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:1848697.3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4535	17270		2.62	5.8E-02	AF096264.1	N	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7578	20247	33352		5.8E-02	5.8E-02 M99150.1	Z	Human polymorphic microsatellite DNA
7578	20247	33353	2.99	5.8E-02	5.8E-02 M99150.1	LN-	Human polymorphic microsatellite DNA
8565		34394	29.0	5.8E-02	5.8E-02 AL163283.2	N	Homo sapiens chromosome 21 segment HS21C083
12084	24590		1.79	5.8E-02	AF220177.1	N	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12373	25396		7.06	5.8E-02	5.8E-02 AA604269.1	EST_HUMAN	no75e11.s1 NCL_CGAP_AA1 Homo saplens cDNA clone IMAGE:1112684 3'
3053	15819	28463	1.36	5.7E-02	5.7E-02 A1081644.1	EST HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo saplens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611 :
3068	1	l	1.29	5.7E-02	5.7E-02 AF119117.1	LN LN	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3694	16448		76.0	5.7E-02	5.7E-02 AF001292.1	FZ	Chironomus thummi thummi globin VIIA.1 (ett-7A.1), globin 9.1 (ett-9.1), globin II-bela (ett-2bela), non- functional globin XIII (ett-13RT), globin XII (ett-12) and globin XI (ett-11) genes, complete ods
3783	16535	29173	2.45	5.7E-02	5.7E-02 AW966791.1	EST_HUMAN	EST378865 MAGE resequences, MAGI Homo sapiens cDNA
4637	17371		1.01	5.7E-02	M95099.1	TN	Bos faurus lysozyme gene (cow 3), complete cds
7438	1		69.0	5.7E-02	5.7E-02 D78003.1	MT	Xenopus laevis mRNA for fourth component of complement, complete cds
7438				5.7E-02	D78003.1	L	Xenopus laevis mRNA for fourth component of complement, complete cds
8055		33880		6.7E-02	AJ296090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
9750	L	32606		5.7E-02	5.7E-02 6681260 NT	NT	Mus musculus ect2 oncogene (Ect2), mRNA
11143	23810	37090	4.42	5.7E-02	5.7E-02 AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo saplens cDNA clone NHTBC_cn18b09 random
11143		37091	4,42	5.7E-02	5.7E-02 AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA cione NHTBC_cn18b09 random
11321	١		1.59	5.7E-02	AL163303.2	닏	Homo sapiens chromosome 21 segment HS21C103
12285	25213		7.24	5.7E-02	D50320.1	LN.	Pig DNA for SPAI-2, complete cds

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Probe SEQ ID NO: 12515	Exon SEQ ID NO: 25283 25387	ORF SEQ ID NO:	Expression Signal 3.18	Most Simi (Top) Hi BLAST E Value 5.7E.	lar Top Hit Acession No. O2 AF217490.1	Top Hit Database Source Source NT	Top Hit Database Source NT Homo saplens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds NT Pan troglodytes apolipoprotein-E gene, complete cds
1518 4595 4648	17330	26951	1.57	5.6E-02 5.6E-02	-02 AF094455.1 -02 AB013100.1 -02 AA290599.1	NT NT FST HIMAN	Hydrocotyle rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product Lycopersicon esculentum LE-ACS6 mRNA for 1-eminocyclopropane-1-carboxylate synthase, complete cds 2245c01.s1 NCI CGAP, GCB1 Homo sepiens cDNA clone IMAGE:700416 3
6562	<u> </u>			5.6E-02 5.6E-02	-02 AW172708.1 -02 AA866182.1	EST_HUMAN EST_HUMAN	x02210.x1 NCI_CGAP_U2 Homo saplens cDNA clone IMAGE:2656050 3' similar to TR:094979 094979 KIAA0805 PROTEIN.; od47712.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element.contains element L1 repetitive element;
7051		32804		5.6E-02 5.6E-02	-02 BE008001.1 -02 Al983738.1	EST HUMAN EST HUMAN	QVO-BN0147-290400-214-g07 BN0147 Homo sapiens cDNA wz34f05.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2559969 3' similar to gb:X06409 RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
8701 8701				5.6E-02 5.6E-02 5.6E-02	-02 A/183583.1 -02 BE542683.1 -02 BE542663.1	EST_HUMAN	qd64g11.xf Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734308 3' 6010g7158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5' 6010g7158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5' 6010g7158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:325245 similar to TR:G769859 G769859
9712 11556 2660 3209			1.09 2.35 6.8 3.93	5.6	=-02 AA482864.1 ES =-02 AF260225.1 NT =-02 X97869.1 NT =-02 6755501 NT	EST HUMAN	LAMINA ASSOCIATED POLYPEPTIDE 1C.; Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternativaly spliced H.aspiens gene encoding La autoantigen Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
5573 5935 7277	18932 18370 19961	33038 33038		5.55 5.55 5.55 7.55 7.55 7.55 7.55	6.5E-02 (20174 SW 6.5E-02 (20174 SW 5.5E-02 (20174 SW 5.5E-02 (20174 SW 5.5E-03 (20174 NT 6.5E-03 (20174 NT	SWISSPROT SWISSPROT NT	Salid neipesvilus mr.v.k. itagnien. TROPOMYOSIN ALPHA CHAIN, NON MUSCLE TROPOMYOSIN ALPHA CHAIN, NON MUSCLE Mus musculus tuffelin (1 fuff.), m. (1 fuff.), m. (1 fuff.), m. (1 fuff.), m. (2 fuff.), m. (2 fuff.), m. (3 fuff.), m. (4 fuff.), m. (4 fuff.), m. (4 fuff.), m. (4 fuff.), m. (4 fuff.), m. (4 fuff.), m. (5 fuff.), m. (5 fuff.), m. (6 fuff.), m. (6 fuff.), m. (7 fuff.), m. (7 fuff.), m. (7 fuff.), m. (7 fuff.), m. (7 fuff.), m. (7 fuff.), m. (8 fuff.), m
9555 9555 9555			0.6	5.5E	-02 AF170911.1 NT -02 10947034 NT -02 10947034 NT -02 U59492.1 NT		Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds Homo sapiens elf-4E-transporter (4E-T), mRNA Homo sapiens elf-4E-transporter (4E-T), mRNA Mus mussulus second (L11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
10943	1				5.5E-02 U09771.1	Z L	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB),>

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
12797		30604	1.49		11421332 NT	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
3019			0.91	5.4E-0	2 AJ277468.1	NT	Oryzza sativa rbbi3-1 gene for putative Bowman Birk trypsin inhibitor
3416			5.78	5.4E-0	8.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
3891		29281	0.76	5.4E-0	5.4E-02 U85806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8024	20719		0.88		Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21); from 2395281 to 2613730
8968	ı		99'0			NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10537	23234	36467	1.62		5.4E-02 AU120889.1	EST_HUMAN	AU120889 HEMBB1 Homo sapiens cDNA clone HEMBB1001630 5'
10598	23292	36530	2.01		5.4E-02 U20790.1	N	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11132	1	L	1.32		5.4E-02 BF371289.1	EST_HUMAN	RC6-FN0112-190700-021-D06 FN0112 Homo saplens cDNA
11132	23800		1.32	ļ	5.4E-02 BF371289.1	EST_HUMAN	RC6-FN0112-190700-021-D06 FN0112 Homo saplens cDNA
1031	1		1.28			EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo saplens cDNA
1031	13791		1.28			EST_HUMAN	QV0-ST0213-021299-062-e09 ST0213 Homo sapiens cDNA
1495	14242			5.3E	T94759.1	EST_HUMAN	ye37112.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2501	L	27961		5.3E-4	32 AJ276408.1	F	Pseudomonas putida ttgS gene
2943			0.95		5.3E-02 M58417.1	TN	Drosophila melanogaster laminin B2 gene, complete cds
2943	L.				5.3E-02 M58417.1	LN	Drosophila melanogaster laminin B2 gene, complete cds
3150	1				5.3E-02 AJ276408.1	TN	Pseudomonas putida ttgS gene
5029					2 M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5236	L				5.3E-02 AE000527.1	LΝ	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5236			1.98		5.3E-02 AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6785					9695413 NT	LN	Lymphocystis disease virus 1, complete genome
6992	L	32733	1	Š	U32832.1	NT	Haemophilus Influenzae Rd section 147 of 163 of the complete genome
7260	19944		2.06	5.3E-02	1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
1111	20399	33514				SWISSPROT	HYPOTHETICAL 130,0 KD PROTEIN IN SNF8-SPO11 INTERGENIC REGION
8304	L		0.7		5.3E-02 U10098.1	LN	Mus musculus 129/Sv cystatin C (cst3) gene, complete cds
9023	L .		1.56		5.3E-02 X03127.1	LΝ	Podospora anserina mitochondrial epsilon-sen DNA
10032	<u></u>	35897			5.3E-02 AB022605.1	INT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-)methyltransferase, complete cds
10032			0.62		5.3E-02 AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-)methytransferase, complete cds
10156	22804		0.63		6.3E-02 Y07907.1	<u>k</u>	D.rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and postsomitogenesis, 20-28 hpf)
10230	П	36090	0.7		5.3E-02 X68432.1	님	B.rerlo pou[c] mRNA for transcription factor

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										_		_		_						_		_		_		_				_			
Onigo Exult Flobes Expressed in plant	Top Hit Descriptor	Branchlostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, excn 2 and partiel cds	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1	Arabidopsis thaliana putative dicarboxylate diron protein (Crd1) mRNA, complete cds	Mus musculus cytokine inducible SH2-containing protein 3 (Cish3), mRNA	Human staroid hormone receptor Ner-I mRNA, complete cds	EST11352 Uterus Homo sapiens cDNA 5' end	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds	wi80e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1	DINA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA.	BINDING GENE 18 PROTEIN)	Homo saplens chromosome 21 segment HS21C004	Turnip mosaic virus genomic RNA for Capsid protein, complete cds	Turnip mosaic virus genomic RNA for Capsid protein, complete cds	OXALOACETATE DECARBOXYLASE ALPHA CHAIN	DKFZp547D073_r1 547 (synonym: hfbr1) Homo saplens cDNA clone DKFZp547D073 5'	Chlamydia trachomatis section 28 of 87 of the complete genome	Homo saplens chromosome 21 segment HS210046	HIV-1 patient 96 from Italy protease (pol) gene, complete cds	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds	Human hypoxanthine phosphoribosytransferase (HPRT) gene, complete cds	Spodoptera littoralis mRNA for 3-dehydroecdysone 3bela-reductase	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)	Candida albicans protein phosphatase Scd1 homolog (SSD1) gene, complete cds	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)	Homo saplens ES18 mRNA, partial cds	Homo sapiens ES18 mRNA, partial cds	Campylobacter Jejuni NCTC11168 complete genome; segment 3/8	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
פופ באטוו רוט	Top Hit Database Source	Ę	NT	LN LN	N	N	날	Z.	EST_HUMAN	Ā	NAMI IL FOR	NUMBER OF	SWISSPROT	Į.	Į.	N	SWISSPROT	EST_HUMAN	۲	TN	ΙN	EST_HUMAN	NT	LN	IN	SWISSPROT	SWISSPROT	LN	SWISSPROT	LN	ΡN	NT	LN
5	Top Hit Acession No.	AF276815.1	5.2E-02 5031908 NT	5.2E-02 AJ277661.1	5.2E-02 AJ277661.1	5.2E-02 AF236101.1	6671757 NT	J07132.1	5.2E-02 AA297940.1	-02 U14731.1	-02 A1830965 1		-02 P36322	5.2E-02 AL 163204.2	210927.1	-02 D10927.1	203030	5.1E-02 AL134071.1	5.1E-02 AE001301.1	-02 AL163246.2		. .		-02 M26434.1	1131966.1	5.1E-02 P02533	-02 P02533	98.1			-02 AF083930.1		-02 AF062467.1
	Most Similar (Top) Hit BLAST ⊑ Value	5.3E-02	5.2E-02	5.2E-02	5.2E-02 /	5.2E-02	5.2E-02	5.2E-02 U07132.1	5.2E-02	5.2E-02	7 00-30 8		5.2E-02	5.2E-02	5.2E-02 D10927.1	5.2E-02	5.2E-02 Q03030	5.1E-02 /	6.1E-02	5.1E-02 /	5.1E-02 A	5.1E-02 E	5.1E-02 M26434.1	5.1E-02 A	5.1E-02 A	5.1E-02 F	5.1E-02 F	5.1E-02	5.1E-02 F	5.1E-02	5.1E-02 A	5.1E-02 A	5.1E-02
	Expression Signal	1.43	160.56	2.34	2.34	1.23	1.19	3.02	6.0	0.61	90 0		3.13	2.19	1.87	1.87	1.93	1.17	1.03	49.38	0.72	1.44	0.84	0.84	1.48	0.58	0.58	6.2	1.89	2.44	2.44	1.3	2.56
	ORF SEQ ID NO:	30964		28516	28517	1		29609		31548			32932		35472	35473			29547		32350				34076	34622	34623	35556	35945	36661	36662	37540	
	Exon SEQ ID NO:	25030	15008							18617	18797)	19860	20789	22282	22282	24795	15086		J	1	- 1	20845	ı	J		21476	22360	22730	23420	23420	24217	24797
	Probe SEQ ID NO:	12776	2283	3112	3112	3919	3921	4245	5053	5828	8018		7174	8095	9629	9629	12414	2364	4179	4960	6575	6760	8161	8151	8245	8783	8783	9709	10082	10733	10733	11620	12421

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Probe							
SEO IO	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12679	24968		1.41	5.1E-02	5.1E-02 AA534104.1	T_HUMAN	nj73f02.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:988139
470	13256	,	1.84	5.0E-02		NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1182	13934	26599	6.54	5.0E-02	02 Z99104.1 ~	NT	Bacilius subtilis complete genome (section 1 of 21): from 1 to 213080
1983	14719	27438	3.91	5.0E-02	02 P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP- 4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
2821			1.28	5.0E-02	-	LΝ	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3332	16092		1.42	5.0E-02	7305610 NT	۲	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3582	16337		1.04	5.0E-02		NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3672	16425	29066	5.83	5.0E-02	2	IN	Antheraea pernyi period clock protein homolog mRNA, complete cds
4770	17502		0.99	5.0E-02	-02 P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
6038	18819	31780	0.95	5.0E-02	-02 AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6216	18990		1.3	5.0E-02	25.1	NT .	Mus musculus Dmp-1 gene, exons 1-6
7437			12.48	5.0E-02		SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
10100	22748	35963	1.28	5.0E-02		۲	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
10521	23167		0.45	5.0E-02		EST_HUMAN	601844753F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070101 5'
11473	24074	37383	2.5	5.0E	-	FZ	Methanococcus jannaschii section 142 of 150 of the complete genome
11956	25246		3.5	5.0E	-02 Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
217	13028		24.03	4.9E-02	02 M14230.1	LΝ	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
380	13158	25800	2.66	4.9E-02		IN	Homo sapiens ABCA1 (ABCA1) gene, complete cds
360	13158		2.66		02 AF275948.1	占	Homo saplens ABCA1 (ABCA1) gene, complete cds
3282	16043		2.53	4.9E-02	02 P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)
2	l		000				2q48a12.s1 Stratagene hNT neuron (#937233) Homo saplens cDNA clone IMAGE:632926 3' similar to
3570	16334	97090	900	4.9E-02	-02 AA00044 1	T	editaris na lepouve dericulario demonitration de la companio del companio de la companio de la companio del companio de la companio del companio del companio de la companio de la companio del companio del companio del companio de la companio de la companio de la companio del comp
3579	L		68.0	4 9E-02	1	T	zf78a03.s1 Sogres testis NHT Homo sapiens cDNA clone IMAGE:728428 3'
4788	į.		1,91	4.9E-02		Г	xg56g10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2632386 3'
4788	l		1.91	4.9E-02		Γ	xg58g10.x1 NCI_CGAP_Ut4 Homo sepiens cDNA done IMAGE:2832386 3/
6286	ľ		1.9		Γ	i i	Rat elastase Il gene, exon 6
5286	18091	30752	1.9	4.9E-02	02 [_00122.1	F	Rat elastase II gene, exon 6
7042	19733	32783	0.91	4.9E-02	-02 AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8513	21205		0.8	4.9E-02		LΝ	Chlamydia muridarum, section 40 of 85 of the complete genome
8652	21344	34489	0.71	4.9E-02	-02 AL161559.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10191	22839		0.48	4.9E		SWISSPROT	TRANSCRIPTION FACTOR E3
10494	23140	36366	0.46	4.9E-02	-02 AL163218.2	Ę	Homo sapiens chromosome 21 segment HS210018

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ſ		Т	Т	Г	Т	Т	т	T^-	Т	Т	Т	Т	Т	Т	Т	Т	T	Т	Т	Т	Г	Т	Т	Т	Т	Т	Т	Т	т	Ţ
טוועס באנון יסטפט באנו פאסטר וויסטפט באנון פאסטר אינון אינון פאסטר אינון פאטטר ינון פאטר אינון פאטר אינון פאטטר אינון פאטטר אינון פאטטר אינון פאטטר אינון פאטר אינון פייי אינון פאטר אינון	Top Hit Descriptor	Homo sapiens prepro placental TGF-beta gene, complete cds	Homo saplens CS box-containing WD protein (LOC55884), mRNA	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete ods	Human mRNA, Xq terminal portion	Human mRNA, Xq terminal portion	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds	zc49b02.s1 Soares, senescent, floroblasts, NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30838 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);	Tetrahymena rostrata histone H3ll and histone H4ll intergenic DNA	S.scrofa gene for skeletal muscle ryanodine receptor	Homo saplens DKFZP434D222 protein (RENT2), mRNA	Homo sapiens DKFZP434D222 protein (RENT2), mRNA	MR2-ST0129-221099-012-b02 ST0129 Homo saplens cDNA	Fugu rubripes rps24 gene	Fugu rubripes rps24 gene	yz97f09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291017 5' sImilar to contains Alu recettifive element:	Rat stalln-related protein (s1) gene, complete CDS	B.faurus mRNA for RF-38-DNA-binding protein	H.sapiens DNA for endogenous retroviral like element	Gallus gallus Wpkci-8 gene, complete cds	B.taurus mRNA for RF-38-DNA-binding protein	601892692F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'	we79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'	Mus musculus ligand of numb-protein X (Lnx), mRNA	Bos taurus paired box protein (pax-6) gene, partial cds	Bos faurus paired box protein (pax-6) gene, partial cds	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533 P90533 LIMA (contains element LTR1 repetitive element;	AV727059 HTC Homo sapiens cDNA clone HTCBWC01 5'
ייין פון	Top Hit Database Source	LN LN	TN	TN	LN	LN	LN	EST HUMAN	LN LN	LN	LZ	l'z	EST_HUMAN		N	EST HUMAN	ZI	N F	N.	FN	NT	EST_HUMAN	EST_HUMAN	TN	TN	LZ	EST HUMAN	LN.	EST_HUMAN	EST_HUMAN
200	Top Hit Acession No.	4.9E-02 AF008303.1	8923880 NT				4.8E-02 AFD03100.1				11693131 NT	11693131 NT	_		4.8E-02 AJ001398.1	E-02 W01153.1				E-02 AB026678.1	E-02 X15543.1	E-02 BF305237.1	E-02 AI873042.1	6754565	E-02 U73621.1	E-02 U73621.1	4.6E-02 BE153583.1			4.6E-02 AV727059.1
	Most Similar (Top) Hit BLAST E Value	4.9E-02	4.9E-02	4.9E-02	4.8E-02	4.8E-02	4.8E-02	4.8E-02	4.8E-02 X17144.1	4.8E-02 Z54280.1	4.8E-02	4.8E-02	4.8E-02	4.8E-02	4.8E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.7E-02	4.6E-02	4.6E-02	4.6E-02	4.6E-02
	Expression Signal	3.22	1.77	3.41	1.54	3.94	96.6	1.82	2.1	1.15	1.03	1.03	1.32	96.0	96.0	3,83	2.02	8.24	96.0	2.68	6.89	0.67	0.57	1.4	1.39	1.39	0.93	2.91	0.99	3.47
	ORF SEQ ID NO:	37285				L	25899		28620		30478	30479				32597		33973			34981						25712	26149		26762
	SEQ D		24752	24912		13123	13262	14997	15966		17863				L	i	19480	ı	21543			22200		23345				13496		14086
	Probe SEQ ID NO:	11378	12345	12598	321	322	476	2271	3203	4623	5144	5144	8037	9027	9027	6731	6819	8149	8852	8875	9127	9547	9635	10654	11545	11545	264	722	1269	1338

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2492	15209	27951	2.31		4.6E-02 AW 236023.1	EST_HUMAN	xn24f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN Q12849 G-RICH SEQUENCE FACTOR-1;
2811	13072		1.0		4,6E-02 BE153583.1	EST_HUMAN	PM0-HT0339-231199-003-g05 HT0339 Homo sapiens cDNA
3325	1	28423	0.74		4.6E-02 BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3487	15774		0.73		4.6E-02 BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-905 HT0339 Homo sapiens cDNA
4103	16846		1.35		4.6E-02 AF220365.1	NT	Mus musculus nucleolar RNA helicase II/Gu (ddx21) gene, complete cds
6121	17839	30455	66:0		4.6E-02 AA079157.1	EST_HUMAN	zm92c10.s1 Stratagene ovarian cancer (#637219) Homo sapiens cDNA clone IMAGE:545394 3' similar to gb:x03212 KERATIN, TYPE II CYTOSKELETAL 7 (HUMAN);
						!	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnrh2)
5647	18442				4.6E-02 AF076962.1	Ł	gene, complete cas
6136	18914	31883			X61624.1	Ł	C.renhardtii atp2 (atbs) mKnA
6136	18914	31884	3.51		4.6E-02 X61624.1	LΝ	C.reinhardtil atp2 (atpB) mRNA
1	-7007		4.47) 30 F	0.0000000000000000000000000000000000000	NAMI IJ FOD	qc60b06.xt Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA olone IMAGE:1713971 3' similar to contains 1 4 13 1.4 repetitive element :
8554	21246	34386			4.6E-02 BE154006.1	EST HUMAN	PM0-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
11379	23986					EST_HUMAN	ol27h09.s1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3
12325	24744		1.88		4.6E-02 AV712871.1	EST_HUMAN	AV712871 DCA Homo saplens cDNA clone DCAAZF07 5'
12705	24985		3.98			NT	Human germline immunoglobulin lambda light chain gene
434	13220	25866	1.72	4.5E-(12 P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1198	13948	26612	1,11	4.5E-4	32 AF005730.1	NT	Marburg virus strain M/S. Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1198	13948		1.11	4.5E-	02 AF005730.1	TN	Marburg virus strain M/S. Africal Johannesburg/1975/Ozolin VP35 gene, complete cds
1797	14537	L	4.57	4.5E-4	12 P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2103	14834	27568	3.76	4.5E-4	32 AE003964.1	L	Xylella fastidiosa, section 110 of 229 of the complete genome
3710	16463		3.66	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
							Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17
6137	18915	31885		4.5E4	4.5E-02 AJ400877.1	TN	gene
8416	19183			4.6E-	02 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
	1						Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdhlA) gene; carbon monoxide
6779	19523	32550	0.61		4.5E-02 L26487.1	TN	dehydrogenase small subunit (odhiB) gene, complete cds
	L_					!	Methanosarcina fitsia carbon monoxide dehydrogenase large subunit (cdhIA) gene; carbon monoxide
6779	1			4.5E-	4.5E-02 L26487.1	LN	denydrogenase small subunit (conib.) gene, complete cos
8282				4.6E	[L	Arabidopsis thaliana CCAA I -box binding factor HAP's nomolog gene, complete cas
9849				4.5E-	-	EST_HUMAN	ES128167 Cerebellum II Homo sapiens CUNA 5 end similar to similar to neuro-04 protein
10000	22648	35860	0.48	4.5E-	02 X95508.1	LN L	A.europaeum mRNA for legumin-like protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vakue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10116	22764		0.85	4.5E-02	-02 AB000470.1	NT	Gallus gallus mRNA for alphat integrin, complete cds
12154	24640		1.94	4.5E-02	TN 8118013 NT	뉟	Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
12537	25290	30733	6.91	4.5E-02	-02 AA191097.1	EST_HUMAN	zq43f11,r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
213	13025		5.52	4.4E-02	-02 BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2089	14821		5.42	4.4E-02	-02 P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2494	15211	27953	2.4	4.4E-02	-02 AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3631	16384	29024	1.95	4.4E-02	-02 AF159160.1	LN TN	Myxxxxxx xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4584	17319	29945	1.24	4.4E-02	-02 AF109907.1	Ľ	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
	L						Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene,
4584		29946		4.4E-02	-02 AF109907.1	NT	partial cds
4693	17427		2.28	4.4E-02	-02 AJ222689.1	N	Ovis aries CCAAT-enhancer binding protein epsilon gene
7018	19710		0.64	4.4E-02	-02 AF095824.1	N	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7018	19710		0.64	4.4E	-02 AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8650	21342			4.46	-02 AA736969.1	EST_HUMAN	nw13h03.s1 NCI_CGAP_SS1 Homo saplens cDNA clone IMAGE:1239221 3'
				I,		l.	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete
11007	_			4.4E-02	-02 AF060669.1	Z	900
11157	Ц	37104	2.78	4.4E-02	-02 AA496739.1	EST_HUMAN	ae33f04,r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
11890	24460		2.57	4.4E-02	-02 AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12067	25406		1.87	4.4E-02	-02 BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4107418 6
763	13536			4.3E-02	-02 AF003249.1	INT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2573	15287	28024	1.23	4.3E-02	-02 AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'
3423		j		4.3E-02	-02 AL 163210.2	TN	Homo sapiens chromosome 21 segment HS21C010
3651	16404		1.37	4.3E-02	E-02 AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5152	17869		26'0	4.3E-02	U11768.1	TN	Grapevine fanleaf virus coat protein gene, partial cds
6404	19173	32171	4.3	4.3E-02	-02 P30427	SWISSPROT	PLECTIN
6404	19173	32172		4.3E	-02 P30427	SWISSPROT	PLECTIN
6633	19395	32410	82'0	4.3E-02	-02 AA652266.1	EST_HUMAN	ns69c12.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1188886
8411	21104	34243	62'0	4.3E-02	-02 AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
8700				4.3E-02	4.3E-02 X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
8700			1.02	4.3E-02	-02 X55322.1	ΤN	H.sapiens NCAM mRNA for neural cell adhesion molecule
803		26238		4.2E-02	-02 AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 6'
846	13616		2:32	4.2E-02	-02 AU123327.1	EST HUMAN	AU123327 NT2RM2 Hamo sapiens cDNA clone NT2RM2000020 5

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Probe NO: NO: NO: 1714 1714 1714 4284 4284 4895 4895 10969 11278 11489 11278 11489 11278 11489 11278 11489 11278		유 G	Signa	Most Simile (Top) Hit BLAST E Value 4.2E-0 4	Vo. Vo. Vo. Vo. Vo. Vo. Vo. Vo. Vo. Vo.	Top Hit Database Source Source Source Source Surissprot SWISSPROT EST HUMAN NT EST HUMAN NT EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN	Top Hit Descriptor W34g01.x1 NCI_CGAP_Pit1 Hono saplens cDNA clone IMAGE:2645694 3' similar to TR:Q63291 Q63291 L1 RETROPCSON, ORPZ MRNA, contains L1.35 L1 L1 repetitive element; TRANISFORMING PROTEIN MAF TRANISFORMING PROTEIN MAGE:2898319 5' TRANISFORMING PROTEIN MAGE:2898319 5' TRANISFORMING PROTEIN MAGE:2898319 5' TRANISFORMING PROTEIN MAGE:2898319 5' TRANISFORMING PROTEIN MAGE:2898319 5' TRANISFORMING PROTEIN MAGE:2898319 5' TRANISFORMING PROTEIN MAGE:2898319 5' TRANISFORMING PROTEIN MAGE:2898319 5' TRANISFORMING TA-280800-009-410 BN0174 Homo saplens cDNA TRANISFORMING TA-280800-009-410 BN0174 Homo saplens cDNA TRANISFORMING TA-280800-009-410 BN0174 Homo saplens cDNA TRANISFORMING TA-280800-009-410 BN0174 Homo saplens cDNA TRANISFORMING TA-280800-009-410 BN0174 Homo saplens cDNA TRANISFORMING TA-280800-009-410 BN0174 Homo saplens cDNA TRANISFORMING TA-280800-009-410 BN0174 Homo saplens cDNA TRANISFORMING TA-280800-009-410 BN0174 Homo saplens cDNA TRANISFORMING T
5556 5556 6783				4.16-	02 BE251894.1 02 BE251894.1 02 X75881.1	EST HUMAN NT	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5 A.thaliana mRNA for plasma membrane protein to accompany to a company of the c
6999	19691 20090	32742	1.25	4.16	02 AE002132.1 NT 02 7662347 NT	F 12	Ureaplasma urealyticum section 33 of 39 of the complete genome Homo sapiens KIAA0867 protein (KIAA0867), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7502	20173	33265	0.98	4.1E-02	4.1E-02 L02110.1	ΤN	Mus musculus provinal retroviral Insertion in the cGMP-phosphodiastarase (rd bata PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7665	20329	33439	3.12	4.1	-02 AF026198.1	Ļ	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosle-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunits
8541	21233	34376	99.0	4.1E	-02 P34687	SWISSPROT	CUTICLE COLLAGEN 34
9052	21741	34899		4.1E-02	-02 AA372398.1	EST_HUMAN	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
12728	25336	30715	4.07	4.1E-02	4.1E-02 AJ271909.1	FZ	Brassica napus gin gene for plastid glutamine synthetase, exons 1-12
3238		28650	3.26	4.0E-02	-02 AB040904.1	Z	Homo sapiens mRNA for KIAA1471 protein, partial cds
3780	16532	29170		4.0E-02	-02 L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
							Homo sepiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
5295	18100	30759	5.4	4.0E-02	-02 AF280107.1	۲	polypeptide 5 (CYP3A5) gene, partial cds
0.70	70000	0.000	0	10,		: :	7n52h07x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:075296 075296
031.0	0890	00010	28:0	4.05-02	-02 BF110434.1	ES HOMAN	K29124_1.;
7590	20258	33366	6.57	4.0E-02	-02 123838.1	TN	Strong/vocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7650	20314		0.86	4.0E-02	-02 AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7666	20330	33440	7.0	4.0E-02	-02 AB000381.1	N.T.	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7666	L	33441	0.7	4.0E-02	-02 AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8617	24300	34451	3.20	4 OF 02	. DOBB640	TOGGSSIMIS	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GRIDASE)
9544			0.78	4.0E-02	-02 BF679376.1	EST HUMAN	602153884F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4294724 5
1998	22220	35406	4.01	4.0E-02	-02 AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A
9884	22534		1.21	4.0E	4.0E-02 D43949.1	N.	Human mRNA for KIAA0082 gene, partial cds
11778			1.54	4.0E	-02 AJ001018.1	FN	Kluyveromyces lactis gene for Ca++ ATPase
12053		30898		4.0E	4.0E-02 AJ001056.1	FZ	Ovis aries mRNA for acetyl-coA carboxylase
1098		26516	2.75	3.9E-02	-02 BF516149.1-	EST_HUMAN	UI-H-BW1-anx-h-08-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1323		26745	2.45	3.9E-02	-02 P41047	SWISSPROT	FAS ANTIGEN LIGAND
1954	14689	27402	2.4	3.9E-02	-02 AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2708	15415		1.69	3.9E-02	4506862 NT	FZ	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
4118		29487	0.93	3.9E-02	8924019 NT	LZ	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
4118	16860	29488	0.93	3.9E-02	8924019 NT	Z	Homo saplens hypothetical protein PRO1163 (PRO1163), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Símilar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
5408	18207	30913		3.9E-02	02 D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5408	18207	30914	0.55	3.9E-02	02 D50608.1	IN	Rat gene for cholecystokinih type-A receptor (CCKAR), complete cds
5644	18439			3.9E-02	BE968841.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo saplens cDNA clone IMAGE:3933642 5'
2766	18557	31484		3.9E-02	3.9E-02 BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5
6957			1.18	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7739	20435		1.14	3.9E-02	-02 BF239613.1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
7959		33778	62'0	3.9E-02	02 AJ229041.1	LN L	Homo saplens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
7959	20654		62'0	3.9E-02	02 AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11386	20396	33511	2	3.9E-02	-02 P48778	SWISSPROT	ANTIGEN GOR
11913	25298		15.38	3.9E	-02 AB042553.1	Ŋ	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
					<u> </u>		Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P,
12543	24883		183	3 QF-02	1166081 1	E	TCRBV19S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1 TCRBV3S1 TCRBV3S2
	1						Mus musculus chromosome X contidB: X-linked Imphocyte requiated 5 gene. Zinc finger protein 275. Zinc
12666	25223		5.31	3.9E-02	02 AL049866.2	뉟	finger protein 92, mmxq28orf
1945	14680	27394	1.16	3.8E-02	02 BE885137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3912215 5'
2114	14845		1.77	3.8E-02	3.8E-02 AJ251973.1	LN.	Homo saplens partial steerin-1 gene
4876	17603	30228	1.1	3.8E-02	3.8E-02 AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo saplens cDNA clone NT2RM2001698 5'
5354	18157	30840	1	3.8E-02	M11228.1	N	Human protein C gene, complete cds
5996			1.32	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7218]	32976		3.8E-02	6005700 NT	LN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8562			1.33	3.8E-02	02 M60675.1	ΝΤ	Human von Willebrand factor gene, exons 23 through 34
10549	23245			3.8E-02	02 AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
971	13736	28401	4.94	3.7E-02	-02 P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
							Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products,
1367	j			3.7E-02	3.7E-02 L14561.1	Z	partial cots
2230				3.7E-02	A1984806.1	EST_HUMAN	wr85e08x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2494502 3'
2582			3	3.7E-02	AB018261.1	TN	Homo saplens mRNA for KIAA0718 protein, partial ods
3045	15811	28457	6.0	3.7E-02	02 P79944	SWISSPROT	EOMESODERMIN
3047	15813		2.99	3.7E-02	02 BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3447	16203	•	1.17	3.7E-02	E680541 NT	L	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Konma3), mRNA
6978	ı		0.83	3.7E-02	3.7E-02 AP000063.1	LV.	Aerobyrum pernix genomic DNA, section 6/7
	1						

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ſ		Т	Т	Т	Т	T	$\overline{}$		_	Т	T	1	T	-	T		Г	Т	Т	Т	Т	r	1	(7	$\overline{}$		
	Top Hit Descriptor	Xylella fastidiosa, section 121 of 229 of the complete genome	al55c09.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1360912.33	601762117F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA	H.vulgare Ss1 gene for sucrose synthase	Homo saplens genomic region containing hypervariable minisatelities chromosome 10[10q26.3] of Homo sapiens	C.glutamicum gap, pgk and tpl genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase	C.glutamicum gap, pgk and toi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and trosephosphate isomerase	Homo sapiens RU2AS (RU2) mRNA, complete cds	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA	CM2-EN0013-110500-192-b10 EN0013 Hamo saplens cDNA	Chromattum vinosum sulfur globule protein Cv2 precursor (sgp2) gene, complete cds	Inw20e05.s1 NCI_CGAP_GCB0 Homo saplens cDNA clone IMAGE:1241024 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN);	MRO-HT0158-030200-003-b08 HT0158 Homo saplens cDNA	Dictyostelium discoldeum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete eds	Dictyostelium discoldeum unknown spare germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete eds	602020453F1 NCI_CGAP_Bm67 Homo saplens cDNA clone IMAGE:4156116 5'	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5	qk48b09.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1872185 3'	Drosophila melanogaster tiggrin mRNA, complete cds	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'	Thermotoga maritima section 85 of 136 of the complete genome	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)	Maize actin 1 gene (MAc1), complete cds
2.6	Top Hit Database Source	N	EST HUMAN	EST HUMAN	L	LN	FZ	۲	Ę	LN	EST_HUMAN	EST_HUMAN	N	EST_HUMAN	EST_HUMAN	ΤN	NT.	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	L	NT	EST_HUMAN	EST_HUMAN	ΝΤ	SWISSPROT	N
	Top Hit Acession No.	-02 AE003975.1	AA782516.1	3.7E-02 BF124974.1	11418392 NT	K73221.1	3.6E-02 AL096806.1	-02 X59403.1	(59403.1	-02 AF181722.1	3.6E-02 AW945516.1	3.6E-02 AW945516.1					720608.1	3.6E-02 BF347586.1	3.6E-02 BF131609.1	3.6E-02 BF131609.1	3.6E-02 AI280966.1	J09506.1	3.5E-02 AF253417.1	3.5E-02 BF678085.1	3F678085.1	3.5E-02 AE001773.1	53780	101238.1
	Most Similar (Top) Hit BLAST E Value	3.7E-02	3.7E-02	3.7E-02	3.7E-02	3.6E-02 X73221.1	3.6E-02	3.6E-02	3.6E-02 X59403.1	3.6E-02/	3.6E-02	3.6E-02	3.6E-02	3.6E-02	3.6E-02	3.6E-02 U20608.1	3.6E-02 U20608.1	3.6E-02	3.6E-02	3.6E-02	3.6E-02	3.5E-02 U09506.1	3.5E-02	3.5E-02	3.5E-02	3.5E-02 /	3.5E-02 P53780	3.5E-02 J01238.1
<u> </u>	Expression Signal	95.0	٦	3.86	1.94	1.38	0.88	0.58	0.58	0.64	24.9	5.47	2.5	2.76	1.03	1.72	1.72	0.83	4.1	1.4	1.46	1.08	1.39	1.55	1.55	1.83	1.27	1.77
	ORF SEQ ID NO:	33368		37811	30813	29039	29046	30806	30823	12608			32725	32967	33298	35130	35131			37081		26314	26413	26991	26992	29559	29647	Ш
	Exon SEQ ID NO:	20260	22563	24506	25193	16399	16407	18144	18144	18212	19370	19370	19678	19891	20203	21958	21958	22165	23803	23803	24436	13644	13751	14303	14303	16929	17020	18905
	Probe SEQ ID NO:	7592	9914	11954	12603	3646	3654	5341	5341	5413	2099	6607	6985	7206	7533	9291	9291	9512	11135	11135	11852	875	988	1556	1556	4188	4281	6127

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olingie Exoli modes Expressed ili pialii	Top Hit Descriptor	yp44e05.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alureneditive element:	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'	Lilactis MG1363 grpE and dnak genes	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'	PM1-CT0326-291299-002-h03 CT0326 Homo sepiens cDNA	PM1-CT0326-291299-002-h03 CT0326 Homo saplens cDNA	601178765F1 NIH_MGC_20 Hamo sapiens cDNA clone IMAGE:3543833 5'	Homo sapiens mRNA for FLJ00013 protein, partial cds	Homo sapiens mRNA for FLJ00013 protein, partial cds	Homo saplens mRNA for FLJ00013 protein, partial cds	Homo sapiens mRNA for FLJ00013 protein, partial cds	xv28d07.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2814253 3' similar to SW:C211 HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C210RF1 PRECURSOR :	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA	yc20e06.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains	MER29 repetitive element	Homo saplens chromosome 21 segment HS21C008	RC3-FN0155-060700-011-d10 FN0155 Homo sepiens cDNA	RC6-UM0015-210200-021-A10 UM0015 Homo saplens cDNA	M.musculus S-antigen gene promoter region	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)	Caenorhabditis elegans mRNA for DYS-1 protein, partial	Human Iysyl oxidase-like protein gene, exon 3	w199d04.x1 NCI_CGAP_Bm25 Hamo sepiens cDNA clone IMAGE:24330313'	nu70f08.s1 NCL_CGAP_AIv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element;contains element MER25 MER25 repetitive element;	zq0411.s1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:628749 3' similar to	TR:G1017425 G1017425	IPISGKPLPKVTLSRDGVPLKATMRFNTEITAENLTINLKESVTADAGRYEITAANSSGTTKAFINIVVLDRPG PPT GPIA/ISDITEENTI KWEPPKYDGGSOVTNYII I KRETSTAAMTEASA TVARTAAKAAKI	OZGORNO VI Source perethyraid himor NAHDA Homo septens CDNA clane IMAGE-1882510 3'	### ### ### ### ### ### #### #########	
JIE CXOII FIODE	Top Hit Database Source	AN HIMAN	Т	NT I		EST_HUMAN P		T_HUMAN				H	EST HUMAN S	1	×	T_HUMAN	H	EST_HUMAN R	EST_HUMAN R		SWISSPROT		NT TN	EST_HUMAN W	EST HUMAN e	Z	<u> </u>	A NAME IN TOR	Т	Т	٦
Tilo	Top Hit Acession No.	02 H29951 1	-		02 BE561042.1	02 AW861641.1	02 AW861641.1	02 BE276948.1	02 AK024424.1			3.4E-02 AK024424.1		5459		02 T57160.1	3.4E-02 AL163208.2	ļ.,	2.1						02 AA664886.1			4042084			
	Most Similar (Top) Hit BLAST E Value	3 55-02	3.5E-02	3.5E-02	3.5E-02	3.5E-02	3.5E-02	3.5E-02	3.4E-02	3.4E-02	3.4E-02	3.4E-02	3.4E-02	3.4E-02		3.4E-02	3.4E-02	3.4E-02	3.4E-02 AW 794952	3.4E-02	3.4E-02	3.4E-02	3.4E-02	3.4E-02 AI868629.1	3.4E-02			о П	9 VE 03	3.3E-02	il man and in
	Expression Signal	0.78	2.7	1.45	0.5	1.82	1.82	5.69	1.14	1.14	6.47	6.47	2.92	7.14		2.06	1.4	0.7	3.19	2.41	3.59	1.2	4.73	3.25	1.36		_	70	600	9.6	2
	ORF SEQ ID NO:		34357	35762	35817	37388	37389		25973	25974		25974	26448			27849	28831		29291	29922		30349	30558		34482						
	Exon SEQ ID NO:	20572		22566	1		24078	1		13346	13346	13346	13789	l		15112	16181	16509	ı			17740	17923	20853				24508	1	1	ł
	Probe SEQ ID NO:	7877	8521	9917	9968	11477	11477	12596	564	564	292	595	1029	1184		2391	3424	3757	3900	4559	2000	5019	8754	8159	8646			7,00	0870	383	3

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5448	18247	31136	1.83	3.2E-02		NT	S.griseocameum whiG-Stv gene
8431	19199	32196	3.13	3.2E-02	02 M32437.1	N	Rat/polyomavirus left junction in cell line W98.14
9	l			000		MAKAI IJI TOD	yd33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Altrespetitive element-cortains 1 TR1 reportitive element
0432	19200	920220	33.40	3.2E-02	7.4	NEWOL TOU	Aut lepeutre delineur, Johnson E. I. A. February delineur, J. Saculturis cedinus fissue kallikrein cene, complete cds.
7682	1			3.2E-02	11424049	Į.	Homo saplens cytochrome P450, subfamily IIB (phenobarbital-Inducible) (CYP2B), mRNA
8189	L			3.2E-02		LN.	Mus musculus kinesin family member 3c (Kif3c), mRNA
8839	L		0.73	3.2E-02		NT	Homo saplens chromosome 3 subtelomeric region
9125	ł	34978		3.2E-02	.02 AI278971.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:1882063 3'
9126	{		1.21	3.2E-02	02 AI278971.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:1882063 3'
9957	22605		4.07	3.2E-02	02 AA719795.1	EST_HUMAN	zg54b12.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gb:L08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
10256	١.,	36114		3.2E-02	Γ	LN	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1237	L.		2.14	3.1E-02	4503416 NT	F	Homo saplens dual specificity phosphatase 4 (DUSP4) mRNA
1282	l_			3.1E-02	-02 P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1885	14622	27332		3.1E-02	10 584 NT	ΤN	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
1967	14703		1.34	3.1E-02	·02 Z50097.1	IN	Drosophila melanogaster mRNA for headcase protein
5182	17990	30506	1.13	3.1E-02	-02 U78104.1	TN	Human leukemia Inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5276	18081	L		3.1E	-02 AA278478.1	EST_HUMAN	2581a06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5561	18358	31268	0.74	3.1E	-02 BF687742.1	EST_HUMAN	602066783F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4065789 6'
	Ι.	_					Netsserla meningitidis DNA for region 2 (fhaB- and fhaC-fromologs, unknown genes) and flanking genes,
5628	_		0.59	3.1E-02	-02 AJ391284.1		strain FAM18
8840		34677	0.46	3.16	BE965092.2	EST_HUMAN	601656879R1 NIH_MGC_69 Homo saplens cDNA clone IMAGE:3886291 3
9931			2.93	3.1E-02	E-02 AF034779.1	LN	Enterococcus faecalis surface protein precursor, gene, complete cds
11765	ii		1.78	3.15	6754241 NT	FZ	Mus musculus histdine rich calcium binding protein (Hrc), mRNA
24	44988		1 08	305	00 AE187105 1	F-2	Physkleines minutus cytochrome oxidase I dene, bartial cds; mitochondrial gene for mitochondrial product
2500	1	28040		3.06		EST HUMAN	立65h03.r1 Soares, testts_NHT Homo saplens cDNA clone IMAGE:727253 5'
3645	1			3.0E	-02 AF247644.1	Z	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3728	1			3.0E	-02 AW 820223.1	EST HUMAN	QV2-ST0296-150200-040-e09 ST0296 Homo saplens cDNA
3929	l		1.42	3.0E		EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
4991	17714			3.0E		TN	Homo saplens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4991	17714	30319		3.0E	-02 AF281074.1	M	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5307	18112		3.43	3.0E	-02 AB046793.1	N	Homo saplens mRNA for KIAA1573 protein, partial cds

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Hit bescriptor Top Hit Descriptor Irce	za39q10.r1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:294906 5' similar to contains JMAN element TAR1 repetitive element;	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element.	Г	Т	JMAN 601512206F1 NIH MGC 71 Homo sapiens cDNA clone IMAGE:3913848 5	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cods	Human dystrophin gene	Т	Г	Т	Omithorhynchus anatinus coagulation factor X mRNA, complete cds	Thermotoga maritima section 109 of 136 of the complete genome	F	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1	Г		!	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds	Homo sapiens mitochandrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene,	T	Т		JMAN yu07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5	Sus scrofa deoxyribonuclease II mRNA, complete ods	MAN 601452661F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3856598 5	Neisseria meningitidis DNA for region 2 (fhaB- and fhaC-homologs, unknown genes) and flanking genes, strain FAM18	JMAN 601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
Top Hit Database Source	EST_HUMAN	EST HUMAN	노	EST_HUMAN	EST_HUMAN	Ϋ́	ΙŽ	Ł	EST_HUMAN	EST HUMAN	EST HUMAN	Ν	Ł	EST_HUMAN	FN.	EST HUMAN	EST HUMAN	EST_HUMAN	۲	ŀ	2 2	EST HUMAN	ESI HUMAN	EST_HUMAN	N	EST_HUMAN	눌	EST_HUMAN
Top Hit Acession No.	-02 N99615.1	3.0E-02 N99615.1	3.0E-02 AJ242906.1	3.0E-02 BE889948.1	-02 BE889948.1	-02 AF213884.1	3.0E-02 AF213884.1	3.0E-02 M86524.1	3.0E-02 BF246361.1	3.0E-02 BF679706.1	3.0E-02 BF353889.1	3.0E-02 AF275654.1	3.0E-02 AE001797.1	3.0E-02 Z21211.1	3.0E-02 M81357.1	3.0E-02 AA483216.1	R32019.1	3.0E-02 AW895565.1	3.0E-02 AF048687.1	1 00F000T	2.9E-02 AF 226/03.1	2.9E-02 BE565644.1	BE565644.1	H72805.1	AF060221.1	-02 BF032233.1	AJ391284.1	29E-02 BE271437.1
Most Similer (Top) Hit BLAST E Value	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	3.0E-02	0	2.95-02	2.9E-02	2.95-02	2.9E-02	2.9E-02	2.9E-02	2.9E-02	2.9E-02
Expression Signal	1.4	1.4	3.32	2.84	2.84	2.15	2.15	1.4	0.59	0.48	99.0	1.8	1.49	0.49	2.73	7.75	2	2.46	2.06		1.27	1.04	1.04	0.89	0.97	7.39	0.56	12.03
ORF SEQ ID NO:	31905	31906		32488	32489	32472	32473	32885			34373		36221	36322	37148	37607	30618			07004	20400	20402	20403	29299	31715	31953	32585	32904
Exan SEQ ID NO:	18937	18937	19609	19467	19467	19453	19453	19819	20155	20720	21231	21384	23004	23092	23862	24285	25389	24909	25383	15504	10004	13/30	00/01	16658	18754	18975	19555	19835
Probe SEQ ID NO:	6160	6160	6692	9089	6806	6971	6971	7132	7483	8025	8539	8692	10357	10446	11197	11690	12243	12587	12629	2438	2000	0887	ORAY	3908	5972	6199	6855	7148

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7897	20282	33723	0.87	2.9E-02	2.9E-02 AF129279.1	NT	Buchnera aphidicola natural-host Schlschtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
7897	20592	33724	0.87	2.9E-02	02 AF129279.1	FN	Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9558	22211			2.9E-4		EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
8998	22211	35397	2.49	2.9E⊣	02 AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9774	22425		0.75	2.9E-		EST_HUMAN	EST388706 MAGE resequences, MAGN Homo sapiens cDNA
10243					4.1	NT	Aeropyrum pemik genomic DNA, section 7/7
10977	L	30590		2.9E-		INT	Sheep gene for uitra high-sulphur keratin protein
552	13335		96.0	-38E	02 AW970153.1	EST_HUMAN	EST382234 MAGE resequences, MAGK Homo sapiens cDNA
3360	16119	28775	1.3	2.8E-(02 AF066063.1	NT	Homo sapiens retinal fascin (FSCN2) gene, exon 2
3360				2.8E-02	32 AF066063.1	NT	Homo sapiens retinal fascin (FSCN2) gene, exon 2
5400		30805	11.62	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
6711				2.8E⊣	02 T78960.1	EST_HUMAN	yd21b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108865 6
8226		34058		2.8€		NT	Craterostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
8915	21606	34749	0.85	7.8E⊣	02 AA280762.1	EST_HUMAN	zs96c06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5
9108	21796	34960	-	2.8E-02	02 AF187872.1	LΝ	Cavla porcellus inwardly-reotifying potassium channel Kir2.1 (KCNJ2) gene, complete ods
9212	21891	35058	0.69	2.8E-(2 AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12528	25229		1.5	7.8E-C	12 R06966.1	EST_HUMAN	y/12h02.r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126675 5'
12530	24876		1.48	2.8E-(02 X06322.1	NT	Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot)
							Human germline T-cell receptor beta chain Doparnine-beta-hydroxylass-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6STP, TCRBV7S1A1N2T, TCRBV7S1A1N2T, TCRBV7S1A1N2T, TCRBV7S1A1N2T, TCRBV7S1A1N2T, TCRBV7S1A1N2T, TCRBV7S1A1N2T, TCRBV7S1A1N2T, TCRBV7S1A1N2T, TCRBV7S1A1N2T, TCRBV7S1A1N2T
1472	14219		1.23	· 2.7E-	32 U66059.1	Z	TCRBV1359/135>
3425	16182	28832		2.7E-4	2.7E-02 AL161494.2	LN.	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4178	16918			L	N47258.1	EST_HUMAN	yy86h12,r1 Soares_multiple_sclerosis_2NbHMSP Homo saptens cDNA clone IMAGE:280487 5
4178	16918		1.92		N47258.1	EST_HUMAN	yy88h12.r1 Scares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5
2252	19159		1.2		2 7E 02 D12246 1	DOT LINAN	y33d09.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:128657 5' similar to SP: IC2284, IC228
5812	1				Τ	L	T. aestivum bTTH20 mRNA for wheat type V thlonin
2000					Τ	1 IV	Ontro cotine mDNA for accordate middee
2020	-		0.0	1	2.7E-02 AD004/88.1	L N	A historic park dane
200	-	1			1	14141	Providence Service Service NIEDLES On Home services CONA alone (IMADE 14604684.3)
6967	19449	32467	2.28		AA8835/1.1	ES HOMAN	Josepho, S. J. Costres, Total Tetta, Indentify By Homo Sapiens Cours Invace; 1024001.5

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	tc28g08.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982.3' similar to contains Alu repetitive element;	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]	Homo sapiens chromosome 21 segment HS21C082	ab02b02.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'	Mus musculus histidine rich calcium binding protein (Hrc), mRNA	Mus musculus histidine rich calcium binding protein (Hrc), mRNA	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes	Chicken dorsalin-1 mRNA, complete cds	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1	xa52b04.x1 NCI_CGAP_Sar4 Homo saplens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN	Q15041 HYPO I HE I I CAL PROTEIN KIAA0069;	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63	qg27f11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'	601493473T1 NIH_MGC_70 Homo sepiens cDNA clone IMAGE:3895578 3'	Vaccinia virus ORF1L, strain Wyeth	Vacchia virus ORF1L, strain Wyeth	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA	ak22f04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'	Homo sapiens KJAA1070 protein (KIAA1070), mRNA	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding milochondrial pene.	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) dans mitrohondrial gene	encoding mitochondrial protein, complete cds	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens radixin (RDX) mRNA	zs84c02.r1 NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:704162 5	UI-HF-BNO-akj-@-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'	602015501F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150944 5'	on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'	on26f06.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
le Exon Probe	Top Hit Database Source		TN TN	TN T	EST_HUMAN a			NT B	NT	N FN		HOMAN	NT A			Г	Г			EST_HUMAN a		S E		⊕ LN			1	Г	EST_HUMAN 6			EST_HUMAN 0
Sing	Top Hit Acession No.	02 AI377036.1	02 543442.1	02 AL163282.2	02 AA490021.1	6754241 NT	6754241 NT	-		-		1	2.6E-02 AL161663.2			2.6E-02 BE621748.1			6981 <i>271</i> NT	02 AA860946.1	11432020 NT	0 P 1 4 4 9 5 9 4				2.6E-02 4506466 NT						
	Most Similar (Top) Hit BLAST E Value	2.7E-02	2.7E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02 AE002014	100	Z.0E-0Z	2.6E-02 /	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.6E-02	2.8E-02 6	2.6E-02	2.6E-02	2 RE-02		2.6E-02	2.6E-02 A	2.6E-02	2.6E-02 4	2.6E-02	2.6E-02	2.5E-02	2.5E-02	2.5E-02
	Expression Signal	1.06	0.49	1.12	3.29	4.49	4.49	1.86	2.25	1.56	C	2.30	0.7	0.59	7.34	1.9	6.0	6.0	7.11	0.71	1.15	0 75		0.75	4.39	1.67	2.33	2.2	2.09	1.75	1.75	15.9
	ORF SEQ ID NO:		li		27825	27827	27828		30200	30332	20004	30204				32089	32593	32594	32494	34232	35182	35453		35454	36165			37465	30615	25935	25936	26224
	Exen SEQ ID NO:	20946	1				15090		17577	17728		ı	- 1	18590	18903				19471		22014	22267		22267	22950	23856	24049	24152		' [- 1	13563
	Probe SEQ ID NO:	8252	8514	558	2366	2368	2368	2916	4847	5005	000	2005	5754	2800	6125	6331	6728	6728	6810	8403	9260	9614		9614	10303	11191	11361	11553	12170	519	519	791

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| Top Hit Descriptor | Homo sapiens hypothetical protein FLJ10844 (FLJ10844), mRNA | Zh83h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3' | Chicken myristoylated alanine-rich Ckinase substrate (MARCKS) mRNA, complete cds | Chicken myristoy/ated alanine-rich Ckinase substrate (MARCKS) mRNA, complete cds | HSAAACKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA

 | Rat gene for uncoupling protein (UCP) | Rat gene for uncoupling protein (UCP) | RC3-ST0186-230300-019-h06 ST0186 Hamo sapiens cDNA

 | Human retrotransposon 3' long terminal repeat
 | yu12c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576.3' similar to contains All repetitive element contains ASR repetitive element. | 1908-641 of Course fold live enlant 4015 C London, | gb K02909 RATSR7K Rat (rRNA);contains A3R.b1 A3R repetitive element; | Borrella burgdorferi (section 11 of 70) of the complete genome | zu91c06.s1 Scares_testis_NHT Homo saplens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET

 | AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR | XTR repetitive element;

 | Arabidopsis thaliana molybdopterin synthase sulphurylase (cnx5) gene, complete cds | Arabidopsis thaliana molybdopterin synthase sulphurylase (cnx5) gene, complete cds

 | AV692954 GKC Home sapiens cDNA clone GKCDSC03 61

 | hh07b12.s1 NCI_CGAP_Thy1 Homo saplens cDNA clone IMAGE:943583 similar to contains Alu repetitive | 1801274962F1 NIH MGC 20 Homo sapiens cDNA clone IMAGE:3615902 5 | | Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23,

 | Muts hamolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes | Mire mineral fire motor historementshills found a place III and an a fact a land and a day and a 1000 | introduction inspects inspects inspects cases in regions have organic pares, parest outs, similarly, GTA, NG25, MutS homolog, CLCP, NG24, and NG26 genes, complete cds; and unknown genes | Bacteriophage blL67, complete genome | Mus musculus DinB homolog 1 (E.
coli) (Dinb1), mRNA | MR0-FT0175-310800-202-a06 FT0175 Homo sapiens cDNA | Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds |
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No. | 8922702 | W86680.1 | M31650.1 | M31650.1 | Z20573.1

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 | H78376 1 | | | |

 | | AA625660.1

 | AF124160.1 | AF124160.1

 | AV692954.1

 | A A AD2804 4 | BE387111.1 | |

 | AF109905.1 | | AF109905.1 | 9627909 | 6753635
 | BE928869.1 | 2.4E-02)U78167.1 |
| Most Similar
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Value | 2.4E-02 | 2.4E-02 | 2.4E-02 | 2.4E-02 | 2.4E-02

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| Expression
Signal | 0.95 | 6.0 | 0.58 | 0.58 | 0.8

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 | 24625 | 24657 |
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| | Exon ORF SEQ Expression (Top) Hit Top Hit Acession Database NO: Signal BLASTE No. Source | Exon
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Single Exul Proces Explessed II brain	Top Hit Descriptor	Raftus norvegicus cAMP-regulated guanine nucleotide exchange factor i (cAMP-GEFI) mRNA, complete cds	Homo saplens SNCA isoform (SNCA) gene, complete cds, atternatively spliced	Caenorhabditis elegans mRNA for Iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds	za84g08.rf Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299294 5'	4 Homo saplens mammary tumor-associated protein INT6 (INT6) gene, exon 4	S.cerevisiae chromosome IV reading frame ORF YDL245c	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3'end	Gailus gailus connexin 45.6 (Cx45.6) gene, complete cds	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds	CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA	xs25d08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2770671 3'	xs25d08.x1 NCI_CGAP_Ut2 Homo saplens cDNA clone IMAGE:2770671 3'	601672279F1 NIH_MGC_20 Homo saplens cDNA clone IMAGE:3955386 5'	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA	carboxylase beta chain (pccB) homolog gene, partial cds	Arabidopsis maiana UNA chromosome 4, contig rragment No. 17	MINO-THE UNDER-UNG-COST IT TO USE TO SENTEND SEPTEMBLE COLVER HE TO USE TO USE SENTENDE TO USE TO USE SENTENDE TO USE TO	Home contains DDX4 data for the Acontaining comments X owns 1.44	and deposits I CA1 gains for apply companied to apply companied to apply companied to apply companied to a second companied to a sec	Homo saplens PDX1 gene for lipoyl-containing component X, exons 1-11	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA cione IMAGE:2302147 3'	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2302147 3'	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR	CHROMOSOME ASSEMBLY PROTEIN XCAP-C	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome	Bacıllus licheniformis isolate N57N1 KerA gene, partial cds
שמוא ווסצם פול	Top Hit Database Source	N R		O 8	T_HUMAN		Г	EST_HUMAN H	Г	NT	NT	EST_HUMAN O	EST_HUMAN C				EST_HUMAN 6	EST_HUMAN 6			Т	NEW COLUMN						П	SWISSPROT C			NT
Sillo	Top Hit Acession No.	02 U78167.1	02 AF163864.1	02 AB008569.1		02 U94165.1	02 274293.1	02 220377.1			02 124799.1		02 BE93525.1					02 BF026487.1			T	02 DE 14 14 / 0. 1	T				0.1		02 P50532			02 AF282894.1
	Most Similar (Top) Hit BLAST E Value	2.4E-02	2.4E-02	2.4E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02		2.3E-02	2.35-02/	205-02	20 30 0	2.35.75	2.3E-02	23E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02	2.3E-02/
	Expression Signal	1.66	1.34	3.88	4.29	10.45	2.08	6.19	8.0	1.06	1.06	0.93	0.88	0.88	1.14	1.14	2.56	2.58		3.63	0.4	80.0	700	to.	0.94	0.68	0.68	0.98	77.0	1.33	1.33	0.46
	ORF SEQ ID NO:	31104					27809	29084		29499	29500	29755	29780	29781	29782	29783	29919	29920		30756	32232	33505	34304	מאבמי	34205	34429	34430	34880	35617	35776	35777	36397
	Exan SEQ (D NO:	24657	24678	24764	14603	14817	15072	16423	18455	16871	16871	17123	17152	17152	17880	17880	17290	17290		18096	2000	20472	24083	3014	21083	21289	21289	21726	22410	22577	22577	23170
	Probe SEQ ID NO:	12186	12218	12360	1865	1880	2350	3670	3702	4129	4129	4386	4415	4415	4418	4416	4555	4555		5281	7700	27.77	8370		8370	8597	8597	9036	8769	8828	8266	10524

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		genes,	cds	cds														93,								ar to contains			omolog, and	ar to contains	
	Top Hit Descriptor	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA	PM2-BT0546-120100-001-f11 BT0546 Homo saplens cDNA	Inc21g03.r1 NCI_CGAP_Pr1 Homo saplens cDNA clone IMAGE:1008820	yx43h07.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264541 5'	PM2-BT0546-120100-001-f11 BT0546 Homo sepiens cDNA	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA	zx63b09.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:7961.21 5'	S.cerevisiae chromosome IV reading frame ORF YDL245c	602015306F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151161 5'	Borrella burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes	wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7	A,thaliana mitochondrial genome, part A	Homo saplens chromosome 21-segment HS21C102	wh54a05.x1 NCI_CGAP_Kld11 Homo saplens cDNA clone IMAGE:2384528 3'	CM4-HT0244-111199-040-h05 HT0244 Homo sapiens cDNA	QV3-GN0058-120900-329-a12 GN0058 Homo saplens cDNA:	Mus musculus sorting nextr 1 (Snx1), mRNA	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element;contains element MER11 repetitive element;	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732.3' similar to contains Alu repetitive element:contains element MER11 repetitive element:	
ביים: יויסאם סופווייס	Top Hit Database Source	FZ	Z	TN	SWISSPROT	SWISSPROT		EST_HUMAN		EST_HUMAN		EST_HUMAN		EST_HUMAN		THUMAN		EST_HUMAN	TN	LΝ				EST_HUMAN	NT		NT	۲	Į,	EST HUMAN	
5	Top Hit Acession No.	J72073.1	2.1E-02 AF204395.1	2.1E-02 AF204395.1	>02438	>02438	502438	2.1E-02 BE072546.1				2.1E-02 BE072546.1	3E072546.1			2.1E-02 BF343655.1	J44914.1	2.1E-02 AI768127.1	Y19213.1	Y08501.1	2.1E-02 AL163302.2	41823432.1	2.1E-02 AW379529.1	2.1E-02 BF086199.1	9790238 NT		2.1E-02 AJ243213.1		-02 129324.1	2.1E-02 AA984288.1	
	Most Similar (Top) Hit BLAST E Value	2.1E-02	2.1E-02	2.1E-02	2.1E-02 P02438	2.1E-02 P02438	2.1E-02 P02438	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02 Y08501.1	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02	2.1E-02]]
	Expression Signal	10.32	1.21	1.21	1.06	1.06	1.06	1.2	1.2	1.32	4.48	1.07	1.07	1	0.81	0.81	1.47	1.53	0.69	4.51	1.05	0.76	1,13	0.88	9.0	0.5	2.61	2.61	1.15	69 0	122.2
	ORF SEQ. ID NO:	26656		26788	27218	27219	27220	27492			26193	27492	27493	28973	29480	29641	29775	29788		30031	30122	30124	31259		34249	35236	L	35369			
	Exen SEQ ID NO:	13989	ļ	14113	14517	14517				15305	13534	14763	14783	16326	!	17014	17147	17157	17197	17396	17494	17501	18350	19448	21110	22065		22184		1 _	1
	Probe SEQ ID NO:	1240	1366	1368	1775	1775	1775	2028	2028	2591	2819	3147	3147	3571	4110	4275	4410	4421	4461	4662	4762	4769	5553	9969	8417	9403	9531	9531	9883	996	990

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Single Exon Probes Expressed in Brain	Exon ORF SEQ Expression (Top) Hit Top Hit Acession Orf Signal BLASTE No. Source Source	24080 37391 1.38 2.1E-02 6754255 NT Mus musculus heat shock protein, 74 kDs. A (Hspage), mRNA	Ę	2.1E-02 L34170.1 NT	F.Z	EST HUMAN	14.4 2.0E-02 AW895565.1 EST HUMAN	3.76 2.0E-02 6753635 NT	25736 2.72 2.0E-02 AA456638.1 EST HUMAN	П	TIM PERSON IN CO DO C	28505 1.0 2.0E-02.ML030000.1	26506 1.17 2.0E-02 8022384 NIT	27349 200 200 200 200	2734.4 239 2.0E-02 8922453[NT	INI 0047780 Z'OL-07	4L161532.2 (NT	12844 25457 2.11 2.0E-02 BF002932.1 EST_HUMAN MER1 repetitive element ;	15905 1.4 2.0E-02 7305474 NT (Seme6b) mRNA	2.0E-02 AF095588.1 NT	29370 1.3 2.0E-02 M18095.1 NT	31254 0.58 2.0E-02 U34778.1 NT	31523 0.7 2.0E-02 L35321,2 NT	33217 1.11 2.0E-02/AP000004.1 NT	33218 1.11 2.0E-02 AP000004.1 NT	2.21 2.0E-02 U70408.1 NT	36117 1.62 2.0E-02 AI640342.1 EST_HUMAN	36469 1.78 2.0E-02 273966.1 NT	37337 2.17 2.0E-02 D88184.1 NT	37598 2.21 2.0E-02 10947055 NT	37599 2.21 2.0E-02 10947055 NT
			20											l			0		<u></u> -	4											
-	be Exon SEQ ID SEQ ID NO:			12339 2516	12714 2498	16 1284	17 1284	262 1306		781 1355	1065 1382		Ļ	T			1087 1087	3077 1284	3141 15905			5548 18348			7450 20126				11344 24034		382 24277
	Probe SEQ ID NO:	£	12	12	12						-	1	Ė	ľ	Ť	ٔ	Ĭ	ĕ	<u>ښ</u> ســــ	3,	ř	ğ	ផ	7,	ř	9	10259	10539	٤	Ĕ	11682

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						2.6	
	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11880		30595	1.9	2.0E-02	2.0E-02 AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12336	15506		1.82	2.0E-02	AL161532.2	L	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
12786	25038		6.4	2.0E-02	T80037.1	EST_HUMAN	yd04c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24675 5'
	1						nf19a07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.t1 L1
677	13452				1.9E-02 AA572764.1	EST_HUMAN	repetitive element ;
1611	14358	27047	1.15	ľ	1.9E-02 P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2032	14767	27496	2.68	1.9E-02	1.9E-02 AL163303.2	Ľ	Homo sapiens chromosome 21 segment HS21C103
2032	14767	27497	2.68	1.9E-02	1.9E-02 AL163303.2	L	Homo sapiens chromosome 21 segment HS21C103
2510	15227	27968	26.0	1.9E-02	1.9E-02 AL161550.2	F	Arabidopsis thallana DNA chromosome 4, contig fragment No. 50
2906			7.48	1.9E-02	1.9E-02 AA713856.1	EST_HUMAN	nw04f05.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
7967	15718	28369	1.66	1.9E-02	1.9E-02 AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLCBLH073'
3598	18351		1.18	1.9E-02	1.9E-02 N52250.1	EST_HUMAN	yz28b02.s1 Soares_multiple_sclerosts_2NbHMSP Homo sapiens cDNA clone IMAGE:284331 3'
3691	16444		85.6	1.9E-02	1.9E-02 BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 6'
							qn04c07.x1 NCI_CGAP_Lu5 Homo saplens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive
3703		29095	0.95	1.9E-02	1.9E-02 Al301183.1	EST_HUMAN	element;
4025			1.49	1.9E-02	40.1	NT	Mycoplasma Imitans VIhA1 precursor (vIhA1) and VIhA2 precursor (vIhA2) genes, partial cds
4170	16910	59539	1.83	1.9E-02		SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4170	16910		1.83	1.9E-02 P09081		SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
1037	47220	62000		100	00 00 01483000 4	HOT LINAMI	148404.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2144551 3' similar to
4054	15227		4.09	1 9E-02		LONDI	Arabidosis thallana DNA chromosome 4 contin francent No. 50
5233	18039			1.9E-02		ż	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5382	18182			1.9E-02	2 L47572.1	Ę	Meleagris galiopavo paraoxonase-2 (PON2) mRNA, complete cds
5701	18495		0.86	1.9E-02	2 AB019507.1	۲	Drosophila kanekol gene for glycerol-3-phosphate dehydrogenase, complete cds
7001	19693		1.38	1.9E-02	2 U19241.1	NT	Homo saplens interferon-gamma receptor alpha chain gene, exon 1
7001	19693	32745		1.9E-02	2 U19241.1	ΤN	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8469			1.23	1.9E-02	2 AL162754.2	LN	Neisseria meninglidiis serogroup A strain Z2491 complete genome; segment 3/7
9230	21909			1.9E-02	2 BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
9613			9.0	1.9E-02	1.9E-02 L10114.1		Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
9945	22593	35796	1.05	1.9E-02	12 BF695832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4076253 5'
10152	22800		0.54	1.9E-02	2 D64001.1	LN-	Synechocystis sp. PCC6803 complete genome, 20/27, 2539000-2644794
10681			1.44	1.9E-02	2 AF008938.1	۲	Vibrio cholerae V86 phage putative replication protein gene, complete cds
12090	i	30903		1.9E-02	2 AF101065.1	Ę	Hirudo medicinalis intermediate filament gliarin mRNA, complete cds
12846	25147		1.36	1.9E-02	1.9E-02 L11068.1	L L	Candida albicans lambda Ca3/B fragment

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Single Exon Probes Expressed in Brain	Top Hit Database Source	hn52c06.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element	Т				EST, HUMAN [1952a09.x1 Soures, NFL T, GBC, S1 Homo saplens cDNA clone IMAGE:2090296.3	EST_HUMAN 4k/24h04.s1 Soares testis_NHT Home sapiens cDNA clone IMAGE:1406835.31	Г	Г		EST HUMAN QV2-NN1073-220400-159-h09 NN1073 Homo septems CDNA		T HUMAN	Ţ		Г	Т					EST_HUMAN 601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'		EST_HUMAN L1.t1 L1 repetitive element;	hf34a03 x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains	NEWDU					EST_HUMAN qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
Buic	Top Hit Acession No.	-02 AW771104.1 E		-02 X17664.1 NT	1.8E-02 AF243382.1 NT	1.8E-02 AE004544.1 NT	1.8E-02 AI805829.1 E	Г	63.1		-	7.1	8943	E-02 BF241924.1					-02 AB002337.2 NT		-02 AP000006.1 NT	-02 U62749.1 NT	-02 BE394869.1 E		-02 AW573183.1 ES	02 018/573483 4	T	1		-02 S74186.1	57495	-02 AI147615.1 ES
	Most Similar (Top) Hit BLAST E Value	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02 P14310	1.8E-02	1.8E-02)	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.7E-02		1.7E-02/	1 7E 02	1 75 02/	1 7 00 7	1./E-02/	1.7E-02	1.7E-02	1.7E-02
	Expression Signal	1.4	0.83	1.32	1.73	1.71	0.94	0.99	1.17	5.02	0.69	0.91	8.0	0.49	0.49	2.41	1.51	1.37	2.31	2.31	1.59	3.32	1.86	. !	2.17	217	2 74	407	10:0	0.99	1.01	1.44
	ORF SEQ ID NO:	25772	26086			28133			29764		33857	-	34242	35225	35226		35815	35987	36409	36410	37535	37545	26323	į	27230	27234				27752		28411
	Exon SEQ ID NO:	13137	13446	13892				16810				21060		22054	22054	22195	22611	22774	23181	23181	24211	24223	13655	,	14524	14524	14602	14837	3	15016	1220	15762
	Probe SEQ ID NO:	336	670	1137	1416	2685	3205	4065	4396	6712	8020	8367	8410	9392	9392	9542	8963	10128	11414	11414	11613	11626	988	Ş	3/8	1783	1864	2108	3 2	1822	949	2996

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3502	16258		4.67	1.7E-02	1.7E-02 AW827368.1	EST_HUMAN	hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens dDNA clone IWAGE:3015534.3' similar to contains MER19.b1 MER19 repetitive element :
3614	16367		0.73	1.7E-02 P04929	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4148	16890		1.23	1.7E-02	AA669618.1	EST HUMAN	ac19f04.s1 Stratagene overy (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element.contains element MER24 repetitive element:
4176	16916		2.04	1.7E-02	1.7E-02 R02506.1	EST_HUMAN	ye86f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124847 5'
4420	17156	29787	1.49	1.7E-02	1.7E-02 AI305279.1	EST_HUMAN	qm08g07.x1 NCI_CGAP_Lu5 Homo saplens cDNA clone IMAGE:1881276.3' similar to gb;X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4491	17227	29856	1.78	1.7E-02	1.7E-02 AW573183 1	EST HUMAN	h/34a03.x1 Seares_NFL_T_GBC_S1 Home sapiens cDNA clone IMAGE:2933740 3' similar to contains
4666	17400	30034	1.61	1.7E-02	1.7E-02 V00641.1	N L	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4763	17495		5.84	1.7E-02	02 AI015076.1	EST_HUMAN	ov51e02.s1 Soares_test(s_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
5007	17730	30334	0.69	1.7E-02	6981289 NT	NT	Rattus norvegicus N-arginine dibasic convertase 1 (Nrd1), mRNA
5096	17815		0.91	1.7E-02	1.7E-02 AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6035	18815	31775	2.07	1.7E-02	1.7E-02 AI769247.1	EST HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6484	19251	32250	1.47	1.7E-02	1.7E-02 Al038280.1	EST HUMAN	oy85h03.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:1672661.31
6950	19432	32448	1.27	1.7E-02	1.7E-02 AF190930.1	FZ	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7103	19791	32856	2.44		8400716 NT	LN⊤	Homo sapiens nebulin (NEB), mRNA
7257	19941	33016	1.06		L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7257	19941	33017	1.06			NT	Human apolipoprotein (a) gene, exon 1
7642	20307		1.78		1.7E-02 AJ010770.1	NT	Homo saplens hyperion gene, exons 1-50
9336	20407	33523	0.98	1.7E-02	1.7E-02 U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9238	22251	35437	1.3	1.7E-02	1.7E-02 AL040554.1 EST_	EST_HUMAN	DKFZp434l0314_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434l0314 5
11801	24391	37724	1.38	1.7E-02	5902007		Homo sapiens serum constituent protein (MSE55), mRNA
12631	25337	30716	2.39	1.7E-02	1.7E-02 AW903482.1	THUMAN	CM4-NN1030-040400-130-106 NN1030 Homo sapiens cDNA
498	13282		3.19	1.6E-02		TN	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1653	14399	27088	1.04	1.6E-02	1	LΝ	Treponema maltophilum flaB2, flaB3 and fliD genes for flagellin subunit proteins and CAP protein homologue
2246	14974	27711	6.0	1.6E-02 Q64176	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2246	14974	27712	6.0	1.6E-02 Q64176	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2570	15284	28022	1.05	1.6E-02	1.6E-02 AJ006345.1	LN	Homo sapiens KVLQT1 gene
2649	15359	28102	1.48	1.6E-02		EST_HUMAN	ne81d06.s1 NCI_CGAP_Ew1 Homo saplens cDNA clone IMAGE:910667
2699	15408		0.96	1.6E-02	1.6E-02 AB014534.1	LN	Homo saplens mRNA for KIAA0634 protein, partial cds

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t Top Hit Acession Database Source	02 AF112282.1 NT Lasaea sp. isolate IBd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product	1.6E-02 AW850652.1 EST_HUMAN IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA	02/AL163301.2 NT Homo sepiens chromosome 21 segment HS21C101	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds: Sacm21 gene, partials	1 EST HUMAN	6671715 NT	1.6E-02 AB015281.1 NT Candida albicans CaGCR3 gene, complete cds		1.6E-02 AB027671.1 NT Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complets cds	1.6E-02 AL 161508.2 NT Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20	1.6E-02 AJ277662.1 NT Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein	X05151.1 NT	AF079764.1 NT	EST_HUMAN	AA572818.1	Z94828.1 NT	1.6E-02 AL161608.2 NT Arabidopsis thallana DNA chromosome 4, contig fragment No. 20	F .	1.6E-02 Al373558.1 EST_HUMAN qz89610.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442.3'	123734 NT	EST_HUMAN	IN	LN	TN	02 BF092942.1 EST_HUMAN MR4-TN0115-080900-201-b12 TN0115 Home sapiens cDNA	1.5E-02 Q09711 SWISSPROT HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I	782 NT	02 11418713 NT Homo sapiens KIAA1009 protein (KIAA1009), mRNA
	AF11228	AW8506	2 AL 16330	AF110520	AW87540		AB01528	AB02757	AB02757	AL161508	AJ277662	X05151.1	AF07976	AA57281	AA57281	Z94828.1	AL161508	AL161508	A1373558		N39521.1	AL161594	AJ006216	AJ006216	BF092942	Q09711	1	
Most Similar (Top) Hit BLAST E Vælue	1.6E-02	1.6E-0	1.6E-0									1.6E-0			1.6E-0	1.6E-0		1.6E-02	1.6E-02		1.5E-02	1.5E-02			1.5E-02		1.5E-02	
Expression Signal	0.71	5.9	1.32	2.49	0.97	1.25	2.05	1.75	1.75	0.86	0.76	1.88	2.72	1.29	1.29	2.38	2.54	2.54	1.54	23.05		1.69	1.6	1.6	96.0	1.56	1.63	1.2
ORF SEQ ID NO:	28431		29215		29640	31241	32316		32518		33847			36184	36185		37124	37125	37407					28468	29103	31955		33060
Exen SEQ ID NO:			16581	16896	<u> </u>	18334	19311		19494	20276	20715	20772	22588	22966	22966	l	23841	23841				1		15823		18977		19984
Probe SEQ ID NO:	3016	3516	3830	4154	4267	5536	6546	6832	6832	7610	8020	8078	9940	10319	10319	10826	11174	11174	11495	734	2138	2172	3057	3057	3711	6201	7219	7301

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Probe SEO ID	Exon SEQ ID	ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit	Ton Hit Descriptor
Ö		Ö Q	Signal	BLAST E Value	Ċ Z	Source	
7773			1.63		1.5E-02 AL163303.2	N	Hamo sapiens chromosome 21 segment HS21C103
7781	20476				11417739NT	TN	Homo sapiens valyf-tRNA synthetase 2 (VARS2), mRNA
8728	21421	34565	6.0		1.5E-02 BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Brn67 Homo sapiens oDNA clone IMAGE:4154504 5'
8368	21943		19'0	1.5E-02	1.5E-02 AF096774.1	IN	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9470			1.47	1.5E-02	D44606.1	FN	Saccharomyces cerevislae chromosome VI plasmid GapC
9711			86'0		R32667.1	EST HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone iMAGE:133531 5'
9711	1				1.5E-02 R32667.1	EST_HUMAN	yn54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
444.04	202.00	00020	07.0		, 0000	<u>}</u>	() - () - () - () - () - () - () - () -
1711	L	90010	0.40		1.0E-02 C+0008.1	1	i asmodali nacipali (i cu ali i co co) variante portire su lace protati (var-z, var-z) gartes, comprete cus s
11163		37109	2.14	1.5E-02	1.5E-02 AL111238.1	Z	Botryds cinerea strain 14 cDNA library under conditions of nitrogen deprivation
11856		37781	1.38	1.5E-02	AL161492.2	⊢N	Arabidopsis thaliana DNA chromosome 4, contig fregment No. 4
12277	25214		1.74		1.5E-02 AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
							w/06h03.x/ NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389493 3' s/milar to contains Alu
12787			1.45		1.5E-02 AI763127.1	EST_HUMAN	repetitive element contains element MER26 MSR1 repetitive element ;
408	13193		2.29	1.4E-02	1.4E-02 AE002230.2	LN	Chlamydophila pneumoniae AR39, section 58 of 94 of the complete genome
1096	13854	26513	4.42		LN 0865022	LN	Homo saplens NESH protein (LOC51225), mRNA
1234	13983		1.24		1.4E-02 U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1275	14025		3.77	1.4E-02	1.4E-02 U67779.1	N	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1376	14123		1.45		AF216854.1	FN	Homo sapiens headpin gene, complete cds
1507	14263		1.26		1.4E-02 AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
							Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-dafactrosidase (anii.)
3207	15970		7	1.4E-02	AF160969.2	۲	genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xylR) gene, partial cds
3383	<u>L</u>	28805	1.07		1.4E-02 AW074212.1	EST_HUMAN	xb09d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3478			6.33	1.4E-02	1.4E-02 AL161586.2	LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3478		28889	6.33	1.4E-02	1.4E-02 AL161586.2	N	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3648	16401	29041	8.63	1.4E-02	E996918 NT	Į.	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4455	17191	29817	7.77	1.4E-02	1.4E-02 AW962688.1	EST_HUMAN	EST374761 MAGE resequences, MAGG Homo sapiens cDNA
4456				1.4E-02	1.4E-02 AW962688.1	EST_HUMAN	EST374761 MAGE resequences, MAGG Homo sapiens cDNA
4821			7.21	1.4E-02	1.4E-02 BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Hamo saplens cDNA clone IMAGE:3842280 5'
4821	17552	30175	7.21	1.4E-02	1.4E-02 BE733142.1	EST HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
. 8324	10001	22070	7 7 2	4 AE	A A EGODO A	HOT LIMANI	nI11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive
1700	1	32010		1.45*74	1.45-02[44338030.1	٦	eren rea k,

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6321	19091	32080	5.47	1.4E-02	-02 AA559030.1	EST_HUMAN	nI11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
8038	20733		1.94	1.4E-02	-02 AL022073.1	F	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
8796		34634	0.75	1.4E-02	M81702.1	N-1	Candida boldinii methanol oxidase (AOD1) gene, complete cds
8083	21742	34900	0.84	1.4E-02	1.4E-02 AJ272265.1	F	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9300	21967	35141	2.27	1.4E-02	1.4E-02 BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10455	23101		0.76	1.4E-02	-02 AL163218.2	L	Homo sapiens chromosome 21 segment HS21C018
11985	24526	37267	2.2	1.4E-02	02 X60459.1	L	Human IFNAR gene for interferon alpha/beta receptor
12331	24747		1.37	1.4E-02	02 AF324985.1	Į.	Arabidopsis thaliana F21,09.2 mRNA, complete cds
12601	24913		2.36	1.4E-02	11426968 NT	Į.	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1948	14683	27395	2.21	1.3E-02	1.3E-02 AL163201.2	N	Homo sapiens chromosome 21 segment HS21C001
3208	15971	28623	2.23	1.3E-02	BF697081.1	EST HUMAN	602129475F1 NIH MGC_56 Hamo saplens cDNA clone IMAGE:4286203 5'
3208	15971	28624	2.23	1.3E-02	02 BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3951	16701		1.31	1.3E-02	-02 AF169288.1		Mus musculus beta-sarcoglycan gene, complete cds
7.07	742.	55000		1			Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV19S1P, TCRBV16S1, TCRBV14S1, TCRBV16S1, TCRBV14S1,
48/4	1/801	30223	0.93	1.3E-02	02 066061.1	L	ICRBV3S1, TCRBV4S1A11, TRY4, TRY6, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
5166	17975	30532	1.31	1.3E-02	02 AL049866.2	NT	Mus musculus chromosome X contgB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5166	17975	30533	1.31	1.3E-02	02 AL049866.2	LN	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
6072	18851	31816	1.05	1.3E-02	02 U80017.1	LN	Homo saplens basic transcription factor 2 p44 (btt2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naio) and sundival motor neuron protein (smn) genes, complete cds
6105	18883		0.88	1.3E-02	02 M62962.1	TN	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
6865	17942		1.33	1.3E-02	02 AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6865	17942	30536	1.33	1.3E-02		NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7477	20150	33244	4.9	1.3E-02	A1031593.1	EST HUMAN	ow08g05.x1 Soares_parathyrold_tumor_NbHPA Homo sapiens cDNA cione IMAGE:1646072.3' similar to contains Alu repetitive element;
8380	21073	34212	1.65	1.3E-02	-02 AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10107		35967	1.91	1.3E-02	02 M63707.1	LN	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10178			0.68	1.3E-02		NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10913	23593			1.3E-02	1.3E-02 AW268563.1	EST_HUMAN	xx34e03.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10913	23593	36839	3.97	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 31

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12337			1.44	1.3	E-02 299117.1	INT	Bacillus subtilis complete genome (section 14 of 21); from 2599451 to 2812870
12437	24807		2.41	1.3E-02	1N 6908896	FZ	Human herpesvirus 6B, complete genome
12607	25145		28.18		1.3E-02 AF152238.1	L	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
							z/65g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 6' similar to contains element
345	- 1	Ì	3.48		1.2E-02 AA059299.1	EST_HUMAN	L1 repetitive element ;
440	13226	25869	1.66		1.2E-02 P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PURS 3'REGION
				_			qd68e12x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.t1 L1
721	. 1				1.2E-02 Al183522.1	EST HUMAN	repetitive element;
2175			1.81			NT	Homo seplens chromosome 21 segment HS21C013
2178			17.1		1.2E-02 AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5
2444	15163	27901	1.39		1.2E-02 AW172350.1	EST HUMAN	x/37e09.x1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 31
2642	15163	27901	1.07	1.2E-02	E-02 AW172350.1	EST_HUMAN	x337e09.x1 Soares_NFL_T_GBC_S1 Home saplens cDNA clone INAGE:2659432 3'
3098	15863		99'9	1.2E-02	1.2E-02 AA075418.1	EST_HUMAN	zm88e03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5/
3281	16042	28691	2.1	1.2E-02	1.2E-02 R62805.1	Г	W11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
3284	16045	28694		1.2E-02	1.2E-02 A1668694.1	EST HUMAN	2b68a07.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:308532.3' similar to contains element: MER22 recettive element:
4675	1_		0.91	1.2E-02	1.2E-02 AI887378.1	T	wm38f04x1 NCI_CGAP_Ut4 Homo saplens cDNA clone IMAGE:2438335 3'
							Human heredijary haemochtomatosis recion histona 24ika notiejn gane haradijary haemochtomatosis
4859	17588	30211	2.03	1.2E-02		L'N	(HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4981	L		1.13	1.2E-02		LZ.	Cynops pyrthogaster CpUbiqT mRNA, partial cds
5025				1.2E-02	1.1	EST_HUMAN	AV731704 HTF Homo saplens cDNA clone HTFBHG11 5'
5666	18481	31375	1.73	1.2E-02	1.2E-02 D78589.1	NT	Rana rugosa mRNA for cairettculin, complete cds
			į			 -	Homo saplens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and
9709			0.72	1.25-02			replication factor C subunit 2 (KFC2) gene, complete cds
6907	- 1		6.46	1.2E-02	1.2E-02 AF175412.1	7	Mus musculus DNA methyttransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7192	ł		1.36	1.2E-02			yj34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7212		32972	10.54	1.2E-02			AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
7458	20130		0.57	1.2E-02	1.2E-02 BF216650.1	EST_HUMAN	601882949F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:4095253 5'
							CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA- GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAO68) (GAL-BETA-1,3-
7896	1		2.18			SWISSPROT	GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
8092	20786	33917					Homo sapiens fringe protein mRNA, partial ods
8092	ı		1.35		1.2E-02 AF193612.1	NT.	Homo sapiens fringe protein mRNA, partial cds

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							43,					PF_HUMAN				se (glnA),	G), YnaH						548328 5'			ir to contains							
Single Exol Flobes Explessed in Brain	Top Hit Descriptor	yd72c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1137743'	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds	Homo sapiens Spast gene for spastin protein	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGUI) (HPER)	C18119 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-557G06 5"	zm69e11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3	H.sapiens LIPA gene, exon 4	H.sapiens LIPA gene, exon 4	602018037F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153808 5	za40e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5'	tq95b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XPF_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA	DKFZp586E0924_s1 586 (synonym: hute1) Homo sepiens cDNA clone DKFZp586E0924	Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GInR (ginR), glutamine synthetase (ginA),	Yna4 (yna4), YnaB (ynaB), YnaC (ynaC), YnaD (ynaD), YnaE (ynaE), YnaF (ynaF), YnaG (ynaG), YnaH	(ynaH), Ynal (ynal), YnaJ (ynaJ), xylan beta-1,4-xylosi>	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA	C04803 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC4040	NEUROGENIC LOCUS NOTCH 3 PROTEIN	zn24a01.r1 Stratsgene neuroepithelium NT2RAMI 937234 Homo saniens cDNA clone IMACE: 5448398 5	EST186494 Colon carcinoma (HCC) cell line II Homo saplens cDNA 5' end	Homo septens T-box 5 (TBX5), mRNA	ab77f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains	RC3-ST0197-120200-015-g11 ST0197 Homo sepiens cDNA	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA	oc22h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone iMAGE:1350495 3'	RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA	601649967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
JIE EXUII FIO	Top Hit Database Source	EST HUMAN	LZ	NT	SWISSPROT	EST_HUMAN	EST_HUMAN	Z.	L	EST HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN			⊢N L	EST_HUMAN	EST_HUMAN	EST HUMAN	SWISSPROT	EST HUMAN	EST HUMAN	N	HOT INAM	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN
JIIO	Top Hit Acession No.	-02 T76987.1	1.2E-02 AB031013.1		-02 015534	E-02 C18119,1	1.1E-02 AA070364.1	1.1E-02 X75491.1	ŀ	3.1				_	1.1E-02 AL048383.2		-	٦		1.1E-02 AW996160.1	1.1E-02 C04803.1	Q61982	1.1E-02 AA082578.1		35505	1 1E-02 4 4668230 1	Ī			1.0E-02 AA806389.1		1	1.0E-02 A1065086.1
	Most Similar (Top) Hit BLAST E Value	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.2E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02		1.1E-02	1.1E-02	1.1E-02			1.1E-02	1.1E-02	1.1E-02	1.1E-02	1.1E-02 Q61982	1.1E-021	1.1E-02	1.1E-02	1 1E-02	1.1E-02/	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02	1.0E-02
	Expression Signal	1.03	2.48	1.35	2.88	8.02	1.49	1.35	1.35	4.92	4.05		1	0,86	1.5			-	2.51	0.91	0.67	6,45	2.03	3.55	3.23	4.18	1.62	9.16	1.56	1.57	2.7	1.49	0.79
	ORF SEQ ID NO:				31112		26662	27143	27144				28924		30132						34558	34639	35682		.			25448	26946		28494		29250
	Exon SEQ ID NO:	21480					13995	14444	14444	14766	15647		16269	-	17510			Į	1		21413	21492	22480	22642	23580	24484	16829	12833	14260	15291	15852	16019	16611
	Probe SEQ ID NO:	8788	9539	9570	12034	12615	1246	1701	1701	2031	2880		3513	4086	4778			6057	7497	8538	8721	880	8828	9884	10900	11923	12678	φ	1513	2577	3087	3257	3861

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3876	16626		0.7	1.0E-02	1.0E-02 AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4726	17458	30094	4.24	1.0E-02	LN 1236378	N _T	Mus musculus corticotropin releasing hormone receptor 2 (Crhr2), mRNA
4793	17524	30146	5.16	1.0E-02	1.0E-02 R96567.1	EST_HUMAN	yq54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 51
5331	1	30793	0.72	1.0E-02	1.0E-02 H52681.1	EST HUMAN	yu36h11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235941 5'
5661	18456	l			1.0E-02 AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6025					1.0E-02 AF257303.1	LN	Mus musculus synaptotagmin II (Syt2) gene, complete cds
8809	18866	31831	2.47		1.0E-02 AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
8809	1			1.0E-02	12 AW 577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6664		32616	1.92	1.0E-02	1.0E-02 Z29642.1	N	Z.mays U3snRNA pseudogene
9293		35133	4.19	1.0E-02	1.0E-02 BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE;3863177 5
9293	21960	35134	4.19	1.0E-02	1.0E-02 BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Hamo sapiens cDNA clane IMAGE:3863177 5'
							Crithidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for
11229	23892		1.97	1.0E-02	1.0E-02 AF157559.1	N	mitochondrial product
							tg55h07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X15183_cds1
							HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5
11263	23925		1.46	1.0E-02	1.0E-02 Al417961.1	EST_HUMAN	repetitive element;
11340		37334	1.97	1.0E-02	1.0E-02 AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12003	25416		1.83	1.0E-02	1.0E-02 Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12059		30811	3.76	1.0E-02	1.0E-02 AW935521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo saplens cDNA
12075	25243		5.93	1.0E-02	1.0E-02 S70330.1	FZ	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12592	25299		3.74	1.0E-02	1.0E-02 X62654.1	LN	H.sapiens gene for Me491/CD63 antigen
12803	25050	30957	1.84	1.0E-02	1.0E-02 AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
	0,007	0,000		L	, 00,001	1 200	wh42k09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
2	13042	ZL802	2.1	9.0E-03	9.0E-03 AI/96126.1	ESI HUMAN	WENZ MENZ repetuve element
1241	13890		2.07	9.0⊑-03	9.0E-03 BE781889.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo saplens cDNA clone IMAGE;3873346 5'
1483	14211	26899	1.1		9.0E-03 AE001270.1	NT	Treponema pallidum section 86 of 87 of the complete genome
2394	15115	27852	2.48		9.0E-03 AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2403	15124		0.92		AF09934.1	NT	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
3659	16412		1.21		9.0E-03 J05184.1	N	S.acidocaldarius thermopsin gene, complete cds
4927	17655	30267			9.0E-03 BE047949.1	EST_HUMAN	1244e10.y1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291466 5'
4964	17689	30297	0.95		9.0E-03 T70044.1	EST_HUMAN	yc17b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
4964	17689	30298			9.0E-03 T70044.1	EST_HUMAN	yc17b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
5720	18512		1.15	9.0E-03	Al809792.1		wf77f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens oDNA clone IMAGE:2361631 3'
6533	19299		4.88	9.0E-03	9.0E-03 BE745988.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo saplens cDNA clone IMAGE:3834752 5'

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			_				_			_			_								,	_	_				_		_	_	_	
ביישני באנו ביישני באנו המיישני באנו ביישני באני באנו ביישני באני באני באני באני באני באני באני בא	Top Hit Descriptor	qh87c12.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA done IMAGE:1853974 3'	Homo saplens hypothetical protein FLJ10650 (FLJ10650), mRNA	DKFZp434L0412_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434L0412 5'	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, atternatively soliced	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN)	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR	Homo saplens NF2 gene	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632181 5'	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3	Homo saplens preprogalanin (GAL1) gene, exons 1, 2, and 3	hw17b09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA	2h30e03.s1 Soares_pineal_gland_N3HPG Homo saplens cDNA clone IMAGE:413596.3' similar to contains	Hame replane adamisation has been somelate some	From Saprens adenyiosuccinate ryase gene, complete cas	Homo sapiens chromosome 21 segment HS21C083	Escherichla coli microcin 24 region, DNA binding protein (mdbA), immunity protein (miti), microcin 24 (mitS), and microcin transport protein (mtA, mtB) genes, complete cds	Homo saplens SCL gene locus	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION	CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA	AU140261 PLACE2 Homo saplens cDNA clone PLACE2000223 5'	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29,	KIFC1, Fas-binding protein, BING1, tapasin, RaiGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and	RPS18 genes, complete cds; Sacm21 gene, partial>	Pyrococcus hortkoshil OT3 genomic DNA, 287001-544000 nt. position (2/7)	PROBABLE PEPTIDASE Y4NA	Human BK virus (strain MM) genome. (Closely related to SV40.)	A.californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end	Tursiops truncatus mRNA for p40-phox, complete cds	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
מוס בעמון ומ	Top Hit Database Source	EST_HUMAN	FN	EST_HUMAN	FN	SWISSPROT	SWISSPROT	FZ	EST_HUMAN	FZ	FZ	EST HUMAN	EST HUMAN	ENT LIMANI	PANOL PIN	2	L	TN	F	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN			⊢ Z	LN	SWISSPROT	TN	NT	ΤN	SWISSPROT
5	Top Hit Acession No.	-03 AI242219.1	8922570 NT	-03 AL039991.1	-03 AF223391 1	-03 P26011	-03 P20908	-03 Y18000.1	-03 BE395380,1	-03 L11144.1	-03 L11144.1	-03 BE348385.1	-03 BF351141.1	A A 723007 4	02 A E408656 4	AF100000.1	-03 AL 163283.2	-03 U47048.1	-03 AJ131016.1	-03 P32644	-03 P32644	-03 BF363327.1	-03 AU140261.1			-03 AF110520.1	-03/AP000002.1	-03 P55577	-03 V01109.1	-03 M17197.1	-03 AB038267.1	P98160
	Most Similar (Top) Hit BLAST E Value	9.0E-03	9.0E-03	9.0E-03	9.0E-03	9.0E-03	9.0E-03	9.0E-03	9.0E-03	9.0E-03	9.0E-03	9.0E-03	9.0E-03	, TO B	0.00	0.00	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03		t	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03 P98160
	Expression Signal	0.57	8.0	1.05	0.65	0.47	1.44	2.07	1.57	1.55	1.55	2.37	23.46	4.08	26.95	30.32	2.2	0.93	1.08	1.21	1.21	4.88	1.09		į	2.82	1.45	4.89	0.95	1.79	2.03	0.63
	ORF SEQ ID NO:		33132			35601				37568							27617											32427		32860		34619
	Exen SEQ ID NO:	20043	20051	20470	20841	22396	22413	23587	23615	24248	24248	25411	24983	13274	13731	5	14884	15726	16113	16418	16418	17089	17802			18235	25085	19413	19481	19795	20119	21473
	Probe SEQ ID NO:	7362	7371	7774	8147	9745	9762	10907	10935	11651	11651	12411	12703	780	3 8	900	2154	2960	3353	3865	3665	4350	5083			5436	6106	6651	6820	7107	7442	8781

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	MR1-ST0111-111199-011-h08 ST0111 Homo saplens cDNA	Campylobacter Jejuni NCTC11168 complete genome; segment 2/8	Mus musculus fusion 2 (human) (Fus2), mRNA	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA	601475819F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'	S.cerevisiae chromosome X reading frame ORF YJR152w	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete ods	ze32e11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360716 5	602013941F1 NCI_CGAP_Bm64 Homo sepiens cDNA clone IMAGE:4149418 5	Oryctolagus cuniculus elF-2a kinase mRNA, complete cds	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1),	Controvered to the second HC-10 second companies and the second to the s	Mossocial in social UC 10 delle complete cuts	O'yprosporation parvim no-tro gene, complete dos	Organia may guarantal o - nanska aso co 1 21 minny, partan cos	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)	ab79b09.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:853145 3'	xx21b02x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'	EST362626 MAGE resequences, MAGA Homo sapiens cDNA	EST362626 MAGE resequences, MAGA Homo sapiens cDNA	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	qf34h02,x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'	UI-H-BI3-akb-c-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens oDNA clone IMAGE:2733691 3'	Rattus norvegicus neuronal nicotinic acetvicholine receptor subunit (Alphario) mRNA. commiete zds	UI-H-BI3-akb-c-10-0-UI.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE: 2733891 3	hh89a05,y1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2969936 5	Homo sapiens chromosome 21 segment HS21C078	yr82g01.r1 Soares fefal liver spleen 1NFLS Homo sapiens cDNA clone INAGE:211624 5' similar to ab:X14723 CLUSTERIN PRECURSOR (HUMAN):	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA	zd33f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 51
le Exon Probe	Top Hit Database Source	EST_HUMAN M	N L		EST_HUMAN Q	Г	Г		-	EST_HUMAN 60	Г	보					EST HUMAN A	SWISSPROT N	EST HUMAN ab	EST HUMAN XX		EST_HUMAN ES	SWISSPROT HI		EST_HUMAN U	_ K	EST HUMAN UP	EST_HUMAN hh	Г	FST HUMAN 9b	Т	EST_HUMAN zd
Suic	Top Hit Acession No.		8.0E-03 AL139075.2	TN 9566876		1.1				-03 BF342436.1	-03 M69035.1	A 20000 A	T	-03 A E007483 4	T	1	-03 AV731712.1	.03 Q61060	-03 AA668298.1 E			7.0E-03 AW950556.1			- .	03 AF196344.1	7.0E-03 AW44463.1		7.0E-03 AL163278.2 N	03 H71106.1 E	19.	
	Most Similar (Top) Hit BLAST E Value	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03	, ev =0 e	7.0E-03.7	7 05-03 /	7.05-03	7 20 70 7	7.0E-03/	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03 4	7.0E-03 F	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03	7.0E-03 A	7.0E-03
	Expression Signal	3.29	0.49	0.58	4.63	1.36	3,58	4.74	22.71	1.36	1.74	12.7	16.15	18 18	3 57	200	3.48	2.67	6.71	3.37	1.24	1.24	1.86	0.71	0.8	1.32	0.83	1.24	217	0.75	4.9	1.47
	ORF SEQ ID NO:	34846	34653	34713		36597		37632		37779			26098	28097	28387	20544	70211		26797	26924	27175	27176	27722	28951	29137	29179	29137					31972
	Exon SEQ (D NO:		21508	21569					24402	24437	24491	24523	13463	13453	13721	1000	13832	14091	14122	14238	14477	14477	15589	16301	16502	16544	16502	17295	17657	18521	25083	18996
	Probe SEQ ID NO:	8808	8816	8878	9848	10666	10906	11715	11814	11853	11933	11980	878	878	858	100	500	1343	1374	1491	1735	1735	2254	3546	3749	3792	4000	4560	4929	6728	6021	6222

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Top Hit Descriptor Top Hit Descriptor Bource Figur Lubrhese zinc finger protein, isolocin, faity acid binding protein, sepiapbarin reductass and vasolocin of genes, complete cds EST HUMAN EST HUMAN COLFED CORDEC-2004-07 BTOGG Home suplems cDNA clone IMAGE:3087754.3° EST HUMAN INT Source parathryoid, tumor, UbHPA Home suplems cDNA clone IMAGE:3087754.3° EST HUMAN INT SOURCE-2002-06-01.4 in 10.1 GGAP Sub8 Home suplems cDNA clone IMAGE:3087754.3° EST HUMAN INT Source parathryoid, tumor, UbHPA Home suplems cDNA clone IMAGE:3087754.3° EST HUMAN INT Source parathryoid, tumor, Colfe Sub8 Home suplems cDNA clone IMAGE:3087754.3° EST HUMAN EST H	Top Hit Database Source Source Source Source Source EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN INT SWISSPROT EST HUMAN INT SWISSPROT SWISSPROT EST HUMAN INT SWISSPROT EST HUMAN INT SWISSPROT EST HUMAN IN	Top Hit Aces: No. No. W37980.1 W37985.1 W37985.1 W37985.1 EE077356.1 EE250108.1 AN847284.2 AA29942.1 AA29962.1 AA2962.1 § C m	Signa	28794 28794 29079 29079 29079 29079 391802 32676 32676 32676 32676 32676 33318 33318 33578 336576 36928			
te91c12.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2094070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE. ;	EST_HUMAN	A142078	6.0E-		36680		10750
Homo saplens hypothetical zno finger protein FLJ14011 (FLJ14011), mKNA	L'N	11545814 NT	6.0E-03	2.54		23402	10713
EST374237 MAGE resequences, MAGG Homo sapiens cDNA	⊷ï	AW962	6,0E				10645
M, thermoformicicum complete plasmid pFV1 DNA		X68366.1	-90'9				10304
cds	LN	AF084555.1	6.0E	1.14			0194
Homo sapiens okadalc acid-Inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete							Γ
Bacillus subtilis fenD gene	LN	AJ011849.1	6.0E			<u> </u>	290
P40429 60S RIBOSOMAL PROTEIN L13A;	EST_HUMAN	AI432661.1	6.0E-	2.13			943
t22c02,x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN						ŀ	
Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein		D10548.1	6.0E			ı	454
601454915F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3858626 5	EST_HUMAN	BF038198.1	90.9	1.58		ı	945
RC0-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA	EST_HUMAN	AW799337.1	-90.6			ŀ	874
contains MER10.b1 MER10 repetitive element;	EST_HUMAN	A1033980.1	90.9				757
ow13a04.x1 Scares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to							Γ
RAS-RELATED PROTEIN RAP-2B	SWISSPROT	P17964	90.9			L_	702
Homo saplens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds	NT	AF128894.1	6.0E-			1	546
EST11949 Uterus tumor I Homo sapiens cDNA 5' end	EST_HUMAN	AA299442.1	6.0E-03				149
EST11949 Uterus tumor I Homo sepiens cDNA 5' end	EST_HUMAN	AA299442.1	6.0E-03			ı	149
601112353F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3353172 5'	EST_HUMAN	BE253748.1	6.0E-03			L	3755
SYNAPSIN III	SWISSPROT	014994	90.0E			L	3718
Variola virus, complete genome	۲N		90.9		L	L	3061
SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)	SWISSPROT	Q62209	_	2.58		1_	5073
EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat	EST_HUMAN	AA324242.1	L			L	1847
ov33c11.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1639124 3'	EST_HUMAN	A1016833.1	<u> </u>	1.84		ı	1331
600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5	EST HUMAN	BE250108.1		1.29		1	3938
RC0-CT0204-240999-021-b10 CT0204 Homo sapiens cDNA	EST_HUMAN	AW847284.1				ı	3902
Mus musculus glucosamine-6-phosphate deaminase (Gnpi), mRNA	⊥N	6754029	6.0E-03				3759
RC1-BT0606-260400-014-a07 BT0606 Homo sapiens cDNA	EST_HUMAN	BE077356.1	-∃0:9				3682
UI-H-BI4-apm-c-06-0-UI.s1 NCI_CGAP_Sub8 Homo saplens cDNA clone IMAGE:30877543'	EST_HUMAN	BF510986.1	-30'9			L	3652
zc13a11.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'	EST_HUMAN	W37985.1	6.0E-03	1.19			3534
genes, complete cds	NT	U90880.1	6.0E-			16136	3377
Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin							Γ
Top Hit Descriptor	Database Source	Ö	BLAST E Value	Signal			
	Top Hit	Ton Hit Aceseion		T. Arreseion			
	שום ביים						

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	Top Hit Descriptor	te91c12.x1 NCL_CGAP_Pr28 Homo saplens cDNA clone IMAGE:2094070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE.;	inc-finger protein mRNA, complete cds	H_MGC_57 Homo saplens cDNA clone IMAGE:3839747 5'	sulatus strain SB1003, partial genome	Methanobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 148) of the complete genome	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds	IH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'	slg gene for S-locus glycoprotein, cultivar T2	Chlamydla trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete ods; complete ORFA, and grpE-like protein, complete ods	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-	plete cds	Chlamydla trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds	ana mRNA for DEAD box RNA helicase,RH3	RNA for KIAA1180 protein, partial cds	IH_MGC_7 Homo saplens cDNA clone IMAGE:3538799 5'	es infant brain 1NiB Homo sapiens cDNA clone IMAGE:22395 3'	ana DNA chromosome 4, contig fragment No. 3	es breast 2NbHBst Homo sapiens cDNA clone IMAGE:155666 3'	artial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene	eruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds	eed storage protein citrin mRNA, complete cds	is tumor I Homo sapiens cDNA 5' end	sed storage protein citrin mRNA, complete cds	OL gene locus	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random	NEL PROTEIN PARA (PARALYTIC PROTEIN)
oligie Exoli Plobes Explessed III braili	Top Hit Descriptor	te91c12x1 NCL_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TF FATTY ACID AMIDE HYDROLASE.;	Mus musculus zinc-finger protein mRNA, complete cds	601572746F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:3839747 5'	Rhodobacter capsulatus strain SB1003, partial genome	nobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 148 te	nocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pog1) ge	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5	Brassica napus sig gene for S-locus glycoprotein, cultivar T2	Chlamydla trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete illee protein, complete cds	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ille protein, complete cds	ydia trachomatis partial ORFB; aminoacyi-tRNA synthase, complete cds; complete	like protein, complete cds	Chlamydla trachomatis partial ORFB; aminoacyt-tRNA synthase, complete cds; complete ilke protein, complete cds	Arabidopsis thaliana mRNA for DEAD box RNA helicase,RH3	Homo sapiens mRNA for KIAA1180 protein, partial cds	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'	yc81f09.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22395 3'	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3	y)86g02.s1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:155666 3'	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds	Citrus sinensis seed storage protein citrin mRNA, complete cds	EST12218 Uterus tumor I Homo sapiens cDNA 5' end	Citrus sinensis seed storage protein citrin mRNA, complete cds	Homo sapiens SOL gene locus	02.X1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_c	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
Seco		te91c	Musn	60157	Rhode	Methano	Pneur	60148	Brass	Chlam like pr	Chlam like pr	Chlam	ike pr	Chlan ike pr	Arabic	Homo				yj86g(Homo	Pseuc	Cifrus	EST1	Citrus	Homo		П
JIE EXOII PIE	Top Hit Database Source	EST_HUMAN	TN	EST_HUMAN	LΝ	ΤN	Ę	EST_HUMAN	N	LΝ	FZ		Ę	LZ	N	NT	EST_HUMAN	EST HUMAN	N	EST_HUMAN	TN	LV	FZ	EST_HUMAN	뒫	NT	EST_HUMAN	SWISSPROT
ilo O	Top Hit Acession No.	-03 AI420786.1	114556.1	6.0E-03 BE737895.1	6.0E-03 AF010496.1	6.0E-03 AE000833.1	J30790.1	6.0E-03 BE788019.1	6.0E-03 AJ245480.1	25105.1	25105.1		25105.1	25105.1	5.0E-03 AJ010457.1	4B033006.1	.1		2	371794.1	5.0E-03 AJ297357.1	5.0E-03 AF147449.2	J38914.1	5.0E-03 AA299675.1	J38914.1	5.0E-03 AJ131016.1	7.1	
	Most Similar (Top) Hit BLAST E Value	6.0E-03 A	6.0E-03 U14556.1	6.0E-03	6.0E-03	6.0E-03	6.0E-03 U30790.1	6.0E-03	6.0E-03	5.0E-03 L25105.1	5.0E-03 1.25105.1		5.0E-03 L25105.1	5.0E-03 L25105.1	5.0E-03	6.0E-03	5.0E-03	5.0E-03 T87623.1	5.0E-03	5.0E-03 R71794.1	5.0E-03 /	5.0E-03	5.0E-03 U38914.1	6.0E-03 (/	5.0E-03 U38914.1	5.0E-03/	5.0E-03	5.0E-03 P35500
	Expression Signal	1.26	4.6	2.81	3.25	6.69	3.17	1.64	1.68	2.7	2.7		3.73	3.73	1.15	2.5	0.88	3.82	2.83	1.3	1.12	4.03	0.85	1.17	0.82	0.73	1.17	5.5
	ORF SEQ ID NO:	36681		36833						26072	26073		26072	26073	26507	28135	28351	28543		28575		29082	29129		29129	29931	30039	31422
	SEQ ID NO:	23435	23583	23584	24563	25174	25235	24898	24910	13432	13432		13432	13432	13848	15397	15702	15898	15915	15927	16033	16440	16494	16704	16494	17304	17404	18501
	Probe SEQ ID NO:	10750	10903	10904	12042	12160	12239	12569	12588	654	654		655	655	1090	2688	2936	3133	3152	3164	3272	3687	3741	3954	4272	4569	4670	5707

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SEQ ID 6 100 100 100 100 100 100 100 100 100 1	Exan SEQ ID NO: 1625 I 1635 I 1645 I 1665 I I 1665 I I665	ORF SEQ ID NO: 28932 28908 28930 30774 30774 31423 31448 31448 31448 31463 31463 3163 3163 3163 3163 3163 31	Expression Signal 0.97 0.97 0.73 1.95 0.73 1.95 0.97 0.99 0.99 0.99 0.99 0.99 0.99 0.99		Top Hit Acess No. No. AW188426.1 G13606.1 AF060868.1 AF060868.1 AM103719.1 AM772898.1 AM773898.1 AM773898.1 AM763278.2 AM7681483.1 AM763278.2 AM163278.2 AM1653278.2 AM1653278.2 AM165328.2	Top Hit Database Source Source Source Source Source Source Source Source Source Source Source Source Surissprot NT SWISSPROT SWISSPROT SWISSPROT SWISSPROT NT NT NT SWISSPROT SWISSPROT SWISSPROT SWISSPROT NT NT NT SWISSPROT NT NT NT SWISSPROT NT NT SWISSPROT NT NT SWISSPROT NT NT NT SWISSPROT NT NT NT SWISSPROT NT NT SWISSPROT NT NT NT NT NT SWISSPROT NT	Top Hit
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Single Exon Probes Expressed in Brain	Exon ORF SEQ Expression (Top) Hit Acession Signal BLASTE No. Source Source	23744 37017 4.09 4.0E-03 AL.163206.2 NT Homo sepiens chromosome 21 segment HS21C006	37700 1.82	1.78 4.0E-03 BE815173.1 EST_HUMAN	4.0E-03 BE298290.1 EST_HUMAN	24694 2.27 4.0E-03 AW 504273.1 EST_HUMAN UI-HF-BN0-alp-g-04-0-UI:11 NIH_MGC_50 Home sapiens cDNA clone IMAGE:3080622 5'	7474c09.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE: 3' similar to contains Alu repetitive lement; 3.41 4.0E-03 BF224125.1 EST HUMAN element; ontains element MER31 repetitive element;	4.0E-03 AW614596.1 EST HUMAN	4.0E-03 11436955 NT	3.0E-03 AF011920.1 NT	13628 26299 5.37 3.0E-03 AF011920.1 NT Homo saplens protein kinase CK2 catalytic subunit alpha gene, exon 1	ACTION TO THE TOTAL CONTRACTOR OF THE CONTRACTOR	1	1.00 PT-00-000.1	6.44 3.0E-03/Z32521.1 NT	27753 1.09 3.0E-03 U46858.1 NT	27754 1.09 3.0E-03 U46858.1 NT	28488 3.31 3.0E-03 BE379296.1 EST_HUMAN	28557 2.52 3.0E-03/AW802687.1 EST_HUMAN	28819 1.72 3.0E-03 U34606.1 NT	5.97 3.0E-03 Y12500.1 NT	29348 6.97 3.0E-03 AV762392.1 EST_HUMAN	29349 6.97 3.0E-03 AV782392.1 EST_HUMAN	29390 1.35 3.0E-03/AI792278.1 [EST_HUMAN	1	29737 5.63 3.0E-03 AJ011432.1 NT	0.73 3.0E-03 BE348739.1	17217 29844 4.97 3.0E-03 A1536141.1 EST_HUMAN xu8.P10.H3 conorm Homo saplens cDNA 3'		30136 2.38 3.0E-03 A 732754.1 EST_HUMAN	30155 7,94 3.0E-03 BE787945.1 EST_HUMAN	30508 3.96 3.0E-03 8922499 NT	18267 31159 1.98 3.0E-03 AJ249981.1 INT Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
		L		385	349	394	144	88					1	702														L					
	Probe Exo SEQ ID SEQ NO:		11777 243	Ш		12246 246	12480 248	<u> </u>	12801 250	362 131	859 136	1857 444	┸	\perp	2292 150			- 1	_ [_1								4482 172	1	1		- 1	5468 182
l	₫ ₩ ²								L			<u> </u>	\perp			_				_											\perp		_

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Top Hit Descriptor	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2- Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds	aa13f10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813163.5'	Kluyveromyces marxianus popi3 gene for purine-cytosine permease	Oryza sativa gene for bZIP protein, complete cds	RC0-BT0812-250900-032-e07 BT0812 Homo sepiens cDNA	RC0-BT0812-250900-032-e07 BT0812 Hamo saplens cDNA	zb27b04.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3/	S.cerevisiae UGA35 gene, complete cds	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN AZ HOMOLOG 1 (HNRNP AZ/A))	Homo sapiens chromosome 21 segment HS21C068	NONSTRUCTURAL PROTEIN V	hh80f10x1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2969131 3' similar to contains L1.f1 L1	repenuve element;	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85	ov03d12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_ma1 HISTONE H2B.2 (HUMAN);	602035980F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183938 5'	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289	PM3-HT0344-071299-003-d07 HT0344 Homo sapiens cDNA	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H)	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;	ENDONUCLEASEJ	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN AZ HOMOLOG 1 (HNRNP AZ(A))	Homo sapiens chromosome 21 segment HS21C103	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA	Oryza sativa gene for bZIP protein, complete cds	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds	Homo sapiens golgin-like protein (GLP) gene, complete cds	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
Top Hit Database Source	Mu	EST HUMAN aar	NT	NT	EST_HUMAN RC	EST_HUMAN RC	EST_HUMAN Zb2	Г	SWISSPROT HE	NT	SWISSPROT NO		EST HUMAN rep		EST_HUMAN HIS	Т	П	T		SWISSPROT CIR		П	ISSPROT			NT		NT		NT Hor	RE SWISSPROT EN
Top Hit Acession No.	3.0E-03 U35323.1	3.0E-03 AA456701.1	Γ		3.0E-03 BF333058.1	:-03 BF333058.1	3.0E-03 N92580.1		Г	8.2				3.0E-U3 AL161589.2	E-03 A1016731.1	5.1	3.0E-03 D90901.1	7:						3.0E-03 AL163303.2	5803028 NT				3.0E-03 AF094481.1	П	
Most Similar (Top) Hit BLAST E Value	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	100	3.00-00	3.05-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03 P03355	3.0E-03	L	3.0E-03 P11369	3.0E-03 P51989	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3,0E-03	3.0E-03 P11369
Expression Signal	66.0	11.75	1.38	3.64	0.82	0.82	1.54	0.51	1.32	1.47	1.29		1.00	*.O.	6.44	0.73	0.83	0.83	0.54	3.88	,	2 8	1.23	3.97	1.9	2.65	1.69	2.52	2.72	2.72	1.58
ORF SEQ ID NO:	31244					33662			34194	34213			24770	0//8	34808	34817		33538			74000	35551	35/40	35906		33187	37346	36422	37372	37373	37452
Exon SEQ ID NO:						20534		20908	21053	21074	21177	24.604	21834	1001	21657	21667	21976			22259	9770	77	240	22688	23437	20099	24043	23191	24065	24065	24143
Probe SEQ ID NO:	5539	6458	7104	7422	7839	7839	8058	8214	8360	8381	8485	0000	2000	2460	8967	8977	8309	9347	9536	9096	2020	CAJA	200	10040	10752	11137	11353	11424	11462	11462	11543

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Table 4
xon Prohee Events

	Top Hit Descriptor	UI-H-BI2-ehi-d-06-0-UI.s1 NCI CGAP Sub4 Homo saniens cDNA clone IMAGE-2726842-21	omo saplens cDNA 5'	ot7b10.s1 Seares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1:t3 MER26 repetitive element :	Homo sapiens gene for CMP-N-scetylneuramInic acid hydroxylase nartial cds.	r connexin36 (cx36 gene)	ELCH PROTEIN)	ELCH PROTEIN)	yd15h03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE-108341 F	bitor gene, exons 6 and 7	nu88f01.s1 NCI CGAP Aiv1 Homo saplens cDNA clone IMAGE 1217593	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete ods	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SF4-1) (CD181 ANTIGEN)	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dloxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA	HAIN PRECURSOR	242a10.r1 Sogres total fetus Nb2HF8 9w Homo sapiens cDNA close IMAGE 780114 F	CM2-HT0183-061099-018-d03 HT0183 Homo saplens cDNA	Mus musculus myelin expression factor-3-like protein gene, partial cds	21 segment HS21C102	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12	UI-H-BI1-adi-g-10-0-UI.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2717010 31	zx42a10.r1 Soares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:789114.5	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14		ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]	Raftus norvegious 5-hydroxytryptamine7 receptor gene, partial cds	UI-H-BW0-air-g-03-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413.3	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
Single Exon Probes Expressed in Brain		JI-H-BI2-ahi-d-06-0-UI.s1 NCI	promrna-5.E07.r bytumor Homo saplens cDNA 5'	ot77b10.s1 Soares_total_fetus_Nb2HF8_contains L1.t3 MER26 repetitive element	Homo sapiens gene for CMP-N-e	Rattus norvegicus mRNA for connexin36 (cx36 gene	RING CANAL PROTEIN (KELCH PROTEIN)	RING CANAL PROTEIN (KELCH PROTEIN)	/d15h03.r1 Soares fetal liver sple	Human alpha-2-plasmin Inhibitor gene, exons 6 and 7	1188f01.s1 NCI CGAP AIV1 Ho	Homo sapiens tumor-related prote	PLATELET-ENDOTHELIAL TET SFA-1) (CD161 ANTIGEN)	Homo sapiens procollagen-lysine, type VI) (PLOD) mRNA	Homo sapiens procoliagen-lysine, type Vi) (PLOD) mRNA	COLLAGEN ALPHA 5/(V) CHAIN PRECURSOR	x42a10.r1 Sogres total fetus N	3M2-HT0183-061099-018-403 H	Aus musculus myelin expression	Homo sapiens chromosome 21 segment HS21C102	Homo sapiens concentrative nur	Homo sapiens concentrative nur	JI-H-Bi1-adi-g-10-0-UI.s1 NCI C	x42a10.r1 Soares total fetus NI	02183960T1 NIH_MGC_42 Hon	I.sapiens DMA, DMB, HLA-Z1, II	genes	INV POLYPROTEIN CONTAIN	attus norvegicus 5-hydroxytrypta	1-H-BW0-air-g-03-0-UI.s1 NCI_(IA0507 Human fetal liver cDNA li
gle Exon Prob	Top Hit Database Source	EST HUMAN	Γ	EST HUMAN	Т	LΝ	SWISSPROT	SWISSPROT	EST HUMAN	Г	EST HUMAN	Г	SWISSPROT			/ISSPROT	EST HUMAN	EST HUMAN	Г		- LN	LN		Г			╗	SWISSPROT	NT TN		EST_HUMAN
Sin	Top Hit Acession No.	AW294812.1	3.0E-03 AI525056.1	-03 AA993154.1	Γ	3.0E-03 AJ296282.1			T70874.1					4557836 NT	4557836 NT		Γ	Γ	2.0E-03 AF302691.1				1		2.0E-03 BF568955.1					.1	-03 A1064746.1
	Most Similar (Top) Hit BLAST E Value	3.0E-03	3.0E-03	3.0E-03	3.0E-03	3.0E-03 /	2.0E-03	2.0E-03 Q04652	2.0E-03 T70874.1	2.0E-03	2.0E-03	2.0E-03 /	2.0E-03 F	2.0E-03	2.0E-03	2.0E-03 P29400	2.0E-03 /	2.0E-03	2.0E-03 /	2.0E-03/	2.0E-03 /	2.0E-03 /	2.0E-03 /	2.0E-03 /	2.0E-03		2.0E-03 >	2.0E-03 P03374	2.0E-03 L	2.0E-03	2.0E-03
-	Expression Signal	1.48	2.86	1.88	2.26	2.71	1.83	1.83	12.31	2.07	1.4	16.16	1.73	1.84	28.	6.31	1.13	1.01	1.57	1.16	4.01	4.01	4.57	4.3	1.13	-	6.62	1.96	11.03	1.12	0.97
	ORF SEQ ID NO:			37256		31066	25919	25920		26766	26768	26777	26906	26938	26939		27207		27445	27713	28007	28008		28818	28823	0,000	29048	29461			29765
	Exan SEQ ID NO:	24374	25196		1	24661	13286	13286	15552	- 1	14093	14102	14220	14252	14252	14332	14506	14610	14724	14975	15272	15272	15298	16169	16174	40440	10410	16835	16936	17130	17134
	Probe SEQ ID NO:	11784	11927	11962	12016	12190	502	502	768	1342	1345	1354	1473	1506	1506	1586	1764	1872	1988	2247	7228	2558	7284	3411	3417	000	200	4093	4195	4393	4397

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					<u>:</u>	SI - 1201 018	Chigge Exoli Plodes Explessed III Drain
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8116			6.07	2.0E-03	-03 N20287.1	EST HUMAN	yx42g06.s1 Scares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442.3' similar to contains L1.b2 L1 repetitive element :
8162	, ,		0.54	2.0E-03	-03 Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C6G9.05 IN CHROMOSOME I
8184			1.19	2.0E-03	-03 P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8239	, ,		0.81	2.0E-03	6005855 NT	L	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8239	20933	_]	0.81	2.0E-03	F005855 NT	N	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8264	- 1	34097	0.86	2.0E-03	-03 AU136679.1	EST_HUMAN	AU136579 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8318			0.91	2.0E-03		FN	Homo seplens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8570	21262		0.54	2.0E-03		LN.	Oroclolagus cuniculus mRNA for eukarvotic bolypeptide chain release factor 3 partial cde
9094			0.74	2.0E-03	2.0E-03 AW 796111.1	EST HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sepiens cDNA
9034	18419	31332	0.74	2.0E-03	Γ	EST HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9139		34992	0.64	2.0E-03	1.7	, LN	Homo saplens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9456	22104		0.89	2.0E-03		EST HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clane IMAGE 104206 2
9426		35277	0.89	2.0E-03		EST_HUMAN	yp98a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194296.3
			•				TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI)
9458	22008	35178	3,46	2.0E-03	03 P24821	SWISSPROT	(GP 150-) (GP 150-) (GP 150-) (GP 150-) (GP 150-) (GP 150-)
9566		35404	1.38	2.0E-03		SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9298	1	35405	1.38	2.0E-03		SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9623	- 1	35464	0.53	2.0E-03		L'N	Homo sapiens caspase recruitment domain-containing protein (BCL 10) gene, complete cds
9623	- 1	35465	0.53	2.0E-03		L'N	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9815	- 1	35668	0.81	2.0E-03	03 AW884269.1	EST_HUMAN	QV3-OT0064-060400-144-e01 OT0064 Homo sapiens cDNA
9942	- 1		5.75	2.0E-03		EST_HUMAN	zs10a05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:6847543
10506	23152	36377	0.45	2.0E-03		EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo sapiens cDNA
10506	23152	36378	0.45	2.0E-03	03 AW361176.1	EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo saplens cDNA
10938	23618		2.97	2.0E-03	1	LZ	Human dystrophin gene
11470	20188	33281	2.56	2.0E-03	03 P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11531	24131		2.14	2.0E-03	03 BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11538	24138	37446	9.1	2.0E-03	03 Z11740.1	NT	H.sapiens variable number tandem repeat (VNTR) locus DNA
11909	24473		3.23	2.0E-03	03 AI625745.1	EST HUMAN	ty65h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE Q26532 VACUOLAR ATP SYNTHASE SUBUNIT G:
11926	24487	37807	2.41	2.0E-03 /		NT	Homo sapiens SEL1L (SEL1L) gene, partial cds

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	Top Hit Descriptor	clone IMAGE:700345 5		coding nuclear protein EBNA2, complete cds	acoding nuclear protein EBNA2 complete cds	ine IMAGE:3943954 5'	ONG-CHAIN COLLAGEN) (LC COLLAGEN)	yyd7h06.r1 Soares melanocyte ZNbHM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains		γy07n06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER8 repetitive element;		lone IMAGE:3875693 3'	isis 1 (TIAM1), mRNA	plens cDNA clone IMAGE:115772 5	ns cDNA	ntromeric end		Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+(Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR),			one IMAGE:3893276 5'	ne, 5' flanking region		zk97c09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to		, exons 2 through 11, and complete cds	soform 3 (PMCA3) gene, 5' flanking region	omo sapiens cDNA clone IMAGE:427810 3'	omo sapiens cDNA clone IMAGE:427810 3'		ΔNOca
Single Exoli Flobes Expressed in brain	Į Į	zs44f01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5	Homo sapiens KVLQT1 gene	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds	601589841F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3943954 5	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)	yy07h06.r1 Soares melanocyte 2NbHM Homo sa	Gement MEKS repetitive element;	yy07h06.r1 Soares melanocyte 2NbHM Homo sa element MER8 repetitive element ;	Mouse nucleolin gene	601657519R1 NIH MGC 68 Homo sapiens cDNA clone IMAGE:3875693 3	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA	yd93a11.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5	QV3:NN1024-260400-171-g05 NN1024 Homo saplens cDNA	Homo sapiens DiGeorge syndrome critical region, centromeric end	Human gene for fourth somatostatin receptor subtype	Homo sapiens X28 region near ALD locus contail protein L18a (RPL18a), Ca2+/Calmodulin-dependent	CDM protein (CDM), adrenoleukodystrophy protein >	Human TRPM-2 protein gene, exons 1,2 and 3	601491081F1 NIH_MGC_69 Hamo sapiens cDNA clone IMAGE:3893276 5'	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region	Homo sapiens partial steerin-1 gene	zk97c09.s1 Soares_pregnant_uterus_NbHPU Hk	contains L1.t1 L1 repetitive element;	Homo sapiens exostoses-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region	zh82e06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone iMAGE:427810.3	zh82e06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3	V.carteri gene encoding volvoxopsin	CM3-LT0079-170200-092-607 T0079 Homo saniens CDNA
gie Exull Flut	Top Hit Database Source	EST_HUMAN	F	Z	Ę	EST_HUMAN	SWISSPROT		EST HOMAN	EST_HUMAN	E	EST HUMAN	Z	EST_HUMAN	EST_HUMAN	Z	LN		NT	LN	EST_HUMAN	LN	LN	*	EST_HUMAN	NT	TN	EST_HUMAN	EST_HUMAN		
	Top Hit Acession No.	03 AA290951.1	03 AJ006345.1	-03 K03332.1	03 K03332.1	03 BE796491.1	03 Q02388	7 7 6 7 7 7	03 N41974.1	03 N41974.1	03 X07699.1	03 BE963839.2	11526176 NT	03 T87761.1	03 AW 902585.1	03 L77570.1	03 D16826.1				03 BE880044.1	03 AF274581.1	03 AJ251973.1			<u>.</u> .			3.1		03 AW840353.1
	Most Similar (Top) Hit BLAST E Value	1.0E-03	1.0E-03 /	1.0E-03	1.0E-03	1.0E-03	1.0E-03		1.05-03	1.0E-03 l	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03		1.0E-03	1.0E-03	1.0E-03	1.0E-03	1.0E-03 /		1.0E-03 /	1.0E-03 /	1.0E-03 L	1.0E-03 /	1.0E-03 /	1.0E-03	1.0E-03 /
	Expression Signal	1.87	3.12	1.85	1.85	0.83	2.07	0	0.0	0.67	2.75	1.07	8.76	1.14	1.7	1.37	2.54		1.8	3.37	0.98	0.83	5.18		-	1.94	0.68	0.61	0.61	1.36	0.62
	ORF SEQ ID NO:		30778	30856	30857	31182	31187	40.00	16216	31252		31711		31990			32805		33308	33382	33429	33608	33673	i	33870	33968	34158	34326	34327		34705
	Exon SEQ ID NO:	18032	18121		18170	18284	18290	10272	3	18343	18714	18750	18877	19016	19086	19418	19743		50209	20274	20320	20484	20545		20737	20836	21022	21184	21184	21534	21560
	Probe SEQ ID NO:	5225	5317	5369	5369	5485	5491	55.76	2	5546	5930	5968	6609	6242	6315	6657	7052		7539	7608	7656	7789	7850	-	8043	8142	8329	8492	8492	8842	8869

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	_						
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8978	21668		0.58	1.00	-03 U52111.2	LN	Homo sepiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9017	L	34868	3.68	1.0E	-03 M30471.1	L	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9017	Ш		3.68		1.0E-03 M30471.1	L	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9507			1.66		1.0E-03 AF011400.1	LN	Thermotoga nespolitana alpha-1,6-galactosidase (agIA) gene, complete cds
9507	22160	35341	1.66		1.0E-03 AF011400.1	Ł	Thermotoga neapolitana alpha-1,6-galactosidase (ag/A) gene, complete cds
9720	22371		0.81	1.0E-03 Q01129	001129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10063	22711	35929	0.65		29.1	Ę	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10068	22718		0.75		1.0E-03 AF097485.1	LN LN	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10214	22862	36075	1.72		1.0E-03 AI024350.1	EST_HUMAN	ov75f08.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1643175.3' similar to contains MER39.b1 MER39 MER39 repetitive element;
2696	35,50		97.0		7 00000	14474	ag93f12.s1 Stratagene hNT neuron (#937233) Homo saplens cDNA clone IMAGE:1142063 3' similar to
1000	1		0.40		1.0E-03 PAY/08/202.1	Т	Contains Aiu repentive element,
10583	23259	36496	179		1.0E-03 AW362393.1	EST HUMAN	RC1-C10279-181099-011-809 C10279 Homo sapiens cDNA RC1-C10279-181099-011-809 C10279 Homo sapiens cDNA
10651	1		2.78	1.0E-03	1.0E-03 BE170859.1	EST HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo saplens cDNA
10725	23413		3.29	1.0E-03	1.0E-03 A1683847.1	EST HUMAN	tt73e12.xt NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2248446.3' similar to TR:Q2e195 Q2e195 PV41 GENE. ;
10808	23491	36727	1.36	1.0E-03	1.0E-03 AW 237482.1	EST_HUMAN	xm72d12,x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE,2689751 3'
11106	23776		3.05		1.0E-03 AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11905		37805	4.48		1.0E-03 BE894488.1	П	801433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12124	24616		1.38	1.05-03	1.0E-03 AV731520.1	EST_HUMAN	AV731520 HTF Homo saplens cDNA clone HTFAJG05 5'
12371	25342		1.98		1.0E-03 Al347355.1	EST HUMAN	to05h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element,
12478		30612	7.05		1.0E-03 BE780572.1	EST HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
12821			1.37	1.0E-03 /	341.1	EST_HUMAN	RC0-CT0205-240999-021-d02 CT0205 Homo saplens cDNA
5130		30465	0.7	9.0E-04 P08548		SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5596	18391		1.26	9.0E-04 P06727		SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6165			9.0	9.0E-04		INT	Homo sapiens KVLQT1 gene
6395		32165	96.0	9.0E-04		ISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
9543	- 1		1.42				Glycyrthiza glabra GgbAS1 mRNA for beta-amyrin synthase, complete cds
1471	14218		1.02	8.0E-04	٦	Ę	X.laevis mRNA for C4SR protein

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Probe SEQ ID NO:	SEQ IO NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
				Value			
4159	16899		4.37			SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4713	17445	30078	2.39			ΤN	Homo sapiens prion protein (PrP) gene, complete cds
11092			2.93				zf24c10.s1 Soares_fetal_heart_NbHH19W Homo saplens cDNA clone IMAGE:377874 31
11266	L		1.96	8.0E-04	8.0E-04 AI571099.1	EST_HUMAN	m85a08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2176310 3'
2398	15119			7.0E-04			Homo saplens prion protein (PrP) gene, complete cds
2719		28184	1.19	7.0E-04		IN	Homo sapiens chromosome 21 segment HS21C010
3274	16035		1	7.0E-04	4885170 NT	L	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
						Γ	ng65g12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1
9005		31748		_	.0E-04 AA516212.1		repetitive element;
6420			2.47	_		EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2367209.3'
7128	L. I		0.78	_	.0E-04 AK024445.1		Homo sapiens mRNA for FLJ00035 protein, partial cds
9703		35549		١.		SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
9703	22354			7	.0E-04 P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
							Homo saplens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
11557	_		2.28	7.0E-04		N⊤	(L44L) and FTP3 (FTP3) genes, complete cds
11586		37500	4.04	7.0E-04			HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12642			2.31	7.0E-04	.0E-04 R17338.1	EST HUMAN	yg13c06.r1 Soares Infant brain 1NIB Homo saplens cDNA clone IMAGE:32298 5'
12669			5.98	7.0E-04	6005855 NT	TN	Homo saplens Retina-derived POU-domain factor-1 (RPF-1), mRNA
3941			1.83	6.0E-04		EST_HUMAN	w/15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3
4068		29440		8.0Ε-04	6.0E-04 K01315.1	TN	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4068	16812			8.0E-04		NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4162			3.79	6.0E-04		NT	Homo sapiens OCR8 chemokine receptor (CMKBR8) gene, complete cds
7478				6.0E-04 Q15034		SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7765	20461		3.33	8.0E-04		SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
7044	20809		080	8 0E-04		NAMI ILI TOR	y694c11.s1 Soares_pineal_gland_N3HPG Homo saplens cDNA clone IMAGE:231956 3' similar to contains
0000	1		3.5	8 05 04	T	EST ULIMAN	DKETHERRANDOL 4 688 (summing brited) Home combase of A class OKETHERRANDOL
2000	22828 8C8CC	35837	200	A OF 04	A OF OA BEDDSASD 1	EST HIMAN	RC2-RN0120-250400-012-614 RN0120 Home samens con A
	ł				T		Lifechinus variedatus embryonic biastocoelar extracellular matrix protein precursor (FCM3) mBNA complete
10238	22886		0.71	6.0E-04			spo
11487		37378		6.05-04	6.0E-04 AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11558	. ,			6.0E-04			UI-H-BI0-aab-e-09-0-UI.st NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11636	24233		2.17	6.0E-04 Q01768			NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
12082	1 (2.81	6.0E-04	6.0E-04 AW380519.1	EST_HUMAN	RC1-HT0269-261199-012-d08 HT0269 Homo saplens cDNA

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Top Hit Descriptor	w/76g11.x1 NOL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element;	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)	QV0-CT0225-021099-030-a07 CT0225 Homo saplens cDNA	nk27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	zo33b08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588863 5'	Gorilla gorilla involucrin gene medium allele, complete cds	qd13f06.x1 Soares_placenta_8bb9weeks_ZNbHP8to9W Homo saplens cDNA clone IMAGE:1723819 3 similar to gb:X51802_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN);contains Alu repetitive element;	ob98e02.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339229 3' similar to contains element MER22 repetitive element:	aj56h03.s1 Soares_tests_NHT Homo saplens cDNA clone IMAGE:1394357 3'	KK2745F Human feta heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 6' similar to REPETITIVE ELEMENT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR	xs08e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'	Human familial Alzheimer's disease (STM2) gene, complete cds	DKFZp386M2024_11 586 (synonym: hute1) Homo saplens cDNA clone DKFZp586M2024	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	nf15h02.s1 NCI_CGAP_Pr1 Homo eaplens cDNA clone IMAGE:913875	Haemophilus influenzae Rd section 63 of 163 of the complete genome	as70b08.x1 Barstead colon HPLRB7 Homo saplens cIDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;	RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C078
Top Hit Database Source	EST_HUMAN	Γ	EST_HUMAN	$\overline{}$		Ŀ	T HUMAN	Г	EST HUMAN	EST HUMAN	Т		SWISSPROT	EST_HUMAN	F.	EST_HUMAN	L L	EST_HUMAN	E	EST_HUMAN	EST HUMAN	Г	П
Top Hit Acession No.	AI817088.1	010341	5.0E-04 AW851844.1	5.0E-04 AA548931.1	5.0E-04 Q9UKP4	5.0E-04 AF248054.1	AA156080.1	5.0E-04 M23804.1	-04 Al188382.1	5.0E-04 AA814519.1	5.0E-04 AA846545.1	5.0E-04 N83765.1	P29128	5.0E-04 AW270938.1	5.0E-04 U50871.1	AL048507.2	5.0E-04 AF248054.1	AA568513.1	4.0E-04 U32748.1	4.0E-04 AI720263.1	4.0E-04 AI720263.1	4.0E-04 AW 753356.1	4.0E-04 AL163278.2
Most Similar (Top) Hit BLAST E Value	6.0E-04	5.0E-04	5.0E-04	5.0E-04	5.0E-04	5.0E-04	5.0E-04	5.0E-04	5.0E-04	5.0E-04	5.0E-04	5.0E-04	5.0E-04 P29128	5.0E-04	5.0E-04	5.0E-04	5.0E-04	5.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04	4.0E-04
Expression Signal	1.34	6.81	4.1	1.35	2.32	2.99	7.89	3.75	5.2	0.98	1.39	0.68	1.44	4.1	0.48	2.38	14.08	5.04	1.48	1.78	1.79	3.18	1.81
ORF SEQ ID NO:		26051		28815	29096	30877	32303	33037	33677	34033	35013	35195	35268	35344			30877		26076	26267	26268	26880	27538
Exon SEQ ID NO:	25058	13415	14237	16166	ł	18186	19298	۱ ۱	20551	20896	1		22096			23577	18186	25184	13435	13597	13597	14196	14807
Probe SEQ ID NO:	12816	938	1490	3408	3704	5386	6532	7276	7856	8202	9177	9271	9418	6056	10177	10897	11713	12020	858	827	827	1449	2075

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_ ω			Most Similar		1	
ŀ	SEQ ID ORF SEQ ID NO:	C Expression Signal	(Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
	14860	1	4.0E-04	AL046704.1	EST_HUMAN	DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
2633 1	15345 28088	88 2.21		4.0E-04 O96615	SWISSPROT	SERICIN-2 (SILK GUM PROTEIN 2)
	15925 285				LZ	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4289	17028 29653	53 3.18	4.0E-(04 AA576331.1	EST_HUMAN	nh10a10.s1 NC_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4289 1	17028 296	3.18		4.0E-04 AA576331.1	EST HUMAN	nh10a10.s1 NOI_CGAP_CO1 Homo sapiens oDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
l	17236 29868			4.0E-04 AA086324.1	EST HUMAN	zn61c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
	17748 3036		4.0E-(14 BE560660.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3878910 5'
7168	19855 32925	1.3	4.0E-0	14 P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7434 2	20111		4.0E-(24 AL161566.2	LZ	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
\	20284 33394		4.0E-(34 AU122079.1	Г	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
	21127 34264	1.07		4.0E-04 BF240712.1	EST_HUMAN	601875985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5'
8442 2	21134 34270		4.0E-(Г	yx39e12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE.264142 5'
		3.24	4.0E-(EST_HUMAN	ov87h03.s1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1644341 3'
	22391	1.22	4.0E-(LN	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
			4.0E-(04 AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
152 1	12967 25608		3.0E-(26.1		DKFZp761J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
					SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
	13629 26300		3.0E-(LN	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
			3.0E-(04 AI262100.1	EST_HUMAN	qz28d03.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1846 1			3.0E-(4.1	EST_HUMAN	th23a02x1 NCLCGAP_Pr28 Homo saplens cDNA clone IMAGE:2119082 3'
_			3.0E-		SWISSPROT	INTERNALIN B PRECURSOR
			3.0E-(34 AA203342.1	EST_HUMAN	zx56a04.r1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:446478 5'
	16696 29335		3.0E-(SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4034	16779	1.33			NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
	16816	1.12			EST_HUMAN	RC0-HT0014-310599-028 HT0014 Homo sapiens cDNA
	17498	4.72	3.0E-(EST_HUMAN	PM0-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
4827 1	17558 30180		3.0E-(EST HUMAN	QV3-DT0045-221299-048-d09 DT0045 Homo saplens cDNA
			3.0E-(EST_HUMAN	nq08g09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1143328 3'
					FZ	Homo sapiens chromosome 21 segment HS21C081
6722 1			3.0E-(78.2		Homo sapiens chromosome 21 segment HS21C078
- 1	20163 33256	56 0.84	3.0E-(14 P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R.PTP-DELTA)

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Oligie LAUI TIODES EXPLESSED III DIGIII	Most Similar Top Hit Acession Database BLAST E No. Source Source	3.0E-04 P22807 SWISSPROT FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)	3.0E-04 AA454055.1 EST HUMAN VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);	04 A1992139.1 EST HUMAN	3.0E-04 AA781201.1 EST_HUMAN RIBOSOMAL PROTEIN L7A (HUMAN);	04 P13816 SWISSPROT	04 4501960	nc38e04.r1 NC!_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.t2 L1 3.0E-04 AA228301.1 EST HUMAN repetitive element;	04 AB018292.1 NT	EST HUMAN	114	04 AF217/96.1 NI	O4 AO 140/07.1	LN.	2.0E-04 M86524.1 NT Human dystrophin gene	04 AI286021.1	2.0E-04 AL163203.2 NT Homo sepiens chromosome 21 segment HS21C003	2.0E-04 AF224268.1 NT Mus musculus 5' flanking region of Pitx3 gene	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV2BS1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1P, TCRBV34S1, TCRBV34S1, TCRBV34S1, TCRBV3S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY8, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,	-04 A1124529.1 EST HUMAN	2.0E-04 5174736 NT Homo sapiens tubulin, beta, 4 (TUBB4) mRNA	2.0E-04 BE082317.1 EST_HUMAN QV2-BT0638-070500-194-b07 BT0636 Homo sapiens cDNA	2.0E-04 AW978441.1 EST_HUMAN EST390550 MAGE resequences, MAGP Homo sapiens cDNA	Г	EST_HUMAN	04 H96265.1 EST_HUMAN	.04 U09226.1 NT	2.0E-04/AB037997.1 NT Danlo rerlo hagoromo gene, exons 1 to 6, partial cds
	<u>≅</u> ≒ ₪	3.0E-04 P22	3.0E-04 AA4	3.0E-04 A199	3.0E-04 AA7	3.0E-04 P13	3.0E-04	3.0E-04 AA2	3.0E-04 AB0	3.0E-04 AL1:	1000	2.0E-04 AFZ	Z.UE-04 AU	2.0E-04 M86	2.0E-04 M86	2.0E-04 A128	2.0E-04 AL1	2.0E-04 AF2		2.0E-04 AI12	2.0E-04	2.0E-04 BE0	2.0E-04 AW	2.0E-04 U01	2.0E-04 H96;	2.0E-04 H96;	2.0E-04 U09	2.0E-04 ABO
	Expression (3.23	1.34	0.65	3.73	0.54	1.38	4.81	3.08	2.75	200	2.05	0 1	10.71	10.71	3.93	2.18	1.12	4.47	1.11	1.1	1.99	0.79	4.93	1.74	1.74	1.63	1.1
	ORF SEQ ID NO:	33983	35673	35943	36220	36367	37466	30617	30818		10000	20024	70007	26324	26325	-			28033	28398	28740	28834	29282	-	2990	29991		30324
	SEQ ID NO:	20851	22471	22726	23003		24154	25386	25230	25000	7900	12384	1070	13856	13656	13911	13917	14563	15295	15752	16088	16186	16642	16864	17355	17355	17474	17721
	Probe SEQ ID NO:	8157	9820	10078	10356	10495	11555	11976	12338	12730	7.17	1/1	3 1	88	887	1158	1183	1824	2581	2986	3328	3429	3892	4122	4620	4620	4742	4998

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Top Hit Descriptor	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds	Kaposi's sarcome-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosyformyglycinamidine synthase, and LAMP (LAMP) genes, complete cds	Kaposi's sarcome-associated herpesvirus ORF 68 gene, partial cds, and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosyfformylglychiamidine synthase, and LAMP II AMP) genes, complete cds.	Equus caballus DNA, chromosome 24q14, microsatellite TKY38	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)	itott11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' sImilar to contains Alu repetitive element;	Mouse alpha 1 type-IV collagen mRNA	AV647727 GLC Hamo saplens cDNA clone GLCBBD04 3'	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	753F Heart Homo sapiens cDNA clone 753	753F Heart Homo sapiens cDNA clone 753	nc02e12.s1 NCL_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:252	nj25a04.s1 NCI_CGAP_AA1 Homo sepiens cDNA clone IMAGE:993486 3' similar to gb:M97252 KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN);contains Alu repetitive element;	qv57d10.x1 NCI_CGAP_Ov32 Homo saplens cDNA clone IMAGE:1985683 3'	qv57d10,x1 NCI_CGAP_Ov32 Homo saplens cDNA clone IMAGE:1985683 3'	ab94g08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854654 3'	w/26e08x/1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)	yd72c08r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:113774 6'	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	Mouse alpha leukocyte Interferon gene, complete cds	UI-H-BIT-aew-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo saptens cDNA clone IMAGE:2720646 3'	UI-H-BI1-aew-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'	Homo sapiens mRNA for KIAA1142 protein, partial cds
Top Hit Database Source	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	Į,	Ę		SWISSPROT	EST_HUMAN	Ę	EST_HUMAN /			SWISSPROT		HUMAN	Г		П	Г	EST_HUMAN	EST_HUMAN	SWISSPROT	THOMAN			ISSPROT	IN		T_HUMAN	
Top Hit Acession No.	1.0E-04 U62918.1	1.0E-04 AF148805.1	10E-04 0E148805 1		062203	2.1	1.0E-04 M14042.1	1.0E-04 AV647727.1	7662015 NT	7862015 NT		1.0E-04 T19615.1			1.0E-04 AA564561.1	4 AI251980.1	1.0E-04 AI251980.1	1.0E-04 AA630453.1		08880	1	10863876 NT				AW 205336.1	1.0E-04 AW205336.1	AB032968.1
Most Similar (Top) Hit BLAST E Value	1.0E-04	1.0E-04	40 H	1.0E-04	1.0E-04 Q62203	1.0E-04	1.0E-04	1.0E-04	1.0E-04	1.0E-04	1.0E-04 P08547	1.0E-04	1.0E-04	1.0E-04	1.0E-04	1.0E-04	1.0E-04	1.0E-04	1.0E-04	1.0E-04 088989	1.0E-04	1.0E-04	1.0E-04 P08547	1.0E-04 P08548	1.0E-04			1.0E-04
Expression Signal	3.12	3.25	3.25	2.09	1.06	0.91	2.11	1.15	1.28	1.28	1.49	0.57	0.57	0.95	0.92	15.6	17.82	0.95	2.27	1.46	0.49	1.86	2.74	1	2.13	2.05	2.05	1.76
ORF SEQ ID NO:		27058	27050	27308	28689	.	29412	29437	30368	30369	31487	31556	31557	32105	32605	İ	32841	33719	35088	35097		35381		35975				37566
Exon SEO ID NO:	14057	14370	14370			<u> </u>	16782	16807	17755	匚	18560	18623	18623	19116		19776	19776	20589	21915	21926	!!	22199		22763	23971			24246
Probe SEQ ID NO:	1309	1623	1803	1854	3278	3719	4037	4062	5036	5036	69/9	5834	5834	6346	6738	7086	7470	7894	9236	9247	9325	9546	10079	10115	11312	11567	11567	11649

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Г		Γ-	_	т-	_	т-	_	τ-	τ	7-	_	_	_	т	_	1	_		_	_		-	Τ-	1	_	_	_			_	_	_	_
	Top Hit Descriptor	Dictyostelium discoideum gene for TRFA, complete cds	Homo sapiens chromosome 21 segment HS21C001	Caenorhabditis elegans Skp1p homolog mRNA, complete cds	Rat cytomegalovirus Maastricht, complete genome	nh93g01,s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966096 3'	EST04984 Fetal brain, Stratagene (cat#636206) Homo saplens cDNA clone HFBED60	Homo saplens sarcoglycan, epsilon (SGCE), mRNA	Homo saplens chromosome X open reading frame 6 (CXORF6) mRNA	Homo saplens chromosome X open reading frame 6 (CXORF6) mRNA	wb54h06x1 NCI_GGAP_GC6 Homo saplens cDNA clone IMAGE:2309631 3' similar to gb:J03260 DNA TOPOISOMERASE I (HUMAN);	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10	H.saplens flow-sorted chromosome 6 HindIII fragment, SC8pA28B10	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)	w50g11.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:2462125	oj80a03.s1 Scares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1504588 3'	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA	zl08c08.s1 Soares, pregnant_uterus_NbHPU Homo sepiens cDNA cione IMAGE.491726 3' similar to contains element MER28 repetitive element;	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR	C4B-BINDING PROTEIN PRECURSOR (C4BP)	C4B-BINDING PROTEIN PRECURSOR (C4BP)	ye28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'	ht37a03.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'	yi59d08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu	repetitive element,contains LTR7 repetitive element;	zk58f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487036 5	MRO-NT0038-250400-001-f09 NT0038 Homo sapiens cDNA	7g28a08.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3307766 3'	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA
	Top Hit Database Source	ΙN	LZ LZ	L	LZ	EST_HUMAN	EST_HUMAN	FZ	LZ	LZ	EST_HUMAN	ĽN	LN	LN LN	SWISSPROT	SWISSPROT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN		EST_HUMAN				EST HUMAN
	Top Hit Acession No.	-05 AB009080.1	-05 AL163201.2	J60980.1	9845300 NT	-05 AA505582.1		10835046 NT	4885170 NT	4885170 NT	-05 AI655241.1	-05 Z84506.1	-05 Z84506.1	-05 AF053630.1	-05 Q12860	-05 Q12860	-05 N72829.1	-05 AA897680.1	-05 BE064410.1	-05 BE064410.1		E-05 AW896629.1	-05 Q60401	-05 P08607			-05 AW627985.1						
	Most Similar (Top) Hit BLAST E Value	7.0E-05	7.0E-05	7.0E-05 U60980.1	7.0E-05	7.0E-05 /	7.0E-05 T07095.1	7.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05	6.0E-05		6.0E-05 F	6.0E-05/	6.0E-05	6.0E-05	5.0E-05
	Expression Signal	5.72	1.71	0.95	0.71	1.09	2.97	3.09	1.69	1.69	1.19	1.1	1.1	3.07	3.61	3.61	1.4	0.95	0.76	0.76	0.62	2.22	0.63	1.21	1.21	0.85	0.59		3.06	3.36	14.34	1.4	10.46
	ORF SEQ ID NO:					33954	35175		27484		28046	28137	28138	26080	31541	31542	32066			33804	34172	34177	34316	35050	35051	35271	35462		36579	37415	30822		26802
	Exon SEQ ID NO:	15919	17078	17149	17598	20818	22003	23782	14755	14755	15309	15399	15399	13440	18611	18811	19081	19496	20678	20678	21035	21040	21171	21882	21882	22099	22274		23340	24103	25239	25053	14129
	Probe SEQ ID NO:	3156	4339	4412	4871	8124	9453	11112	2020	2020	2595	2690	2690	2817	5822	5822	6309	6834	7983	7983	8342	8347	8479	9151	9151	9421	9621		10849	11502	12387	12810	1382

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		7	7	$\overline{}$	$\overline{}$	$\overline{}$	-	$\overline{}$	7	_	_	$\overline{}$	_	_	_	_	_	-1-	_	_	_	_		_	_	_		-	 -		_	
סייקט באסור ויספס האף מספט וו בי מון היים היים היים היים היים היים היים היי	Top Hit Descriptor	Homo saplens 22kDa paroxisomal membrane protein-like (LOC55895) mRNA	PROTEIN MOV-10	Homo saptens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT) exp. 1	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)	Human MLC1emb gene for embryonic myosin alkaline light chain. 3'LITR	AV653544 GLC Homo saplens cDNA clone GLCDMA06 3'	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spilload	Mus musculus gene for calretinin, exon 1	RETINAL-BINDING PROTEIN (RALBP)	RETINAL-BINDING PROTEIN (RALBP)	Human renin (REN) gene. 5 flanking region	RETINAL-BINDING PROTEIN (RALBP)	RETINAL-BINDING PROTEIN (RALBP)	Cryptosporidium parvum isolate Zaire 15 kDa diveoprotein do 15 gene, partial eds	Drosophila melanogaster senseless protein (sens) gene, complete cds	Macaca mulatta haptodlobin (HP) gene. 5 region	Homo sapiens PP1200 mRNA, complete cds	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;	BETA-GALACTOSIDASE PRECURSOR // ACTASEV/ACID RETA. GALACTOSIDASEV	hi36c07.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2974380 3' similar to contains	element MIR repetitive element;	xd93e09.x1 Soares_NFL_T_GBC_S1 Homo saptens cDNA clone IMAGE:2605192 3	zv01e11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746252 3'	qh64c10.x1 Soares_feta_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:1849458 3' similar to	XXZ4003.X1 Soares NEL T GBC S1 Home seniers cDN4 close MAGE:084.446.01	601461463F1 NIH MGC 66 Homo sepiens cDNA clane (MA GE-98644.2 F)	601461463F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3865142 5	qi91g11.x1 Sogres_NhHMPu_S1 Home sapiens cDNA clone IMAGE:1879748 3' similar to TR:008632 008632 GI YCINE TYROSINE-RICH HAIR PROTIEIN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA	PM1-HT0621-120200-001-e10 HT0621 Homo sapiens cDNA
01 1000	Top Hit Database Source	ΡN	SWISSPROT	LN LN	SWISSPROT	SWISSPROT	LN	EST_HUMAN	LN	LN	SWISSPROT	SWISSPROT	LN	SWISSPROT	SWISSPROT	N	LN LN	LZ LZ	N.	TOGGOOIMS	SWISSPROT		EST_HUMAN	EST_HUMAN	EST HUMAN	FST HIMAN	EST HUMAN	EST HUMAN	EST_HUMAN			EST_HUMAN
	Top Hit Acession No.	8923891 NT	1	-05 AJ251884.1	226422	226422		-05 AV653544.1			249193					4.0E-05 AF164488.1								4.0E-05 AW117580.1	٦		3.0E-05 AW273851.1		1	3.0E-05 AI288919.1		-05 BE169211.1
	Most Similar (Top) Hit BLAST E Value	5.0E-05	5.0E-05 P23249	5.0E-05	5.0E-05 Q26422	5.0E-05 Q26422	5.0E-05	5.0E-05	5.0E-05	5.0E-05	5.0E-05	5.0E-05	4.0E-05 U12821.1	4.0E-05 P49193	4.0E-05 P49193	4.0E-05 /	4.0E-05	4.0E-05	4.0E-05 AF202635.1	4 05-05	4.0E-05 P23780		4.0E-05	4.0E-05/	4.0E-05/	3.0E-05/	3.0E-05/	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05
	Expression Signal	1.2	1.1	2.41	0.72	0.72	13.38	3.75	0.99	0.87	3.64	4.72	3.84	0.73	0.73	1.16	0.75	0.74	7.57	0.47	0.59		4.18	3.48	1.7	9.	0.86	1.01	1.01	0.73	7.98	7.98
	ORF SEQ ID NO:		28001		30408	30409			31822					29809	29810		30289	32528		35745	36168	000	30288	+		26082	26457	26523	26524		29719	29720
	Exen SEQ ID NO:	14593		16710	17793	17793	18237	18688	18855	19916	24810	24810	13032	17185	17185	17551	17681	19503	22101	22550	22953	02000	23338 24630	87047	75041	13441	13797	13866	13866	16048	17088	17088
	Probe SEQ ID NO:	1855	2551	3961	5074	5074	5438	5903	9209	7231	12175	12440	2810	4449	4449	4820	4955	6841	9423	9901	10306	70000	9000	04121	12/89	965	1037	1109	1109	3287	4349	4349

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		_	_				_	_	_					_		_						_	_				_				_	_
Top Hit Descriptor	EST79996 Placenta I Homo sapiens cDNA similar to similar to p53-associated profein	EST79996 Placenta I Homo saplens cDNA similar to similar to no 53-associated protein	Homo sapiens chromosome 21 segment HS21C102	CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)	dh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:1849458 3' similar to contains Air repatitive element contains a lament transfer a lament transfer and the contains a lament transfer and	AU125721 NT2RM4 Homo septions CDNA clone NT2RM4002075 5'	Mus musculus myosin light chain 2. precursor lymphocytespecific (AAAc2ni) mRNA	Homo sapiens SYBL1 gene, exons 6-8	Homo sapiens SYBL1 gene, exons 6-8	801567451F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3842292 5	zs60b05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE-701841 3'	hl94e08.x1 NCI CGAP Lu24 Homo saplens cDNA clone IMAGE:3009638 3	Homo sapiens Interleukin-1 receptor aniagonist homolog 1 (IL1HY1), mRNA	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE 8 ANTIGEN)	Human Alu-family cluster 5' of albha(1) acid alveoprotein gene	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end	wg36f09.x1 Soares NSF F8 9W OT PA P S1 Homo saniens cDNA clone MAAGE-2387200 3	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)	Homo sepiens DiGeorge syndrome critical region, centromeric end	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains	MER3.b2 MER3 repetitive element ;	Human adenosine deaminase (ADA) gene, complete cds	2446a12.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to	Contains Alu repetitive element; contains element L1 repetitive element;	NCC-5 105 15-120200-014-106 B 10519 HOMB septens CDNA	Homo sapiens p47-phax (NCF1) gene, complete cds	H.saplens DNA for endogenous retroviral like element	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV	DKFZp566l084_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566l064 5	601236455F1 NIH_MGC_44 Homo sapiens oDNA clone IMAGE:3608653 5'	Homo sapiens TNNT1 gene, exons 1-11 (and loined CDS)
Top Hit Database Source	EST HUMAN	EST HUMAN	Ľ.	SWISSPROT	EST HUMAN	EST HUMAN	LN	LN	L	EST_HUMAN	EST HUMAN	EST HUMAN	TN	SWISSPROT	LN	EST HUMAN	T	Г	SWISSPROT	LZ		EST_HUMAN	NT		ES HOMAN	Т			NT	EST_HUMAN	T_HUMAN	Г
Top Hit Acession No.	-05 AA368679.1	-05 AA368679.1	-05 AL169302.2	-05 P97468	AI248061.1	-05 AU126721.1	11072102 NT	-05 AJ225782.1	-05 AJ225782.1	05 BE733157.1	-05 AA284049.1	-05 AW770982.1	6912431 NT	05 P43361		05 AA372562.1	05 AI769331.1	05 Q62918	05 Q62918	05 L77570.1		-	05 M13792.1	2000	T	Ī			05 X95465.1	05 AL039107.1		05 AJ011712.1
Most Similar (Top) Hit BLAST E Value	3.0E-06	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-06	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05	3.0E-05		2.0E-05/	2.0E-06	2000	205-03/	20.70.0	Z.UE-U3 /	2.0E-05)	2.0E-05)	2.0E-05/	2.0E-05	2.0E-05
Expression Signal	0.94	0.94	66.0	1	0.82	0.97	1.66	1.17	1.17	2.33	1.47	1.58	1.23	0.51	0.56	1.22	292	0.98	0.98	1.77		1.09	2.43	1	2 2	2 2	0.93	1.22	0.71	0.78	1.09	1.92
ORF SEQ ID NO:	29798			30065	26082	30144	31181	32433	32434	33616	34082	34630	34633	34638		35068			38304		· ·	2//84	28037		28544	70757	±0.707	28779				31382
SEO ID NO:	17170		17285	17420	13441	17522	18269		19419	20494	20944			21491		21899	22216		_	24585		1	16301	15425	15899	П	ŀ	- 1	ı	16539	17377	18467
Probe SEQ ID NO:	4434	4434	4550	4686	4785	4791	5470	6659	6869	7799	8250	8791	8795	8799	9029	9220	9563	10433	10433	12072	- 600	5252	žę,	2718	3134	3343	2 0	3362	3485	3787	4643	5672

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Top Hit Descriptor	Homo saplens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	RENAL SODIUMDICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)	qc72a02.x1 Soares, placenta_8to8weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1716114.3 similar to contains L1.t3 L1 repetitive element;	nw06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'	P.falciparum mRNA for AARP1 protein, partial	qz47b06.x1 NCI_CGAP_Kid11 Hamo sapiens cDNA clone IMAGE:2030003 3' similar to TR:002711 002711 PRO-POL-DUTPASE POLYPROTEIN ;	wu35h07.x1 Soares_Dleckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE;2622077 3'	Heterodonius francisci Hox410 (Hox410), Hox49 (Hox49), Hox47 (Hox47), Hox46 (Hox46), Hox46 (Hox46), Hox46 (Hox44), Hox43 (Hox44), Hox43 (Hox44), Hox44 (Hox4	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA8 (HoxA6), HoxA5 (HoxA4), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds	Homo sapiens Indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds	tg20h05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE,2109369 3'	TCBAP2E1590 Pecliatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590	TCBAP2E1599 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)	Homo sapiens chromosome 21 segment HS21C007	7175g09.y1 NCI_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'	Homo sapiens otase gene, exon 1-alpha	Homo sapiens dase gene, exon 1-alpha	yw91a08.r1 Scares_placenta_8tx6weeks_2NbHP8tx3W_Homo espiens cDNA clone IMAGE:259570 5
Top Hit Database Source	Ä	SWISSPROT	SWISSPROT	EST HUMAN	EST HUMAN	LY	EST_HUMAN	EST_HUMAN	TN	TN	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	SWISSPROT	SWISSPROT	Į.	EST_HUMAN	LN	TN	EST_HUMAN
Top Hit Acession No.	2.0E-05 AF029308.1	013183	2.0E-06 Q13183	2.0E-05 AI149272.1	AA714330.1	2.0E-05 Y08926.1	AI492960.1	2.0E-05 AI991025.1	2.0E-05 AF224262.1	AF224262.1	AF128847.1	2.0E-05 AI381040.1	-05 BE244840.1	BE244840.1	2.0E-05 P49457	P49457	AL163207.2	2.0E-05 BF055939.1	2.0E-05 AJ131024.1	AJ131024.1	2.0E-05 N41751.1
Most Similar (Top) Hit BLAST E Value	2.0E-05	2.0E-05 Q13183	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-06	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05
Expression Signal	69.0	0.76	0.76	0.61	2.26	3.27	1.12	9.37	1.93	1.93	0.83	1.71	.0.63	0,53	0.58	0.58	0.49	0.87	0.54	0.54	1.98
ORF SEQ ID NO:		31606	31607	31808	32297	32483	32497		32806	32807		33605	34862	34863	L		L	35900	36333	36334	36362
Exon SEQ ID NO:	18616	18666	`	18844	19293	19462	19475	19485	19744	}	1	20480	21710	21710	1_	1	١_		23103	23103	23135
Probe SEQ ID NO:	5827	5880	5880	6065	6527	6801	6814	6824	7053	7053	7267	7785	9020	9020	9167	9167	9823	10035	10457	10457	10489

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								_	_	_				_	_		_	_		_	_	_		_			
Single Excit modes Expressed in Brain	Top Hit Descriptor	W91a06.1 Soares, placenta, 8tc8weeks, 2NbHP8tc9W Homo sapiens cDNA clone IMAGE:259570 51	wu35h07 x1 Soares_Dleckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'	ti30h09.x1 NCI_CGAP_Gas4 Homo saplens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.	130h09.x1 NCI_CGAP_Cas4 Home sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.	RC5+HT0582-280300-012-E12 HT0582 Homo saplens cDNA	Iww21a03.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:3183532 3' s/milar to TR:Q12832 Q12832 GLYCOPHORIN HEP2 :	Homo saplens ABCA1 (ABCA1) gene, complete cds	Human gene for L-histidine decarboxylase, complete cds	PUTATIVE SERINETHREONINE-PROTEIN KINASE P78	Homo saplens chromosome 21 segment HS21C082	Drosophila melanogaster strain Lamto 120 Suppressor of Hairless (Su(H)) gene, partial cds	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	MOSAIC PROTEIN LGN	Homo saplens chromosome 21 segment H\$210003	zw69g04.r1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:781494 5	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'	Homo sapiens Spast gene for spastin protein	Ins19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1		From Sapiens prospholipase AZ, group X (PLAZG10) mKNA, and translated products	Home capiers chromosome 24 commit LE24(202	236H12.31 Soares, total fetus, Nb2HF9.94 How sophers cDNA clone IMAGE:788519 3' similar to the control of the c	zso5e11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu	repetitive element;contains element TAR1 repetitive element;	AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5'	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2912043 3' similar to contains OFR.tl OFR repetitive element ;
gle Exori Fic	Top Hit Database Source	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	NT	LN	SWISSPROT	٦	NT	FZ	SWISSPROT	LN.	EST_HUMAN	EST_HUMAN	TN	MALLILL TOO	NAMOL 181	NI	TOUR SERVICE	NOT IN		EST_HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	2.0E-05 N41751.1	2.0E-05 A1991025.1	2.0E-05 A1493285.1	A1493285.1	2.0E-05 BE175801.1	2.0E-05 BE348229.1	2.0E-05 AF275948.1	2.0E-05 D16583.1	-05 P27448	-05 AL163282.2	-05 AF088273.1	-05 AF223391.1	-05 P81274	-05 AL163203.2	-05 AA431119.1	-	-05 AJ246003.1	A A & 44 9 4 8 4	101	4000844	27.0			-05 AA236110.1	-05 AV732190.1	-05 AW510902.1
	Most Similar (Top) Hit BLAST E Value	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	2.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	1.0E-05	4 DE 08	1.01-03	1.00.00	1 OF-05	4 0 1 0 5		1.0E-05	1.0E-05	1.0E-05
	Expression Signal	1.98	2.42	1.33	1.33	2.27	4.86	2.27	1.44	3.22	1.6	1.91	1.02	9.2	1.2	2,52	1.81	1.22	896	00.7	1 48	2 24	3.02		12.45	0.62	0.74
	ORF SEQ ID NO:	36363		37243								29034		29337	29523			32428	32530			<u> </u>	34799		35022	35189	35593
	Exon SEQ ID NO:	23135	19485	23948	23948	23197	25168	25155	25247	14991	15603	16394	16545	16699	16894	16985	17530	19415	10805	10875	20344	21505	21849		21857	22020	22389
	Probe SEQ ID NO:	10489	10541	11287	11287	11430	12185	12342	12674	2265	2700	3641	3793	3949	4152	4244	4799	9653	RORO	Caoa	7877	8813	8958		9187	9566	9738

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-		_	_	_		
Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9738 22389	35594	0.74	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Seares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR:t1 OFR repetitive element :
9816 22467	35669	1.16	1.0E-05	AW 291521.1	EST_HUMAN	UI-H-BI2-agk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
9816 22467	35670	1.16	1.0E-05	AW291521.1	EST_HUMAN	UI-H-BI2-agk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:27243983'
22732		1.87	1.0E-05	AW466995.1	EST_HUMAN	ha07c10.x1 NCI_CGAP_Kld12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.t2 L1 repetitive element;
10836 23518	36760	1.97	1.0E-05	U91328.1	۲N	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
23518	36761	1.97	1.0E-05	U91328.1	LΝ	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
24438	37780	1.38	1.0E-05	AF111167.2	LΝ	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
2678 15387	28129	4.8	9.0E	AI583811.1	EST_HUMAN	tt73a06.x1 NCI_CGAP_HSC3 Homo saplens cDNA clone IMAGE:2246386 3'
3092 15857	28498	3.53	9.0E-06	A1218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1759191 3'
		2.82	9.0E-06	M61755.1	IN	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
1	31532	2.61	90E-06		TN	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
		0.8	9.0E-06		EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
20021	33099	0.85	9.0E-06		SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
20337		13.94	9.0E		EST_HUMAN	ox20g01.xt Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens oDNA clone IMAGE::1656912.3' similar to contains Alu repetitive element;
21056		1.1	9.0E-06		NT	Homo sapiens chromosome 21 segment HS21C009
21572	34715	2.69	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
24572			90508	063769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
21810			9.05-06		NT	Human apolipoprotein E (APOE) gene, hepatic control region HOR-2
23538	36784	3.46	9.0E-08	010364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
15597	27986	1.27	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
23076	36298	0.75	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
23076	36299	0.75	8.0E-08	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYL'INOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
(1008) 9816 (1008)	NO: NO: 22389 22467 22467 22458 15867 1 15867 1 15867 21672	SEQ. ID ORI NO: 10 DRI NO: 22389 22467 22467 22458 15857 15857 16609 20021 20021 20021 20037 20337 21572 21572 21572 21572 21572 23638 15597 23676 23676	SEQ ID ORF SEQ Expression of the color of th	SEQID ORF SEQ Expression (Compared to the compared to the comp	SEQ ID ORF SEQ Expression (Top) Hit Top Hit Acession Value (Top) Hit Top Hit Acession Value 22389 35594 0.74 1.0E-05 AW510902.1 22467 35699 1.16 1.0E-05 AW291621.1 2247 35690 1.16 1.0E-05 AW291621.1 22732 1.87 1.0E-05 AW466995.1 23518 36761 1.97 1.0E-05 AW466995.1 15387 28498 3.53 9.0E-06 AW33811.1 15387 28498 3.53 9.0E-06 AIS83811.1 16360 31532 2.61 9.0E-06 AIS83811.1 16509 31532 2.61 9.0E-06 AIS8381.1 20021 33099 0.85 9.0E-06 AIS8381.1 21650 34197 1.1 9.0E-06 AIS3209.2 21651 34197 1.1 9.0E-06 AIS3209.2 21810 34876 </td <td> CART SEQ Expression (Top) Hit Top Hit Accession Detaprial Plants No. Signal BLASTE No. Source Value Value Source Source Value 1.0E-05 AW510902.1 EST_HUMAN 22467 35696 1.16 1.0E-05 AW221521.1 EST_HUMAN EST_H</td>	CART SEQ Expression (Top) Hit Top Hit Accession Detaprial Plants No. Signal BLASTE No. Source Value Value Source Source Value 1.0E-05 AW510902.1 EST_HUMAN 22467 35696 1.16 1.0E-05 AW221521.1 EST_HUMAN EST_H

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
958	13723		2.69	7.0E-	06 AA669729.1	19.1 EST_HUMAN	ab90f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.t1 MER20 repetitive element;
1419	14167	26851	3.42	7.0E-06		N	Hamo sapiens KIAA0555 gene product (KIAA0555), mRNA
	l						qw16g09.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive
2876	15643		5.93	7.0E-	06 AI368252.1	EST_HUMAN	element;
3551			0.92	-30'L		EST_HUMAN	EST99205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
6099	18405		5.68	-30'L	11.1	EST_HUMAN	QV2-OT0062-250400-173-h01 OT0062 Homo saplens cDNA
5715	18508	31429	1.01	7.0E-	06 N98645.1	EST_HUMAN	ly65c07.r1 Soares_multiple_sclercsis_2NbHMSP Homo sapiens cDNA clone IMAGE:278412 5'
8688	21380	34524	0.7	7.0E-06	T1420709 NT	Ł	Homo saplens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
9800	22451		0.45	7.0E-	06 Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
11930	25356	30808	2:32	7.0E-	06 BF215972.1	EST_HUMAN	801881522F1 NIH_MGC_57 Home saplens cDNA clone IMAGE:4093972 5'
2918	15684		1.28		6.0E-06 BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3680	16433	29078	1.08	€.0E	6.0E-06 BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4705	15708	28359	16.1	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4710	17442	30074	166	80E-08	A1040089 1	NAMIN TRE	ox08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MFR8 t2 MFR8 reportitue element
5285	1	30700		6.0E	D6 AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
6324	18127	30787	1.06		Q02040	SWISSPROT	PROTEIN XE7
9226		.			6.0E-06 AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo saplens cDNA
12755	25018	30979	2.27		11418157 NT	N-	Homo sapiens calclum channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
2970	18752	31713		5.0E⊣	J6 AL163246.2	LN LN	Homo sapiens chromosome 21 segment HS21C046
6245	19019	31993	2.31	5.0E-06	U07561.1	TN	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7134		32887	1.1	5.0E-06	AB007548.1	NT	Homo saplens gene for LECT2, complete cds
8359	21052	34192			5.0E-08 AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Hamo sapiens cDNA
8359	21052	34193	0.53		36 AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10002	22650	35862	6.16		5.0E-08 AA313820.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo saptens cDNA 5' end
10410	23056	36273)-30'S	D6 P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12649	24953	30987	2.83	5.0E-(J6 A1065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
632	13411	26046	6.1	4.0E-06	4.0E-06 R16267.1	EST HUMAN	ya48c03.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element;
828	13596	26266	7.07	4.0E.	36 AW103354.1	EST HUMAN	xx89g12.x1 NCI CGAP_Eso2 Homo saplens cDNA clone IMAGE:2589574.3' similar to contains Alu repetitive element; contains element MER21 repetitive element;

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1311	14059	26733	4.64	4.0E-	06 Al334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1311	14059		4.64	4.0E-	06 Al334928.1	EST_HUMAN	[tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1457	14204	26889	1.8	4.0E-	06 BF365612.1	EST HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo saplens cDNA
2261		27728	2.17	4.0E-	06 AW015401.1	EST_HUMAN	UI-H-BI0-aat-f-05-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3060	15826	28471	6.0	4.0E→	06 AF198349.1	LN-	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3874	16624	29262	,	4.0E-	06 AW848295.1	EST HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo saplens cDNA
							w194c10.x1 NCI_CGAP_Brn25 Hamo sapiens cDNA clone IMAGE:24325623' similar to contains element
4756	17488	30115		4.0E-	06 AIB86939.1	EST_HUMAN	MER22 repetitive element ;
8397	21090	34225	0.56	-30'₽	06 015393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
8699	21391	34536		+30'4	06 AF009660.1	ΝΤ	Home sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
2096	22260	35446			4.0E-06 AJ272265.1	N	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11427	23194	36425	4.21		4.0E-06 AB007955.1	IN	Homo saplens mRNA, chromosome 1 specific transcript KIAA0486
2460	44000	70020		200			234b08.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to
2	14090	71074	1./3	3.05-	36 AA 700562.1	EST HUMAN	contains L1.t1 L1 repetitive element;
2160	14890	27625	1.75	3.0E-	06 AA7005621	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element;
2263	14989		1.44	3.0E⊣	06 AF202635.1	N-	Homo sapiens PP1200 mRNA, complete cds
2922	15688	28332	1.05	3.0E-	06 AA868218.1	EST_HUMAN	ak48g11.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1409262 3' similar to contains LTR1.t3 LTR1 repetitive element;
3259	16021		2.05		3.0E-06 AI857779.1	EST HUMAN	W22a05.X1 NCI_CGAP_Ut1 Homo septens cDNA cione IMAGE.2425616 3' similar to TR:060734 060734 LINE-1 LIKE PROTEIN :contains L1.12 L1 repetitive element :
3763	16515		1,13		3.0E-06 BE047094.1	EST_HUMAN	hq64d12.x1 NCI_CGAP_HN13 Homo sepiens cDNA clone IMAGE:3124151 3'
3763	16515	29153	1.13	3.0E-	D6 BE047094.1	EST_HUMAN	hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4524	17259	29893	3.74		3.0E-06 X54816.1	LV	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N- terminus.)
8988	18847	31811	66.0	3.0E-06	3.0E-06 AU159412.1	EST HUMAN	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3
7129	19817		2.43		P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7981	20676	33801	0.83	3.0E-(DE BE 562964.1	EST_HUMAN	601336213F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3690314 5'
8584	21276	34413	99.0	3.0E-(P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
12349	24755		3.84	3.0E-∢	D6 AW385262.1	EST_HUMAN	RC0-LT0001-261199-011-A03 LT0001 Homo sapiens cDNA
197	13010		2.81	2.0E-06	D6 P54366	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1561	14308		4.45	2.0E-(D6 P21414	SWISSPROT	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE)
2376	15098	27838	4.8		2.0E-06 AI672138.1	EST_HUMAN	wa04a03.x1 NC_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.51 MER30 repetitive element;
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Probe SEQ ID NO: 2469 3744 3763 3763 3788 6028 6028 6028 6028 6028 6116 9116 9116 9116 9116 9116 9116 911	Exon SEQ ID NO: 15285 16285 16520 1 16510 16510 16520 1 16520 1 16510 16	ORF SEQ ID NO: 27926 28023 2819 2819 28141 28144 28144 28144 28168 34969 34970 34970 34970 25477 25050 28886 28886 28947	Expression Signal Signal Signal Signal 1.12 2.37 1.68 1.159 0.83 0.83 0.657 0.657 0.65 0.65 0.65 0.65 0.65 0.65 0.65 0.65	(Top) Hit Pop Hit BLAST E Value 2.0E-06 P04829 2.0E-06 P06719 2.0E-06 P06719 2.0E-06 AA47735 2.0E-06 AA87482 2.0E-06 AA87482 2.0E-06 AA87482 2.0E-06 AA87244 2.0E-06 AA77244 2.0E-06 AA77245 2	40. AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TOP HIT Database Source SWISSPROT SWISSPROT SWISSPROT EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN SWISSPROT SWISSPROT SWISSPROT NT	TOP HIS Deletese SWITSSPROT PROBS EXPRESSED IN DYBLINE TOP HIS Deletese SWITSSPROT PROBLES AND THE CHROSOR SWITSSPROT RINDLE-RICH GLYCOPROTEIN PRECURSOR SWITSSPROT RINDLE-RICH GLYCOPROTEIN PRECURSOR SWITSSPROT RINDLE-RICH GLYCOPROTEIN PRECURSOR SET HUMAN AVESTED GLC Horne superins cander (19537219) Horne superins cDNA done IMAGE:3759176 3: IN IN THE REGISTARIES OF CLC HORNE SWITSSPROTEIN SWITSSPROT SET HUMAN WITH SWITSSPROT TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE: EST HUMAN WITHOUT COAP LLIS HORN capters CDNA done IMAGE:159800 3 similar to contains Alu repetitive testifica. Searce NPT TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE: EST HUMAN WITHOUT COAP LLIS HORN capters CDNA done IMAGE:2410083 3: EST HUMAN WITHOUT COAP LLIS HORN capters CDNA done IMAGE:2410083 3: EST HUMAN WITHOUT Source overy tumor NUHOT Horne suplems cDNA done IMAGE:2310083 3: EST HUMAN WITHOUT Source overy tumor NUHOT Horne suplems cDNA done IMAGE:2310083 3: EST HUMAN WITHOUT Source overy tumor NUHOT Horne suplems cDNA done IMAGE:2310083 3: EST HUMAN WITHOUT Source overy tumor NUHOT Horne suplems cDNA done IMAGE:2310083 3: EST HUMAN WITHOUT Source overy tumor NUHOT Horne suplems cDNA done IMAGE:2310083 3: EST HUMAN WITHOUT Source overy tumor NUHOT Horne suplems cDNA done IMAGE:2310083 3: EST HUMAN WITHOUT SOURCE INTOXICLE FALE (HUMAN); INT Horne suplems glypican 3 (GPC3) given, partial dots and flanking repeat regions WITSSPROT PROTEIN WOY-to ORGANIC CATTOW/CARRITINE TRANSPORTER 2 (SOLUTE CARRITER) MATCH STORE SOURCE SURFACE PROTEIN CANDITINE COTRANSPORTER) MATCH HORNESPROT PROTEIN MOY-to SWITSSPROT MEROZOITE SURFACE PROTEIN MATCH SOURCE SURFACE PROTEIN MATCH SOURCE SURFACE PROTEIN MATCH SOURCE SURFACE PROTEIN MATCH SOURCE SURFACE PROTEIN MATCH SOURCE SURFACE PROTEIN MATCH SOURCE SURFACE PROTEIN MATCH SOURCE SURFACE PROTEIN SWITSSPROT MEROZOITE SURFACE PROTEIN SWITSSPROT MEROZOITE SURFACE PROTEIN SWITSSPROT MEROZOITE SURFACE PROTEIN SWITSSPROT SOURCE SURFACE PROTEIN SWITSSPROT SOURCE SURFACE PROTEIN SWITSSPROT SOURCE SURFAC
1564	14311	26997	1.27	1.0E-06 /	41.1	EST_HUMAN EST_HUMAN	contains Alu repetitive element; 2008a12.s1 Source_fetal_liver_spieen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element; 2008a12.s1 Source_fetal_liver_spieen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1578	14325		1.34	1.0E-06 P27625	27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT

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Table 4
Single Exon Probes Expressed in Brain

Top Hit Descriptor	Homo sapiens p47-phox (NCF1) gene, complete cds	Homo saplens p47-phox (NCF1) gene, complete cds	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA	MR3-FN0004-090500-001-e04 FN0004 Homo saplens cDNA	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA	15 KDA SELENOPROTEIN PRECURSOR	CM0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA	ol29c08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA done IMAGE:1524878 3'	qp54e02.x1 NCI_CGAP_Co8 Hamo saptens cDNA clone iMAGE:19268423'	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element	vIR repetitive element;	za55e01.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:298472.3'	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM	Homo sapiens shox gene, alternatively spliced products, complete cds	Homo saplens shox gene, alternatively spliced products, complete cds	2017e08.r1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'	zx04d11.s1 Soares_total_fetus_Nb2HF8_3w Homo saplens cDNA clone IMAGE:785493 3' similar to gb:Dz8129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);	Homo sapiens chromosome 21 segment HS21C003	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA	zq42c02.s1 Stratagene hNT neuron (#897233) Homo sapiens cDNA clone IMAGE:632354 3' similar to SW:POL_SMSAV P03359 POL POLYPROTEIN ;	zq42c02.s1 Statagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632354 3' similar to	SW.POL_SMSAV P03359 POL POLYPROTEIN;	Homo saplans p47-phox (NCF1) gene, complete cds	Homo sapiens p47-phox (NCF1) gene, complete cds	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions	Homo sapiens chromosome 21 segment HS21C080	Homo sapiens chromosome 21 segment HS21C081
Top Hit Database Source	TN.	ΝŢ	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST HUMAN	}_	EST_HUMAN	EST_HUMAN	SWISSPROT	IN	L	EST HUMAN	EST HUMAN	Į.	EST_HUMAN	EST HUMAN		T HUMAN	NT	NT			LN	٦N
Top Hit Agession No.	E-06 AF184614.1	E-06 AF184614.1	J07561.1	1.0E-06 BF333015,1	E-06 BE834518.1	1.0E-06 BE834518.1	E-06 060613	1.0E-06 BE063527.1	E-06 P02671	E-06 BE185330,1	E-06 AA912623.1	E-06 Al347010.1		1.0E-06 AI287878.1	174635.1	139575	E-06 U82668.1	E-06 U82668.1	E-06 AA132611.1	1.0E-06 AA449257.1	1.0E-08 AL163203.2	1.0E-06 AW890941.1	E-06 AA164914.1		1.0E-06 AA164914.1	1.0E-06 AF184614.1	1.0E-06 AF184614.1	9.0E-07 AF003529.1	9.0E-07 AF003529.1	9.0E-07 AL163280.2	NL 163281.2
Most Similar (Top) Hit BLAST E Value	1.0E-06 /	1.0E-06	1.0E-06 U07561.1	1.0E-06	1.0E-06	1.0E-06	1.0E-06	1.0E-06	1.0E-06	1.0E-06	1.0E-06/	1.0E-06		1.0E-06/	1.0E-06 N74635.1	1.0E-06 Q39575	1.0E-06 L	1.0E-06	1.0E-06	1.0E-06	1.0E-06/	1.0E-06/	1.0E-06		1.0E-06 /	1.0E-06/	1.0E-05 /	9.0E-07	9.0E-07	9.0E-07	9.0E-07 /
Expression Signal	5.09	5.09	12.81	5.07	0.93	0.93	1.22	0.78	6.91	0.63	0.77	1.2		1.31	0.94	0.55	4.28	4.28	4.76	3.37	1.68	3.85	1.38		1.38	1.79	1.79	2.24	2.24	0.53	2.87
ORF SEQ ID NO:	27443	27444	29703	30638	30665		30881		32545			33997		34215	35255	32205		35418	35470				37641		1	27443	27444	25790			37161
Exon SEQ ID NO:		14723	17075		18038			18500	19517	25427							22234	22234	22280	22340		24245	24318		24318	14723	14723	13150	13150	1	23875
Probe SEQ IO NO:	1987	1987	4336	5208	5232	5232	5389	2206	6773	7644	7900	8171		8387	9204	9279	9581	9581	9627	9688	10385	11648	11724		11724	12390	12390	351	351	8306	11212

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11733			1.3	9.0E-C	17 AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
4719		30084		8.0E⊣	17 AI288596.1	EST_HUMAN	ql82g07.x1 Soares_NhHMPu_S1 Homo saplens cDNA done IMAGE:18788763
4719		30085		₽.0E-	07 AI288596.1	EST_HUMAN	ql82g07.x1 Soares_NhHMPu_S1 Homo saplens cDNA clone IMAGE:18788763'
5796			9.43	8.0E-	8.0E-07 P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
7901	20598		6.73	≻30'8	07 AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11622	24219		6:59	8.0E-	37 T07770.1	EST_HUMAN	EST05660 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBEN89
11912	24476		8.22	8.0E-∢	07 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1858	14596	27312	0.91	7.0E-07	07 AF167341.1	LZ	Homo sapiens membrane interieukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5432	l .	30944		L	F005700 NT	뉟	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5432	18231	30945			6005700 NT	FN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1905	14642	27352	2.98	⊬30'9	17 AW855558.1	EST_HUMAN	CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
							Homo saplens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-
							hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKi2W), RD, complement factor B
2488	- 1	27956			6.0E-07 AF019413.1	FZ.	(Bf), and complement component C2 (C2) genes,>
3955	16705		1.83	6.0E-07	07 P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
9040	21730	34885	1.52	6.0E-07	6.0E-07 BF001867.1	EST_HUMAN	7g94f07.x1 NCI_CGAP_Co16 Homo sepiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L.;
11836	24420	37761	1.3		6.0E-07 BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
12156	25307		2.28		6.0E-07 AW903222.1	EST_HUMAN	CM4-NN1029-260300-121-h12 NN1029 Homo sapiens cDNA
318	13121		1.94		07 AIB31893.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2385547 3'
1035	13795		4.25		5.0E-07 AA380630.1	EST_HUMAN	EST93615 Supt cells Homo sapiens cDNA 5' end
3028	15794		0.88	5.0E-07	5.0E-07 AI831893.1	EST_HUMAN	wh64f10:x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2385547 3'
6029	18809	31769	6.0		5.0E-07 U65067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, parttal cds
7000	97707	50700		, 20 5	A 200000	147711111 200	tg06b05.x1 NCI_CGAP_CLL1 Home sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu
Š B	1.	37400	8.	0.0	7 Alsesson. I	EST HUMAIN	repende densationalis definitives deligning
6964	19448	32464	1.69	5.0E-07	07 Al393981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo saplens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element.contains element A3R repetitive element;
7248	19933	33008	11	5.0E-07	5.0E-07 AW070885.1	EST HUMAN	xa31a02.x1 NCI_CGAP_Br18 Homo saplens cDNA clone IMAGE:2568362 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
	l						ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
8173	_ 1	33999	0.74	5.0E-07	5	SWISSPROT	MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8388				5.0E-07		SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10265	22913	36123	4.94	5.0E-07	17 Al908587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA

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Top Hit Descriptor	NE TRANSCRIPTASE HOMOLOG	PHA 1(1) CHAIN PRECURSOR	q pseudoautosomal region; segment 1/2	0400-204-b12 CT0383 Homo sapiens cDNA	CGAP_Co3 Homo saplens cDNA clone IMAGE:2504697 3'	PP2 gene for secreted phosphoprotein 24 precursor, exons 1-8	ETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)	SETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)	Tomosome 21 segment HS21C007	CGAP Lu34.1 Homo saplens cDNA clone IMAGE:2858548 3'	H_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'	H_MGC_21 Homo sepiens cDNA clone IMAGE:3959651 5'	tromosome 21 segment HS21C018	CGAP Kid12 Homo sapiens cDNA clone IMAGE 2399703 3'	CGAP Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'	0300-003-e12 BN0083 Homo sapiens cDNA	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced	200	g pseudoautosomal region; segment 1/2	The microsalentia DIVA	loup I genining gene, exons I and Z, v-region O Briefe	nioobo9.s1 NCI_CGAP_OV2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element:contains L1.t3 L1 repetitive element :	thic microsatellite DNA	0300-001-f11 BN0115 Homo sapiens cDNA	0300-001-f11 BN0115 Homo sapiens cDNA	is fetal liver spleen 1NFLS Homo sapisns cDNA clone IMAGE:111895 67	63 & KD DEOTEIN IN CLITTLEMA INTERDENIO DECION DE CALIDRODE	Homo sarions of No. 61 COOD64 at	es NF T GRC S1 Homo sablens CDNA clone IMA GF: 23.47067.31	vo14h09.s1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:80705 3' sImilar to similar to che similar to similar to similar to similar to similar to similar to similar to similar to similar to che similar to	
Top Hit Descriptor	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	COLLAGEN ALPHA 1(1) CHAIN PRECURSOR	Homo sapiens Xq pseudoautosomal region; segment 1/2	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA	ws84h05.x1 NCI_CGAP_Co3 Homo septens cDNA clone IMAGE:2504697 3'	Homo saplens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)	Homo sapiens chromosome 21 segment HS21C007	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'	Homo saplens chromosome 21 segment HS21C018	wi81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'	wi81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA	i microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and al	univansialed exons	Homo sapiens Xq pseudoautosomal region; segment 1/2	Francial polyntolphia microsatellite DNA	יופר פתראומת ו אפורווווו או אפור באחוז באחוז ביותר לי אין באומוס בוופוב	niooooys.s1 NCI_CGAPOv2 Homo sapiens cDNA clone IMAGE:980825 similar to contal element:contains L1.t3 L1 repetitive element :	Нитап polymorphic microsatellite DNA	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA	yd50f12.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:111695 6	HYPOTHETICAL 63 8 KD PROTEIN IN GLITT-RIMA INTERCENIC BECION DESCRIBES	AVERDO4 GLC Home serviews CDNA Jone GLCCCD04 3	we86b12 x1 Sogres NFI T GBC S1 Homo sapiens clove that the 23470s73	vo14h09.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' slmil db:M62982 ARACHIDONATE 12-LIPDXXQENASE (HI IMAN)	vc14h09 s1 Stratagene ling (#037240) Homo seniese c DNA close 1846 GE 80706 5' closica to
Top Hit Database Source	SWISSPROT LINE	SWISSPROT COLL	NT	EST_HUMAN QV0-	_	NT	SWISSPROT HIST	Γ	NT Homo	EST_HUMAN xy49g		Γ	Γ	Г	Г	EST_HUMAN PM1-			Homo			EST HUMAN elemen	Т	EST_HUMAN MRO-	Г	Т	T	T	Т		T
Top Hit Acession No.			Γ		Γ	5.1							4.0E-07 AL163218.2		-07 AI765528.1 E	-07 BE001828.1 E			3.0E-07 AJ271735.1			-07 AA526763.1 E		2.	Γ	3.0E-07 T84704.1		+	Γ		Ī
Most Similar (Top) Hit BLAST E Value	5.0E-07	5.0E-07	5.0E-07	5.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	4.0E-07	0	0.0E-0.0	3,0E-07	2000	2000	3.0E-07	3.0E-07	3.0E-07	3.0E-07	3.0E-07	3 0F-07	3 0F-07	3.0E-07	3.0E-07	
Expression Signal	1.28	4.04	2.52	3,48	2.02	0.83	1.74	1.74	9.0	5.41	0.47	0.47	0.49	3.14	3.14	1.66	0	6.6	2.12	202	2	1.42	1.83	7.61	7.61	1.16	1 45	CA 7	0.86	13	
ORF SEQ ID NO:	36493				29364	L						35891	36084	_	36782		2000	20002	25978				27749	27930	27931	28443	28566	30047	30075	30330	
Exon SEQ ID NO:	23256	24101	24173					19854	20518	21640	22675	22675	22871	23536	23536	23849	7,004	175	13350	14360		14773	15011	15190	15190	15797	15920	17412	17443	17777	
Probe SEQ ID NO:	10560	11500	11574	12561	3981	7078	7167	7167	7823	8949	10027	10027	10223	10856	10856	11184	707	2	569	1622		2039	2286	2472	2472	3031	3157	4678	4711	5004	

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						,	
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5580	18377	31290	12.43	3.0E-	708880	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
5883	18669	31610	0.83	3.0E-	07 042280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
6603	19366		5.57	3.0E-	07 AA815175.1	EST_HUMAN	oc04c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7409	20086	33170	3.48	3.0€~	07 AW 797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
7561	20231		62.0	3.0E-	07 AI591065.1	EST_HUMAN	tw28f11.x1 NCI_CGAP_Ov35 Homo saplens cDNA clone IMAGE:2281037 3' similar to contains Alu repetitive element;contains element MSR1 MSR1 repetitive element:
9028	21718	34872	0.85	-30.€	07 P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (OF-1 64 KD SUBUNIT)
9028	21718	34873	0.85	3.0E	07 P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
11484	24085		1.45	3.0E-	07 BE439409.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
11656			1.75	3.0E⊣	07 AF029308.1	FZ	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trousingen gene families
12791	25043		5.1	3.0E-07	3.0E-07 AJ132352.1	۲Z	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
27	12855	25471	4.15	2.0E-(07 AF262988.1	Ę	Homo saplens TRF2-Interacting telomenic RAP1 protein (RAP1) mRNA, complete cds
150		25606	6	2.0E-07	07 L77569.1	Z	Homo sapiens DiGeorge syndrome critical region, telomeric end
150		25607	6	2.0E-07	7 L77569.1	LN	Homo sapiens DiGeorge syndrome critical region, telomeric end
17		25629	44.15	2.0E-C	07 U38849.1	LN	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
731	13505	26160	2.45	2.0E-(7 AF003530.1	LN	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
731	13505	26161	2.45	2.0E-(07 AF003530.1	LN	Homo saplens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
744	13517		0.82	2.0E-07)7 P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
82	13689	26353	3.73	2.0E-07	2.0E-07 AA223260.1	EST HUMAN	z/08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to obi.131880 GI YCOPHORIN A PRECLIRSOR (HIMAN) population also sensitive algorithms.
923	13690	26354	2.15	2.0E-07	2.0E-07 T63042.1	EST HUMAN	vo15g04.s1 Stratagene lung (#937210) Homo saplens cDNA clone IMAGE:80790 3' similar to contains L1 repotitive element:
1140	13895	26556	1.37	2.0E-07 Q26768		SWISSPROT	J/6 AUTOANTIGEN
1596	14342	27032	2.96	2.0E-07		Т	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME
3676	16429	29070	15.93	2.0E-07		Z	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5059	17778	30395	0.84	2.0E-07	2.0E-07 AW 070995.1	EST HUMAN	xa05h07.x1 Soaras_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567486 3' similar to WP:C38H2.1 CE00923 PROBABLE RABGAP DOMAINS:
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33320 0.67 1.0E-07 R530801 EST_HUMAN 33321 0.67 1.0E-07 R5375909.1 EST_HUMAN 33321 0.67 1.0E-07 R5375009 1 EST_HUMAN	0.87 1.0E- 5.24 1.0E- 5.24 1.0E-	2.1 EST_HUMAN 2.1 EST_HUMAN 2.1 EST_HUMAN 1.1 EST_HUMAN 1.1 EST_HUMAN 1.1 EST_HUMAN 1.1 EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1) GLYCOPROTEIN GPV Homo sepiens chromosome 21 segment HS21 C082 AV718682 GLC Homo sepiens cDNA clone GLCFNF04 5' AV718682 GLC Homo sepiens cDNA clone GLCFNF04 5' ZINC FINGER PROTEIN 180 ZEGGGLAT Scares retina N2b4HR Homo sepiens cDNA clone IMAGE:363026 5' AV718682 GLC Homo sepiens cDNA clone sepiens cDNA clone IMAGE:363026 5' AV718682 GLC Homo sepiens cDNA clone IMAGE:363026 5' AV718682 GLC Homo sepiens cDNA clone IMAGE:263026 5' AV718682 GLC Homo sepiens cDNA clone IMAGE:2291339 5' E26302L1 Scares retina N2b4HR Homo sepiens cDNA clone IMAGE:2291339 5' E43406 y1 NCI_CGAP_Brn52 Homo sepiens cDNA clone IMAGE:2291339 5'
20218 33321 0.67 1.0F-07 RE375000 1 FET UTIMAN	33320 9.08 1.0E-	EST_HUMAN EST_HUMAN	W43c07.s1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3' PM4-TN0024-0308co-002-b05 TN0024 Homo sapiens cDNA
NUMBER OF STREET	33321 0.67 1.0E-(PMA TNOOZA OROBOO OOS FOE TNOOZA FINONA LI
		EST HUMAN	IF IMPERIOUS CONTRACTOR INVITATION CONTRACTOR IN THE INVITATION CONTRACTOR

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Single Exon Probes Expressed in Brain

		,			: +		
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7721	20385		0.64	1.0E-07	1.0E-07 AL163203.2	LN	Homo sapiens chromosome 21 segment HS21C003
8114		33941			P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8114	20808		2.73		P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8853	21544	34691			1.0E-07 AA693576.1	EST_HUMAN	251e10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:434346 3'
9170	21840	35005	26.0	1.0E-07 P57110	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
						-	huzano6.x1 NCI_CGAP_Mel15 Homo saplens cDNA clone IMAGE:3171419 3' similar to contains MER18.t3
9517	- (35353		2	E-07 BE327843.1	EST HUMAN	MEK18 repetuve element;
9836	22487	35689	2.77	1.0E-07	E-07 BF674524.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
9844	22495	35696	1.21	1.0E-07	E-07 AA386311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens oDNA
10362	53009		1.28		1.0E-07 AL163282.2	TN	Homo sapiens chromosome 21 segment HS21C082
	l					ŀ	hr33c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:095722 095722
12212	Į	30810	3.83		1.0E-07 BE048770.1	EST HUMAN	[DJ1]63J1.1 ;
12514			1.87		1.0E-07 X51755.1	LN	Human lambda-immunoglobulin constant region complex (germline)
7181	19867	32940	0.84	9.0E-08	9.0E-08 A/539362.1	EST HUMAN	te51b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
9787	22438	35645	1.88		9.0E-08 AV734819.1	EST_HUMAN	AV734819 cdA Homo sapiens cDNA clone cdABFB06 5'
	l						wn30a07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.t2
11136		37082		į	9.0E-08 AI891052.1	EST HUMAN	OFR repetitive element ;
11668	24263	37587	2.8		9.0E-08 AL163301.2	NT	Horno sapiens chromosome 21 segment HS21C101
12188	24648		4.44		9.0E-08 AJ251973.1	LN.	Homo saplens partial steerin-1 gene
88	15546		3.7	8.0E-08	8.0E-08 AI911352.1	EST_HUMAN	wd16b05.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273.3'
1028			0.72		8.0E-08 BE795469.1	EST_HUMAN	601690133F1 NIH_MGC_7 Hamo sapiens cDNA clone IMAGE:3943976 5'
3532	16288		1.53		BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo saplens cDNA clone IMAGE:3943976 5
8638	21330	34474	3.05		8.0E-08 AI752367.1	EST_HUMAN	on15002.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8638	21330	34475	3,05		8.0E-08/A/752367.1	EST HUMAN	en15c02.x1 Normal Human Trabecular Bone Cells Homo saplans cDNA clone NHTBC cn15c02 random
9527	١.	35364			8.0E-08 AW970693.1	EST_HUMAN	EST382776 MAGE resequences, MAGK Homo saplens cDNA
	L					·	
10461	┙	36338			8.0E-08 AF111167.2	Z	Homo sapiens fun aimerzetan protein gene, partai cos; cros gene, complete cos; and unknown gene
11211	┙			_ [AF253417.1	N	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
78					7.0E-08 Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1340	ı	26764			X04809.1	NT	Rat mRNA for ribosomal protein L31
3563	16318	١	1.15	7.0E-08 P15305	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)

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	Most Similar Top Hit Acession Database BLAST E No. Source Source	7.0E-08 P15305 SWISSPROT DYNEIN HEAVY CHAIN (DYHC)	7.0E-08 A1835743.1 EST HUMAN cong3.P11.A5 conorm Home saplens cDNA 3'	7.0E-08 U24070.1 NT	7.0E-08 P15305 SWISSPROT	7.0E-08 P15305 SWISSPROT DYNEIN HEAVY CHAIN (DYHC)	7.0E-08 AJ131016.1	6.0E-08 AL163248.2 NT Homo sapiens chromosome 21 segment HS21C048	6.0E-08 AL163248.2 NT	6.0E-08 BE144398.1 EST HUMAN	6.0E-08 7662473 NT	6.0E-08 AL163248.2 NT	6.0E-08 P08547 SWISSPROT		6.0E-08 AA827075.1 EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEÍN (CONTAÍNS: REVERSE TRANSCRIPTASE ; 6.0E-08 P11369 SWISSPROT ENDONUCLEASE)	6.0E-08 AL163209:2 NT	08 AL163303.2 NT	- Louis	5.0E-08 P06681 SWISSPROT	5.0E-08 AW851878.1 EST HUMAN	4.0E-08 P25723 SWISSPROT	4.0E-08 P25723 SWISSPROT	4.0E-08 AL079581.1 EST_HUMAN	LN .	4.0E-08 P52624 SWISSPROT URIDINE PHOSPHORYLASE (UDRPASE)	4.0E-08 O15393 SWISSPROT	4.0E-08 L42571.1 NT	4.0E-08 P08547 SWISSPROT	4.0E-08 AI016342.1 EST_HUMAN	4.0E-08 A1050027.1 EST_HUMAN
-	Most Similar (Top) Hit BLAST E Value	7.0E-08 P1	7.0E-08 AIS	7.0E-08 UZ	7.0E-08 P1	7.0E-08 P1	7.0E-08/AJ	6.0E-08 AL	6.0E-08 AL	6.0E-08 BE	6.0E-08	6.0E-08 AL	6.0E-08 Po	-	6.0E-08 AA	6.0E-08.P1	6.0E-08 AL	5.0E-08 AL	A 0 E 0 B	5.0E-08 PO	5.0E-08 AW	4.0E-08 P2	4.0E-08 P2	4.0E-08 AL	4.0E-08 UB	4.0E-08 P5	4.0E-08 O1	4.0E-08 L42	4.0E-08 PO	4.0E-08 AIO	4.0E-08 AI0
	Expression Signal	1.15	1.67	5.17	2.98	2.98	1.89	2.88	2.88	2,97	0.81	86.0	69.0		0.56	2.24	133	3.72	, 82	8.36	2.54	0.97	0.97	1.09	1.04	1.08	0.63	1.05	0.71	0.68	3.87
	ORF SEQ ID NO:	28966		37589	28965					١,	28469	29588			_	37299		25547	70976		31085		27196		29284		34533	34881			36147
	Exon SEQ ID NO:		23405	24267	16318	16318	24975				15824	16963	20546	L	21906	23997	24120	12809	14057	L	L			15655		Н		21727	22198	22876	22932
	Probe SEQ ID NO:	3563	10716	11672	12619	12619	12690	798	798	2363	3058	4222	7851		9227	11391	11520	ន	2228	11914	12099	1754	1754	2888	3894	6311	8697	9037	9545	10228	10284

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Top Hit Descriptor	278b08.11 Soares, testis, NHT Homo septens cDNA clone IMAGE:728247 5' similar to TR:0505579 G505579 NA/CA,K-EXCHANGER.;	2/78b08.1 Soares, testis, NHT Homo saplens cDNA clone IMAGE:728247 5' similar to TR.G503579 G505579 NA/CA,K-EXCHANGER.;	602248024F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4333300 5'	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'	zol65g03.r1 Soares, fetal_heart_NbHH19W Homo sapiens cDNA cione IMAGE:345556 5' similar to contains L1.t1 L1 repetitive element;	tb95a11.X1 NO_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2082076 3' similar to contains MER18.b3 MER18 MER18 repetitive element;	bb79a10.y1 NIH_MGC_10 Homo sepiens cDNA clone IMAGE:3048570 5' similar to TR:Q8Z158 Q9Z158 SYNTAXIN 17.;	qs76f11.y5 NCI_CGAP_Pr28 Homo saplens cDNA clone IMAGE:1944045 5	Homo saplens chromosome 21 segment HS21C046	th93h09x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA done IMAGE:2126273 3' sImilar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;	Homo sapiens MHC class 1 region	qh21a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845294 3'	yp12b10.s1 Soares breast 3NbHBst Homo saplens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT- BINDING PROTEIN-1 (HUMAN);	vp12b10.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT-BINDING PROTEIN-1 (HUMAN);	yg02f04.r1 Soares Infant brain 1NIB Homo saplens cDNA clone IMAGE:30948 5' similar to contains Alu repositive element:	xr87f06.x1 NCI CGAP Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'	zw48f07.1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317.5' similar to contains Alu repetitive element;contains element MER15 repetitive element;	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	MR0-OT0080-240200-001-g08 OT0080 Homo saplens cDNA	MR0-OT0080-240200-001-908 OT0080 Homo saplens cDNA	601155321F1 NIH_MGC_21 Hamo saplens cDNA clane IMAGE:3138863 5	Homo sapiens chromosome 21 segment HS21C047	601570463F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3845199 5'
Top Hit Database Source	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	LZ	EST HUMAN	LZ.	EST_HUMAN	EST_HUMAN	EST_HUMAN	HST HIMAN	EST HUMAN	EST HUMAN	N.	EST_HUMAN	EST_HUMAN	EST_HUMAN	L	EST_HUMAN
Top Hit Acession No.	4.0E-08 AA393627.1	8 AA393627.1		4.0E-08 BF692493.1	4.0E-08 W76159.1		3.0E-08 BE018348.1	3.0E-08 AI792737.1		3.0E-08 AI436352.1	8 AF055066.1	3.0E-08 AI218001.1	R86279.1	R86279.1	R18420 1	96.1				2.0E-08 AW886438.1		2.0E-08 AL163247.2	
Most Similar (Top) Hit BLAST E Value	4.0E-08	4.0E-08	4.0E-08	4.0E-08	4.0E-08	4.0E-08	3.0E-08	3.0E-08	3.0E-08	3.0E-08	3.0E-08	3.0E-08	3.0E-08	3.0E-08	3.05-08	2.0E-08	2.0E-08	2.0E-08	2.0E-08	2.0E-08	2.0E-08	2.0E-08	2.0E-08
Expression Signal	1.7.1	1.71	4.02	4.02	4.31	2.18	2.22	4.24	1.66	3.56	0.52	1.32	61.58	61.58	76.6	9.03	9.14	1.01	13.62	13.62	24.4	2.38	12.18
ORF SEQ ID NO:	36939	36940					31222		33205			36877	37477	37478				25905		26063		26743	
Exon SEQ ID NO:	23681	23681	_		25334	24887	18321	17955	20116	20313	22449	23626	24165	24165	24459	1	ſ	13269	13424	13424	13735	14069	14476
Probe SEQ ID NO:	11009	11009	11031	11031	11919	12549	6523	68879	7439	7649	86/6	10948	11566	11566	11888	Ŕ	123	484	645	645	696	1320	1734

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1	178			Adica	7 7 1000 1010	14 40 61 61 61 61 61	TOO DOT HAVE HEAVE HE SALE HERE
100	١		4.11	Z.0E-08	Z.UE-U8 AW Z/UZ/1.1	ESI HOMAN	XP43711X1 NOL CGAP HN11 Homo sapiens CONA clone IMAGE:2/43149 3
2545	15260		1.71	2.0E-08	08 K00216.1	NT	Sheep His-RNA-GUG
3202	15965		7.94	2.0E-08	08 042280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3202	15965		7.94	2.0E-08	08 042280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3840	16591		1.76	2.05-08	08 AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-b03 ST0197 Homo saplens cDNA
							aa26c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.t2 L1
4373	17111		2.48	2.0E-08	08 AA459040.1	EST_HUMAN	repetitive element;
, in							her7h08.x2 NCI_CGAP_CML1 Homo saplens cDNA clone IMAGE:2919327 3' similar to contains Alu
4903	•		2.38	2.05-08	38 AW 57 2881.1	EST_HUMAN	repetitive element;
6649	18346	31255	1.19	2.0E-08	2.0E-08 AA813204.1	EST_HUMAN	ai80h11.s1 Soares_festis_NHT Homo sapiens cDNA clone 1377189 3'
							xd32c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3
5742		31457		2.0E-08	AW088924.1	EST_HUMAN	MER18 MER18 repetitive element;
7903		33728		2.0E-08	2.0E-08 P10272	SWISSPROT	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE)
8008	20704			2.0E-08	08 AA490121.1	EST_HUMAN	ab02g06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
8883	21673		6.0	2.0E-08	08 AU139978.1	EST_HUMAN	AU139978 PLACE1 Homo saplens cDNA clone PLACE1011719 5'
							W72f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains
10416	23062	36281	0.79	2.0E-08	2.0E-08 N78097.1	EST_HUMAN	LTR1.b3 LTR1 repetitive element;
97707		COCOC	6	L C	7 2000214	100	W72f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains
5	1		9.0	4.0E-00		ESI DOMAIN	LINITED LINITED BEILDING
12184			1.54	2.0E-08	-08 AL163284,2	L	Homo sepiens chromosome 21 segment HS21C084
1499			1.16	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE)
1768		27211	1.45	1.0E-08	1.0E-08 AF125348.1	NŢ	Homo saplens caveolin 1 (CAV1) gene, exon 3 and partial cds
2044			2.31	1.0E-08	08 BE141959.1	EST_HUMAN	PM2-HT0130-150989-001-f12 HT0130 Homo saplens cDNA
5512	1			1.0E-08	08 AJ010770.1	ĹΝ	Homo sapiens hyperion gene, exons 1-50
7668			1.26	1.0E-08	08 P19474	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
7934	20629	33756		1.0E-08	08 AL163302.2	ĹΝ	Homo sapiens chromosome 21 segment HS21C102
							Homo saplens mannosidase, beta A, lysosomal (MANBA) gene, and ublquitin-conjugating enzyme E2D 3
8028	20723	33855	0.64	1.0E-08	08 AF224669.1	⊢ V	(UBE2D3) genes, complete cds
							Homo sapiens mannosidase, beta A, lysosomal (WANBA) gene, and ubiquitin-conjugating enzyme E2D 3
8028	١	33856	0.64	1.0E-08	08 AF224669.1	LN	(UBE2D3) genes, complete cds
8445	Į	Í		1.0E-08	1.1	EST_HUMAN	ot35a05.s1 Soares_lestis_NHT Homo sapiens cDNA clone IMAGE:1618736 31
9104				1.0E-08		SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9105	21793	34956	0.78	1.0E-08	08 BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-d02 BT0546 Homo sepiens cDNA

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		-	т-	1	т	_	_	_		т—	_	_		_	_	_	Τ-	_	_	_	_	т-	_	_	_		_	
Top Hit Descriptor	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN)	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	Homo sapiens major histocompatibility locus class III region	Human lambda-immunoglobulin constant region complex (germline)	Homo capiens chromosome 21 segment HS21C079	Homo sapiens chromosome 21 segment HS21C079	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'	qu86c11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1978964 3' similar to contains L1.t3 L1	repetitive element;	qd42e07.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164.3' similar to contains MSR1.t1 MSR1 repetitive element	CM0-NN1004-100300-273-e06 NN1004 Homo saniens cDNA	op74d08.s1 Soares NFL T GBC S1 Homo sabiens cDNA clone IMAGE:1682575.3	Homo sapiens DNA for 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional nuclein exen 2-3	745e10.x1 Soares_NSF_F8_8W_OT_PA_P_S1 Homo sepiens cDNA clone IMAGE:3524443.3' similar to contains MFR29.b2 MFR29 renefitive element:	z/80c05.r1 Scares_NhHMPu_S1 Homo saplens cDNA clone IMAGE:681992 5' similar to contains L1.t2 L1	repetitive element;	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region	601111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5	zf58e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE;381156 3' similar to contains L1.t2 L1	repetitive element;	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1219183'	DKFZp434C0514_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0514 5'	PM1-HT0527-160200-001-h05 HT0527 Homo saplens cDNA	xn85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'	MR3-HT0446-260300-201-h12 HT0446 Homo sapiens cDNA	Homo sapiens fibrobiast growth factor receptor 3 (achondroplasia, thanatrohoric dwarfism) (FGFB3) mBNA	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds	745e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
Top Hit Database Source	SWISSPROT	SWISSPROT	N	LN L		FZ	"HUMAN		EST_HUMAN	EST HUMAN	Т	Т		EST HUMAN	Т	EST_HUMAN	N F	EST_HUMAN	П	П			Г	Г	EST_HUMAN N		LN	EST_HUMAN o
Top Hit Acession No.	08 P79110	08 P98063	08 AF044083.1		2.0		39 T97950.1		8.0E-09 AI270615.1	8.0E-09 AI183500.1	Γ	8.0E-09 AA938892.1		7.0E-09 BF108755.1			7.0E-09 L09709.1									4503710 NT	6.0E-09 AF200923.2	6.0E-09 BF108755.1
Most Similar (Top) Hit BLAST E Value	1.0E-	1.0E-08	1.0E-08	1.0E-08	9.0E-09	9.0E-09	9.0E-09		8.0E-09	8.0E-09	8.0E-09	8.0E-09	7.0E-09	7.0E-09		7.0E-09	7.0E-09	7.0E-09	-	7.0E-09	7.0E-09	6.0E-09	6.0E-09	6.0E-09	6.0E-09	6.0E-09	6.0E-09	6.0E-09
Expression Signal	1.2	0.77	4.14	2.82	4.65	4.65	0.52		0.62	7.66	2.65	2.65	1.73	0.61		0.82	2.91	1.42		0.5	1.49	0.99	3.12	11.59	0.93	1.96	3.76	1.44
ORF SEQ ID NO:	35712		37241		29583					32920	33726							35946					30263	30760	34311	34925		36561
Exon SEQ ID NO:					Н		22610		19158	19851	20594	1	16346	20497	ı	- 1	21829	22731	0	78077	23268	14879	17650	18101	21167	21763	22824	23324
Probe SEQ ID NO:	9868	10453	11285	12282	4218	4218	9965	- 6	6380	7164	7899	8887	3583	7802		7948	9129	10083	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	102	105/1	2149	4922	9236	8475	9074	10176	10632

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Probe SEO ID NO: 11798 11798 11798 11798 11798 11799 1		ORF SEQ ID NO: 37722 26818 27298 32071 34321 35855 35856 377479 277485 35856 37764 36943 36704 36943 28733	Signal Signal Signal Signal 1.37 1.37 1.37 1.37 1.37 1.37 1.37 1.37	Most Similar (10p) Hit BLAST E Value (10p) Hit BLAST E SinE-09 (5.0E-09 (5.	8 - 505 5000 5000 500 50 50 50	Top Hit Database Source EST HUMAN INT SWISSPROT EST HUMAN INT INT INT INT INT INT INT INT INT IN	Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor EST HUMAN HUNGS0003782 Human adult (K.Okubo) Home expiens dDNA EST HUMAN HUNGS0003782 Human adult (K.Okubo) Home expiens dDNA Home suplers chromosome 21 segment HS210384 EST HUMAN HUMS0003782 Human adult (K.Okubo) Home expiens dDNA EST HUMAN Human qemiline T-cell receptor begate than Dopamine-beta-hydroxylass-like, TRY1, TRY2, TRY3 TGRBVS2781 TGRBVS2821, TGRBVS283421, TGRBVS1841, TGRBVS284297, TGRBVS28341, TGRBVS283421, TGRBVS284297, TGRBVS28341, TGRBVS283421, TGRBVS283421, TGRBVSS3421, TGRBVSS3421, TGRBVSS3421, TGRBVSS3421, TGRBVSS3421, TGRBVSS28421, TGRBVSS3421, TGRBVSS3
4076				3.0E-09	3.0E-09 X16674.1	L L	H sapiens PADPRP-I gene for NAD(+) ADP-ribosytransferase
4476	17129	29761	3.42	3.0E-09	E-09 AF175325.1 E-09 Q9Y3R6	SWISSPROT	Homo septens eukaryotic initiation factor 4AI (EIP4AI) gene, partial cds 258.1 KDA PROTEIN C210RF5 (KIAA0933)
	ł			1,7,5	20.00		

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			_	_	_		_	_	_	_		_		1 .6	_		_		_	_		,		,	_					
Top Hit Descriptor	hx80a02.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:3194090 3' similar to TR:O55091 O55091 IMPACT PROTEIN ;	Homo saplens chromosome 21 segment HS21 C047	7172c08.x1 Soures_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'	772c08x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyftransferase	Homo sapiens chromosome 21 segment HS21C084	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'	258.1 KDA PROTEIN C210RF5 (KIAA0933)	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR	Human transposon-like element mRNA	ot47b09.s1 Soares_tests_NHT Homo saplens cDNA clone IMAGE:1619897.3	Homo sapiens chromosome 21 segment HS21C049	EST66142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat	zx63h06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE;796187 5' similar to contains	Alu repetitive element;	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	MR1-CT0352-240200-105-b06 CT0352 Homo saplens cDNA	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo sapiens chromosome 21 segment HS21C048	H.saplens PADPRP-I gene for NAD(+) ADP-ribosyltransferase	nc11c02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;	Homo sapiens shox gene, alternatively spliced products, complete cds	zd79d03.s1 Soares, fetai, heart, NbHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);	Homo saplens CCAAT-box-binding transcription factor (CBF2) mRNA	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nain) and survival motor neuron protein (sun) genes complete cds.	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds	Homo saplens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
Top Hit Database Source	EST_HUMAN	ΙN	EST_HUMAN	EST_HUMAN	NT	TN	EST_HUMAN	SWISSPROT	SWISSPROT	ΙN	EST_HUMAN	NT	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	ΤN	IN	LN	EST HUMAN	LN	EST HUMAN	N	LN	LN	Ę	L	NT	EST_HUMAN
Top Hit Acession No	BE465780.1	AL163247.2	BF109943.1	BF109943.1	X16674.1	AL163284.2	AL118573.1	Q9Y3R5	060241	M23161.1	Al004062.1	AL163249.2	AA357407.1		AA461430.1	W28834.1	_	AJ271735.1	AL163248.2	X16674.1	AA226070.1	U82668.1	W78152.1	5031624 NT	5031624 NT	AJ229041.1	1 1800-17 1	M28699.1	M28699.1	BE535440.1
Most Similar (Top) Hit BLAST E Value	3.0E-09	3.0E-09	3.0E-09	3.0E-09		2.0E-09	2.0E-09	2.0E-09	2.0E-09	2.0E-09	2.0E-09	2.0E-09	2.0E-09		2.0E-09	2.0E-09	2.0E-09	2.0E-09	2.0E-09	2.0E-09	2.0E-09	2.0E-09	1.0E-09	1.0E-09	1.0E-09	1.0E-09	10,00		1.0E-09	1.0E-09
Expression Signal	1.19	1.7	4.8	4.8	2.43	7.99	7.46	1.1	3.01	0.85	0.55	0.57	0.93		8.4	0.68	0.62			22.07	2.41	1.75	0.72			1.17	7	3.25	3.25	0.7
ORF SEQ ID NO:	33617	60098	36873			26653		27787			31341				33110	33188	33494		37183						26504		28304			
Exen SEQ ID NO:	20495	22795	23624	1		13984	14401			17795	18428	18838	19599		20032	20100			23896	13566	25403	24934		l	13845	14376		1		1 1
Probe SEQ ID NO;	7800	10147	10945	10945	794	1236	1855	2326	3918	5076	5633	8909	6682		7351	7423	1117	8612	11233	12428	12495	12634	974	1087	1087	1630		2928	2926	3034

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4744	17476		6.4	1.0E.4	09 AA719297.1	EST HUMAN	2h35b03.s1 Soares_plusel_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element.contains element MER22 repetitive element:
5416	18215	30923	99.0	1.0E-09	09 AL163283.2	N.	Homo saplens chromosome 21 segment HS21C083
6740	18532		1.89	1.0E-	09 U07000.1	LN	Human breakpoint cluster region (BCR) gene, complete cds
6053	18833	31795	3.13	1.0E-	09 P26694	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8289	20983	34124	מא ט	-30 t	00 4 688474 4	TOT LIMAN	wd39b05x1 Scares_NFL_T_GBC_S1 Homo seplens cDNA clone IMAGE:2330481 3' similar to contains
10212	L		2.92	1.06-	09 AL 163283.2	LZ LZ	Homo saniens chromosome 21 serment HS2/Ch83
11799	24389		1.68	1.0E-09	09 AL163283.2	Į.	Homo saplens chromosome 21 segment HS21C083
12333	25344	30717	2.25	1:06-	11418127 NT	FZ.	Homo saplens GTP binding protein 1 (GTPBP1), mRNA
12503	24857		1.35	1.0E-	09 T93176.1	EST HUMAN	ye24e05.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118688 5/
1286	14036	26707	3.74	9.0E-	10 AW867740.1	EST HUMAN	MR0-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2838	15606	28256	4.41	9.0E-10	10 AI870071.1	EST HUMAN	we78h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29 HUMAN P47914 60S RIBOSOMAL PROTEIN 129 :contains element PTR5 renefitive element
6735	19569	32601	4.78	9.0E-10	10 A1452982.1	EST HUMAN	148b09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IWAGE:2144537 3' similar to TR:000372 PUTATIVE P150.:
142	12957	25599	13.27	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3337	16097	28748	0.88	8.0E-10	8.0E-10 BE080748.1	EST_HUMAN	QV1-BT0631-150200-071-f01 BT0631 Homo sapiens cDNA
4177		29544	3.17	8.0E-10	10 AA376832.1	EST HUMAN	EST89564 Small Intestine I Homo sapiens cDNA 5' end
9865	22515		2.44	8.0E-	10 U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
685		26107	9:36		7706225 NT	NT	Homo saplens TPA inducible protein (LOC51586), mRNA
982		26108	9:36	7.0E-10	7706225 NT	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1618	. 1	27055	2.24	7.0E-10	10 Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2013			3.17	7.0E-	10 P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2564			24.23	7.0E-	10 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3086	1	28491	2.19	7.0E-	10 X00856.1	TN	H.sapiens DHFR gene, exon 3
6092	- 1	31836	4.18	7.0E-10	10 AA345220.1	EST_HUMAN	EST51247 Gall bladder II Homo saplens cDNA 5' end
7316	- 1	33078	1.08	7.0E-10	10 BF352883.1	EST_HUMAN	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
7556	ı		1.48	7.0E-10		SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7875	ł	33696	1.6	7.0E-	٠	LΝ	Homo sapiens presenilin-1 gene, exons 1 and 2
7875	- 1	33697	1.6	7.0E-	1.2	NT	Homo saplens presentlin-1 gene, exons 1 and 2
10209	22857	36073	1.67	7.0E-10	10 L08895.1	NT	Homo sapiens MADS/MEF2-family transcription factor (MEF2C) mRNA, complete cds

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Top Hit Database Source	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene	HUMAN	HUMAN	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) SWISSPROT (LEUKOCYTE-ENDOTHELIAL GELL ADHESION MOLECULE 2) (LECAM2) (CD62E)	E-SELECTIN PREGURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) SWISSPROT (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)	SWISSPROT ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)		HUMAN	SSPROT	T Homo sepiens WRN (WRN) gene, complete cds	EST_HUMAN 601822184F1 NIH_MGC_75 Home sapiens cDNA clone IMAGE:4042413 5	Г	SWISSPROT HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III	qg08f09.x1 Soares_placenta_8to8weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1759049.3' EST_HUMAN similar to contains LTR8.b2 LTR8 repetitive element;	EST HUMAN Inf64e01.s1 NCI_CGAP_Co3 Homo saplens cDNA clone IMAGE:924649 3'		Homo sapiens chromosome 21 segment HS21C103	Homo septens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) censes, complete cds	HOMAN	HUMAN				Homo sapiens chromosome 21 segment HS21C003	EST_HUMAN yz11908.s1 Soarss_muliple_scierosis_2NbHMSP Homo sapiens cDNA clone IMAGE:282782 3	1	EST_HUMAN ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
Top Hit Acession No.	0 AJ400877.1	0 Al424405.1 EST	0 AW853719.1 EST	0 P33730 SW	0 P33730 SW	0 P98073 SW	0 AW971923.1 EST	0 AL046804.1 EST			0 BF105159.1 EST	0 P34678 SWI	D P34678 SWI	A1221083.1 EST		AW594709.1 EST	D AL163303.2 NT	AF224669.1 NT				7005150.1 NT	AL163203.2 NT	AL163203.2 NT	N50109.1 EST		BE302970.1 EST
Most Similar (Top) Hit BLAST E Value	6.0E-10 A.	6.0E-10 A	6.0E-10 A	6.0E-10 P:	6.0E-10 P.	8.0E-10 P	6.0E-10 A	5.0E-10 A	5.0E-10	5.0E-10 A	5.0E-10 BI	5.0E-10 P	5.0E-10 P	4.0E-10 A	4.0E-10 A	4.0E-10 A	4.0E-10 AL	4.0E-10 A	4.0E-10 A	4.0E-10 AI	3.0E-10 N36113.1	3.0E-10 AY005150.1	3.0E-10 AL	3.0E-10 AI	3.0E-10 N	3.0E-10 P2	
Expression Signal	3.5	1.21	2.7		-	0.46	2.18	7.27	2.5	1	1.51	1.89	1.89	1.17	0.74	1.31	3.73	25.71	0.49	0.89	3.55	4.72	1.04	1.04	1.24	2.52	3.43
ORF SEQ ID NO:	26327	28132		34518	34519	35373			28878	30269		35288	35289		25976	27446	28032	32831	35957	36208	26329		29864	29865		l	32007
Exon SEQ ID NO:			17423	21374	21374	22187	24503	13518		17659	19907	22114	22114		13348	14725	15294	19767	22743	22990	13663	14078	17234	17234	18169	18887	19032
Probe SEQ ID NO:	893	2684	4689	8682	8682	9534	11950	745	3468	4931	7222	9438	9436	109	287	1989	2580	7076	10095	10343	895	1329	4498	4498	5368	6110	6258

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PCT/US01/00667

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4108	16851	29477	6.1	1.0E-10	0 U62111.2	FN	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2*/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4108	16851	29478	5.1	1.0E-10	10 U52111.2	L Z	Homo saplens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2≁/CalmodulIn-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4113	16856	29484	1.94	1.0E-10	1.0E-10 AB031069.1	N	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4149	16891		1.84		1.0E-10 M30629.1	LN	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5085	17804		1.51	1.0E-10	1.0E-10 AI797745.1	EST_HUMAN	we82f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.t1 MER31 repetitive element;
6720	19635	32678	99'0	1.0E-10	0 AF003528.1	N TN	Homo sapiens X-linked anhidrolitc ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7375			0.65		0 P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7583	20251	33357	0.55		1.0E-10 AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8138		33966		1.0E-1	0 AW408990.1	EST_HUMAN	fB 6A4 Fetal brain library Homo sapiens cDNA
8553	21245		1.07	1.0E-10	1.0E-10 A[268340.1	EST_HUMAN	qm04s10.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874.3' similar to contains L1.t1 L1 repetitive element;
10102	22750		4.01	1.0E-10	AA081868.1	EST_HUMAN	zn23g06.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548314 5'
10831	23513	36754	2.65	1.0E-10	1.0E-10 Ai038280.1	EST_HUMAN	oy85h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
11896	17913		17.1	1.0E-10	1.0E-10 X87344.1	NT	H.sapiens DMA, DMB, HLA•Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
255	13063	25702	1.59	9.0E-11	1 BE145600.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2097	14828	27561	6.12		9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: htbr1) Homo sapiens cDNA clone DKFZp547D225 5'
2097	1	27562			9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'
3378		28795			9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'
3378		28796	2.45	9.0E-1	1 AL 134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'
4465					1 AA775985.1	EST_HUMAN	ae78f01.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5487			3.83		9.0E-11 BE079780.1	EST_HUMAN	RC8-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
10054	22702				9.0E-11 AA324960.1	EST HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10054			ļ	9.0E-1	1 AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12258			3.9	9.0E-1	1 C16635.1	EST_HUMAN	C16635 Clontech human sorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-508B08 5'
3114	15879		8.33	8.0E-11	8.0E-11 H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element ;

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Top Hit Descriptor	Im54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'	yw48e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE;255298 3'	xf45h11.x1 NCI_CGAP_Bm50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.t1	MER10 repetitive element;	EST34392 Embryo, 6 week I Homo saplens cDNA 5' end	Homo sepiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE)	Human matrix Gla protein (MGP) gene, complete cds	Human matrix Gla protein (MGP) gene, complete cds	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G8PD) gene, complete ods's	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	AV727859 HTC Homo sapiens cDNA clone HTCASC06 5'	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C083	Homo sapiens chromosome 21 segment HS21C083	ALDEHYDE OXIDASE	Homo sapiens chromosome 21 segment HS21C013	Homo saplens protocadherin beta 3 (PCDHB3), mRNA	zu01b12,r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 5'	Homo sapiens chromosome 21 segment HS21C047	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2	zv59f10.r1 Soares, lestis, NHT Homo sapiens cDNA clone IMAGE:757963 5' similar to TR:G1055250 G1055250 PHEROMONE RECEPTOR VN4.;	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	RC1-HT0256-210100-013-108 HT0256 Homo sapiens cDNA	t82g12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP.ZK353.1 CE00385;
Top Hit Database Source	Г	EST_HUMAN \			EST_HUMAN E	노			±N ±N	Т	Ł	SWISSPROT	EST HUMAN A	Γ			ISSPROT	TN.			EST_HUMAN 6	₩ H	EST_HUMAN IF	Г		± 5	T HUMAN	
Top Hit Acession No.	8.0E-11 AH78617.1	N23712.1		8.0E-11 AW166158.1	AA330642.1	7.0E-11 AJ277546.2	7.0E-11 AF163864.1	! !	-	6.0E-11 M55270.1	-11 L44140.1	-11 P08547	-11 AV727859.1	6.0E-11 BE063509.1		33.2		5.0E-11 AL163213.2	11416799 NT	-11 AA436042.1	-11 BE885900.1	-11 AL163247.2	-11 D44666.1	-11 P20095	-11 AA442630.1	-11 AF224669.1		-11 AI609753.1
Most Similar (Top) Hit BLAST E Value	8.0E-11	8.0E-11		8.0E-11	7.0E-11	7.0E-11	7.0E-11	7.0E-11 P11369	6.0E-11	6.0E-11	6.0E-11	6.0E-11	6.0E-11	6.0E-11	5.0E-11	5.0E-11	5.0E-11 P48034	5.0E-11	5.0E-11	4.0E-11	4.0E-11	4.0E-11	4.0E-11	4.0E-11	4.0E-11	4.0E-11	4.0E-11	4.0E-11
Expression Signal	. 0.7	4.88		0.65	1.75	1.03	2.05	1.17	7.01	7.01	0.67	3.65	7.81	0.52	1.49	1.9	1.36	1.63	14.05	1.94	7.14	1.16	0.85	3.2	0.82	5.4	1.79	6.0
ORF SEQ ID NO:	29334				26862					25838	32398	33369	34095	35059		25451	29571	32187	33194		28238	28385	29939	32153	32686	_		35402
Exen SEQ ID NO:		16768		_	14177	16802	21089	77.122	13188	13188	19384	20261	20956	21892	12838	12838	16944			14127	15498	15735	17311	19153	19641	19958	21962	22215
Probe SEQ ID NO:	3945	4022		6574	1430	3852	9688	10129	403	403	6622	7583	8262	9213	11	3359	4203	6423	7430	1380	2793	2969	4576	6384	£069	7274	9295	9562

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Table 4
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. Top Hit Descriptor	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA	EST180120 Liver, hepatocellular carcinoma Homo saplens cDNA 5' end	qf36c04xf Soares_testis_NHT Homo sapiens cDNA clone IMAGE:17521023' similar to contains MER10.13	MER10 repetitive element;	yg43e12.r1 Soares infant brain 1NIB Homo sapiens cDNA done IMAGE:35144 5'	yg43e12.r1 Soares infant brain 1NIB Horno sapiens cDNA clone IMAGE:35144 5'	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3'beta (COR3'beta) genes, complete cds	Gallus gallus rho-globin, beta-H-globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein	COR3'beta (COR3'beta) genes, complete cds	qc51c10.x1 Soares_pregnant_uterus_NbHPU Homo saplens cDNA clone iMAGE:1713138 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);contains L1.t1 febetitive element:	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)	tm54c08 xt NCL CGAP Kid11 Homo saplens cDNA clone IMAGE-2161g36 3	POLYPEPTIDE N-ACETY GALACTOSAMINY LTRANSFERASE (PROTEIN-UDP	ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-11)	(All 12)	none separa Franco Cultillori ilaggie region, Gadenosire improspirate riyarorasa (FRII.) gene, exon o	KC3-B10310-170200-014-605 B10316 Homo sapiens CLINA	Homo sapiens chromosome 21 segment HS21C027	QV2-BT0258-281099-014-e01 BT0258 Homo sapiens cDNA	QV2-PT0073-280300-109-h08 PT0073 Homo sapiens cDNA	nc83h05.r1 NCI_CGAP_GC1 Homo sapiens cDNA done IMAGE:797433 5' similar to SW.PR16_YEAST P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16.;	7j97c03.x1 NCI_CGAP_GC6 Homo saplens cDNA clone IMAGE:3442565 3'	OLFACTORY RECEPTOR-LIKE PROTEIN COR6	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
Top Hit Database Source			EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	ż		LN	EST HIMAN	Т	L	Т	SWISSPROT		Т	HOMAN		EST_HUMAN (EST_HUMAN (EST_HUMAN		I LN	SWISSPROT		EST_HUMAN
Top Hit Acession No.	11545732 NT	TN 220075	11 AA309248.1		11 Al150502.1	11 R24807.1	11 R24807.1			11 1174321	11 8126371 1	T	1		11 010473		S.UE-II AFUZUSUS.I	T		11 BE062558.1	11 AW877806.1	11 AA581028.1	11 BF592945.1	11 P37072		Γ		٦
Most Similar (Top) Hit BLAST E Value	4.0E-11	3.0E-11	3.0E-11		2.0E-11	2.0E-11	2.0E-11	2.0E-11		2.0E-11	2 0E-11	2.0E-11	2 OF-11		20E-11	1 0	2.05-11	2.0E-11	2.0E-11/	2.0E-11	2.0E-11/	2.0E-11	2.0E-11	2.0E-11 F	2.0E-11	2.0E-11	2.0E-11 /	2.0E-11
Expression Signal	1.47	2.8	1.04		1.97	3.99	3.99	4.86		4.86	124	7.58	111		0.93		10.7	0.68	0.72	1.77	1.02	1.87	0.59	0.56	1.14	5.44	1.12	1.12
ORF SEQ ID NO:	31029	26908			26372	26580	26581	27042		27043	27048	28607	28730		28771	Į.					31785	31968						36278
Exon SEQ ID NO:	24830	14222	16984		13707	13916	13916	14354	1	14354	14359		18080		16118	1	Т	- (- 1	17609	18824	18992	ı	1	21811		ı	23059
Probe SEQ ID NO:	12462	1475	4243		940	1162	1162	1608		1608	1612	3191	3320		3358	3	8 3	440g	4587	4882	6044	6218	7095	7782	9123	10184	10413	10413

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11056	23726		1.48	2.0E-11	-11 AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo saplens cDNA clone IMAGE:471794 3'
11056			1.48	2.0E-11	-11 AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11090	23760	32035	1.57	2.0E-11	2.0E-11 AA261956.1	EST_HUMAN	zs18b04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685519 5'
12017			1.54	2.0E-11	-11 AA704195.1	EST_HUMAN	277e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12048			3.54	2.0E-11	-11 AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo saplens cDNA
12073		31123		2.0E-11	-11 BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-901 TN0140 Homo sapiens cDNA
12332	24748		2.67	2.0E-11	-11 D25217.2	F	Homo saplens mRNA for KIAA0027 protein, partial ods
12479	24840		3.14	2.0E-11	-11 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12781			3.37	2.0E-11	11417966 NT	۲	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
661		26078		1.0E-11	-11 AJ131016.1	N	Homo sapiens SQL gene locus
1195		26811	3.35	1.0E-11	-11 AL163279.2	F	Homo sapiens chromosome 21 segment HS21C079
1485	14232		2.36	1.0E-11	-11 AF119914.1	Į,	Homo saplens PRO3078 mRNA, complete cds
2030			1.13	1.0E-11	-11 P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2122	14853	27582	2.91	1.0E-11	-11 AF000573.1	۲	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
3490	16246		1.2	1.0E-11	-11 BE004315.1	EST_HUMAN	CM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5249	18055	30683	16.93	1.0E-11	-11 AL 163247.2	F	Homo saplens chromosome 21 segment HS21C047
							7p57d01,x1 NCi_CGAP_Pr28 Homo saplens cDNA clone IMAGE:3648945 3' similar to contains MER10,b3
5741	18533	31456		1.0E-11	-11 BF222646.1	EST_HUMAN	MER10 repetitive element :
8101		33926	3.15	1.0E-11	4885546 NT	NT	Homo saplens PHD finger protein 2 (PHF2) mRNA
8480	L	34317	5.44	1.0E-11	-11 R13174.1	EST_HUMAN	y73d08.r1 Soares infant brain 1NIB Homo saplens cDNA clone IMAGE:28166 5'
8946		34782	1.89	1.0E-11	-11 BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Homo saplens cDNA
8946				1.0E-11	.11 BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
11257				1.0E-11	-11 BF680078.1	EST_HUMAN	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
2695	22348	35542	1.07	9.0E-12		TN	Homo saplens chromosome 21 segment HS21C100
9697		35543	1.07	9.0E-12	.12 AL 163300.2	LΝ	Homo sapiens chromosome 21 segment HS21 C100
9237	1		66.0	8.0E-12	-12 BE074720.1	EST_HUMAN	IL 5-BT0678-130300-036-G12 BT0578 Homo sapiens cDNA
12125			16.8	8.0E-12	-12 AJ271736.1	ΙN	Homo saplens Xq pseudoautosomal region; segment 2/2
4613				7.0E-12	12 005904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11322	24013	37316		7.0E-12	-12 AA704735.1	EST_HUMAN	223g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE;451152.3'
3535	16291		0.71	6.0E-12	12 AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAW F06 5'
4314	17053	29678	8.52	6.0E-12	12 AA732516.1	EST HUMAN	nz88f11.s1 NCL_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element:
R.70F	10088	32054	22.0	2 TO 8		NT.	Homo seriene EDASB common fearlis radion diadensarine statements to trides (FUIT) sees
0290	1		7.70	0.05-12	1		notice september MASD continues trapher region, biademostric improspinate hydrolase (FILL) gene, exon 3

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	Т	$\overline{}$	Ť	_	Т	7	т	_	Т	_	Т.		Т	Т	т	T -	_	$\overline{}$	Т	Т	т-	Τ-	T.	т-		т-	_	,
Top Hit Descriptor	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds	od10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.t2 MER29 repetitive element:	EST04462 Fetal brain, Stratagene (cat#936206) Homo sabiens cDNA clone HFBDV33	1242b05.y1 NCI_CGAP_Bm52 Homo saplens cDNA clone IMAGE:2291217 5	Homo sapiens Xq pseudoautosomal region; segment 2/2	Homo sapiens chromosome 21 segment HS21C078	Homo saplens chromosome 21 segment HS21C078	EST386850 MAGE resequences, MAGN Homo sapiens cDNA	DKFZp434B1615_s1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434B1615 3'	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'	zf01g12.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA olone IMAGE:375718 3' sImilar to contains	L1.t3 L1 repetitive element ;	RC1-OT0086-220300-011-b07 OT0086 Homo sapiens cDNA	DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5	Homo sapiens Xq pseudoautosomal region; segment 1/2	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)	Homo saplens chromosome 21 segment HS21C103	Homo sapiens chromosome 21 segment HS21C102	Rattus norvegicus Deleted in colcorectal cancer (rat homotog) (Dcc), mRNA	274911.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'	274g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'	b28h05.x1 NC]_CGAP_Lu24 Homo saplens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.	nad21b03.x1 NC _CGAP_Lu24 Homo saplens cDNA clone IMAGE:3388077 3' similar to contains MER7.b2 MER7 repetitive element :	Homo seplens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene,	partial cds	Bos taurus Mtch2 mRNA for mitochandrial carrier homolog 2, complete cds	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	Homo saplens Bruton's tyrosine kinase (BTK), alpha-D-galectosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
Top Hit Database Source	FN	EST HUMAN	EST HUMAN	EST HUMAN	ΝT	LN	L	EST_HUMAN	EST_HUMAN	EST_HUMAN				Γ.	N	SWISSPROT	LN			1	EST_HUMAN	EST HUMAN	EST HUMAN		NT	LN⊥	Į.	TN
Top Hit Acession No.	6.0E-12 AF003249.1	6.0E-12 AA847898.1	T06573.1	5.0E-12 BE047779.1	5.0E-12 AJ271736.1	5.0E-12 AL163278.2	5.0E-12 AL163278.2	5.0E-12 AW974760.1	4L040739.1	5.0E-12 AL040739.1			-12 AW887037.1	-12 AL079581.1	-12 AJ271735.1	-12 P34982	33.2		6978754 NT	-12 AA700326.1	-12 AA700326.1	-12 AI689984.1	-12 BF445140.1			-12 AB042815.1	-12 AJ229043.1	-12 U78027.1
Most Similar (Top) Hit BLAST E Value	6.0E-12	6.0E-12	5.0E-12 T06573.1	5.0E-12	5.0E-12	5.0E-12	5.0E-12	5.0E-12	5.0E-12	5.0E-12		5.0E-12	5.0E-12	5.0E-12	5.0E-12	5.0E-12	5.0E-12	5.0E-12	5.0E-12	4.0E-12	4.0E-12	4.0E-12	4.0E-12		4.0E-12	4.0E-12	4.0E-12	4.0E-12
Expression Signal	1.04	1.67	3.52	1.61	5.03	6.41	6.41	11.33	0.94	1.16		1.33	0.55	0.54	2.93	0.96	4.45	0.76	0.44	4.2	4.03	0.8	0.72		3.2	0.87	4.2	2.76
ORF SEQ ID NO:	34723		26442	28801	29104					32439	0.00	33959			34847	35161		36120	36344	25686	25686	29940				34418	36954	
Exan SEQ ID NO:	21585	21949	13780	16144		18715			19424	19424	00000	20822	21258	21584	21696	21990	22823	22910	23114	13047	13047	17312	20190		20835	21279	23691	24774
Probe SEQ ID NO:	8894	9374	1020	3385	3713	5931	5931	පෙවෙ	6933	6942	00.70	8128	9266	8833	9006	9323	10175	10262	10468	237	238	4577	7519		8141	8587	11019	12375

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					· · ·	100 DE	Origin Lives Lypinessed in Diam
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
602	13380	26011	4.27	3.0E-12	3.0E-12 AW341683.1	EST_HUMAN	hd13d01.xi Soeres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.;
602	13380	26012	4.27	3.0E-12	-12 AW341683.1	EST_HUMAN	hd13d01.X1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.;
5084		30421	0.81	3.0E-12	3.0E-12 AL163268.2	Ν	Homo sapiens chromosome 21 segment HS21C068
5365	1		1.52	3.0E-12	3.0E-12 AF111168.2	NT	Homo sapiens serine paintitoy transferase, subunit II gene, complete cds; and unknown genes
7854			0.83	3.0E-12	3.0E-12 AW854328.1	EST_HUMAN	RC3-CT0255-031099-011-h02 CT0255 Homo sapiens cDNA
8273		34109		3.0E-12 035453	035453	SWISSPROT	SERINE PROTEASE HEPSIN
9004	1 1		0.52	3.0E-12 035453	035453	SWISSPROT	SERINE PROTEASE HEPSIN
10551	1 1	36483		3.0E-12	3.0E-12 U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10551	1 1			3.0E-12		LN	Human prostate specific antigen gene, 5' flanking region
1649	14395			2.0E-12		EST_HUMAN	LL5-UM0071-120400-065-a05 UM0071 Homo sapiens cDNA
4094		29462		2.0E-12		LΝ	Rat U3A small nuclear RNA
4094	16836	29463		2.0E-12		ΝΤ	Rat U3A small nuclear RNA
4387	17124		2.03	2.0E-12	2.0E-12 BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
4840	17570	30192		2.0E-12 O70306	070306	SWISSPROT	TBX16 PROTEIN (T-BOX PROTEIN 15)
4840	17570		1.18	2.0E-12 O70306	070306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
1	İ						RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
5169	-1	30491	0.77	2.0E-12 P11369	P11369	SWISSPROT	ENDONUCLEASE
6385	19154	١		2.0E-12	2.0E-12 AW971857.1	EST_HUMAN	ES I 383946 MAGE resequences, MAGL Homo sapiens cDNA
7075	- 1			2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bento S <i>care</i> s Homo sapiens cDNA clone HIBBA13 5' end
7244		33005	Ì	2.0E-12	2.0E-12 BE173035.1	EST HUMAN	MR0-HT0559-200400-015-e08 HT0559 Homo sapiens cDNA
7558	1		2.2	2.0E-12	11422229 NT	L'N	Homo sapiens Ao-like transposable element (ALTE), mRNA
9208			1.84	2.0E-12	2.0E-12 AF196864.1	LΝ	Homo saplens putative BPES syndrome breakpoint region protein gene, complete cds
9886	22535		11.12		BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo saplens cDNA
4042	BUCC	2070	70.0	0 TO C	200 12 12 12 12 2	TOT LEADING	9407f02.x1 Sogres_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1931835.3' similar to TR:Q13538
1000	1	L	20.0	20170	1	EG! TOWN	TOTAL OF THE TOTAL
7503	1		70.7	Z-120.2	l		ndilo sapiens dillomosane zi segmen nozinoos
12223	24680		2.5	2.0E-12	2.0E-12 11418248 NT	٦	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
Ç	9000	25570	ć	i c	A NEGEORGIA	HOTEL HOD	h/90a09.x1 NC_CGAP_GU1 Home sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11
2	1			1.05-12	1.0E-12 AWGZ/G/4.1	NEW TOUR	יאובראוס ושלומיות אינויים אינוים אינוים אינוים אינוים אינוים אינוים אינוים אינוים אינוים אינוים אינוים אינוים
1980	14716		1,39	1.0E-12	1.0E-12 AI871726.1	EST_HUMAN	wm51f07,x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element ;
3087	L	28476		1.0E-12	1	TN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds

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Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
15833	28477		1.0E-1		F	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
16805		2	1.0E-1	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
			1.0E-1		EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
18663		2.25	1.0E-1		TN	Homo sapiens ataxla telangiectasía (ATM) gene, complete cds
18732		1.93	1.0E-1	Q9Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
19206	32202		1.0E-		LΝ	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
19708	32764	2.07	1.0E-		NT	Hamo saplens putative BPES syndrome breakpoint region protein gene, complete cds
19741	32802	11.32	1.0E-	AI248533.1	EST_HUMAN	qh68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA done IMAGE:1849614.3' slimilar to gb:M19503 LiNE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.t1 MER10 repetitive element;
19741	32803		1.0E-	Al248533.1	EST HUMAN	qh66a04.X1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614.3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.t1 MER10 repetitive element;
21298	34442		1.0E-	AA782323.1	EST_HUMAN	ac26d05.s1 Stratagene overy (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
23834		1.72	1.0E-1	AW 468478.1	EST_HUMAN	he38f07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921317 3' similar to contains element LTR3 repetitive element;
24497	37809	4.54	1.0E-1	AW962164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Hamo sapiens cDNA
24637		1.52	1.0E		EST_HUMAN	wi33h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
25308		2.92	1.0E		NT	Homo sapiens chromosome 21 segment HS21C068
16371			9.0E-13		NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
16677	29320	0.96			INT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
22154		2.67			EST_HUMAN	za26b06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:293651 3'
13475		7.37	8.0E-13		NT	Homo sapiens prion protein (PrP) gene, complete cds
13475		7.37	8.0E-13		NT	Homo saplens prion protein (PrP) gene, complete cds
14569	27281	2.94	8.0E-13		LN	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naio) and survival motor neuron protein (smn) genes, complete cds
20706	33834			AI884398.1	EST HUMAN	wm31h09.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:24376013'
20708	33835	0.76	8.0E-1		EST_HUMAN	wm31h09.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437601 3'
22694		3.08			LΝ	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
100 100 100 100 100 100 100 100 100 100	Exon NO: 15833 15805 16805 18605 18732 18741 19741 19741 19741 19741 19776 13475 13475 13475 13475 13475 13475 13475	ğ _α	ORF SEQ Express ID NO: Sign 28477 28243 28243 28243 282803 32764 282803 32764 28123 26123 26123 26124 27281 33834 33835	ORF SEQ Expression (Top) H D NO: Signel Signel Value 28477 1.29 1.0E 29242 2.43 1.0E 29245 2.25 1.0E 32202 0.62 1.0E 32202 0.62 1.0E 32202 1.132 1.0E 32202 1.132 1.0E 32202 1.132 1.0E 32202 1.132 1.0E 32202 1.132 1.0E 32202 1.0E 32202 1.0E 32202 1.0E 32202 1.0E 32202	ORF SEQ Expression (Top) Hit Top Hit Acess Signal BLAST E No. 28477 1.29 1.0E-12 AP000891.1 29243 2.26.43 1.0E-12 AP132248.1 2.25 1.0E-12 AP132248.1 2.25 1.0E-12 AP132248.1 2.25 1.0E-12 AP132248.1 2.25 1.0E-12 AP132248.1 1.0E-12 AP132248.1 1.0E-12 AP132248.1 1.0E-12 AP132248.1 1.0E-12 AP132248.1 1.0E-12 AP132248.1 1.0E-12 AP132248.1 1.0E-12 AP132248.1 1.0E-12 AP132248.1 1.0E-12 AP132248.1 1.0E-12 AP132248.1 1.0E-12 AP132248.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13223.1 1.0E-12 AP13233.1 1.0E-13 AP132333.1 1.0E-13 AP132333.1 1.0E-13 AP132333.1 1 1.0E-13 AP132333.1 1.0E-13 AP132333.1 1.0E-13 AP132333.1 1.0E-13 AP132333.1 1.0E-13 AP1323333.1 1.0E-13 AP1323333.1 1.0E-13 AP1323333.1 1.0E-13 AP13233333333333333333333333333333333333	ORF SEQ Expression (Top) Hit Top Hit Acession Database Source Signel A-STE No. 28477 1.29 1.0E-12 AF000891.1 NT Source Source Source Source Source Source Source Value 28242 26.43 1.0E-12 AL132249.1 EST_HUMAN 22643 1.0E-12 AL132249.1 EST_HUMAN 32764 2.07 1.0E-12 AF196864.1 NT SOURCE

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Exon SEQ ID NO: 15092 15201 16945 16945 18251 18251 18251 20670 20670 20670 20670 23270 23270 23270 13996 15771 16771 16771 16036

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
3232			0.84	9.0E-14	9.0E-14 AA781159.1	EST_HUMAN	aj 24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232.3' similar to contains MER19.t1 MER19 repetitive element;
3778			6.85	9.0E-14	D14547.1	LZ.	Human DNA, SINE repetitive element
4707	17439		1.66	9.0E-14	9.0E-14 AJ002153.1	LZ	Saguinus cedipus gene for seminal vesicle secreted protein semenogelin i
3489	Щ		1.27	8.0E-14	8.0E-14 BE468263.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3213424 3'
3837			2.67	8.0E-14	8.0E-14 R76269.1	EST_HUMAN	y/2e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
9348	1	33539	15.04	8.0E-14	8.0E-14 X89211.1	LN	H.sapiens DNA for endogenous retroviral III/a element
9460			3.69	8.0E-14	8.0E-14 AA219316.1	EST_HUMAN	zq17c10,s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629970 3'
11410			1.72	8.0E-14	_	EST_HUMAN	QV2-BT0256-261099-014-a01 BT0258 Homo sapiens cDNA
12302	24727	31056	2.48	8.0E-14	8.0E-14 AI688118.1	EST_HUMAN	wc92h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3'
							xf67e10.x1 NCI_CGAP_Gat4 Homo sapiens cDNA done IMAGE:2823146 3' similar to contains MER10.t2
1625			4.77	7.0E-14	7.0E-14 AW151673.1	EST_HUMAN	MER10 repetitive element;
8818	21510		10.57	7.0E-14	7.0E-14 AL163285.2	ΙN	Homo sapiens chromosome 21 segment HS21C085
358	13156	25797	14.14	6.0E-14	6.0E-14 AF020503.1	Ę	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
0220		35570		8 OF 14	6 OE-14 AE030503 1	HV	Homo confere ED 838 common femilia racion, disdensarias triches holes holes (FUIT) and also
	1			1	1 000000		מינים מלומנים במינים מיניים במינים במינים מינים
9722	22373	35573	2.6	6.0E-14	6.0E-14 AF020503.1	NT	Homo sepiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
909	13382	28014	5,46	5.0E-14 Q63120	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MÜLTIDRÜG RESISTANCE. ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
	L						xb03b05.x1 NCI_CGAP_GU1 Homo saplens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1
4993	- 1		1.41	5.0E-14	5.0E-14 AW073791.1	EST_HUMAN	repetitive element;
5446		31133	5.77	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1101	15560		2.18	4.0E-14 P04928	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1870	14608	27319	5.9	4.0E-14	AJ007973.1	LN	Homo sapiens LGMD2B gene
3735	16488		0.87	4.0E-14	4.0E-14 AA046502.1	EST_HUMAN	zk87a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 51
				-			yy73c12.s1 Soares_multiple_sclerosis_ZNbHMSP Homo saplens cDNA clone IMAGE:279190 3' similar to
4269	17000	29630	1.05	4.0E-14	4.0E-14 N46328.1	EST_HUMAN	contains L1.t3 L1 repetitive element;
							H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14
7858	20553		0.59	4.0E-14	-14 X87344.1	Z	genes
12626	25414		7.02	4.0E-14	4.0E-14 AI886224.1	EST_HUMAN	wm08c03.x1 NCI_CGAP_Ut4 Homo saplens cDNA clone IMAGE:2435332.3' simiter to conteins Alu repetitive element;
930	1	26361	1.88	3.0E-14	3.0E-14 X95466.1	NT	R.narveglous mRNA for CPG2 protein

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Top Hit Descriptor	xxx45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE.2743343 3' similar to contains Alu repetitive element;contains element MER9 repetitive element;	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), mRNA	te91c12:x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE.	teg1c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.:	Homo sapiens chromosome 21 segment HS21C048	yy07b10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270523 5'	601511530F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3913087 5'	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;	Homo sapiens chromosome 21 segment HS21 C085	Homo sapiens Xq pseudoautosomal region; segment 2/2	Homo saplens Xq pseudoautosomal region; segment 2/2	Homo sapiens chromosome 21 segment HS21C103	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA	Нато sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA	Homo sapiens chromosome 21 segment HS21 C009	hv90g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element:	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA	ta78h01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.t3 L1	repeutive element;	Human beta globin region on chromosome 11	RC3-BN0072-240200-011-a06 BN0072 Horno sapiens cDNA	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11) mRNA	ZINC-FINGER PROTEIN NEURO-D4	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA	L2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA	wr59g10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;	AV741648 CB Hamo sapiens cDNA clone CBFBBF04 5'
Top Hit Database Source	EST_HUMAN		EST_HUMAN		1	EST_HUMAN	HUMAN	EST HUMAN	Т	FN	FZ		EST_HUMAN I		LNT	EST HUMAN	Т	Γ		HOMAN	┑	THUMAN		П	Г	EST_HUMAN I		1 1
Top Hit Acession No.	14 AW265354.1	3864	14 A1420786.1				4 BE888016.1	14 AW265354.1						7657529 NT	4 AL163209.2	2.0E-14 BE222432.1		2.0E-14 BF380661.1				14 BE000550.1	4585709 NT			4 BE158761.1	4 AI978795.1	
Most Simllar (Top) Hit BLAST E Value	3.0E-14	3.0€-14	3.0E-14	3.0E-14	3.0E-14	3.0E-14	3.0E-14	3.0E-14	3.0E-14	2.0E-14	2.0E-14	2.0E-14	2.0E-14		2.0E-1		2.0E-14	2.0E-14	77 20 0	2.0E-14	20E-14	2.0E-14	2.0E-14	2.0E-14 P56163	2.0E-14	2.0E-14	2.0E-14	2.0E-14
Expression Signal	0.92	0.97	1.49	1.49	0.62	0.87	1.28	7.19	1.68	3.71	3.71	9.05	1.49	2.15	1.19	1.14	0.95	0.8	6	0.92	3.42	0.91	0.62	1,25	22.12	22.12	0.57	0.53
ORF SEQ ID NO:			32411	32412		·	36840	30220			25812				27983	•		30950	900.40	31230	31342		32724	32945	33167	33168	35671	
Exan SEQ ID NO:	17597	17600	19397	19397	25099		23594	17597	25282	13168	13168	15548	15108	15185	15245	15256	l .	18236		İ	18429	19528	19677	19871	20084	20084	22468	1
Probe SEQ ID NO:	4870	4873	6635	6635	6744	8686	10914	11201	12539	381	381	674	2387	2467	2529	2542	2681	5437	000	200	5634	6784	6984	7185	7407	7407	9817	10317

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Probe SEQ ID NO:	_	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
10679	23370	36612	4.88	2.0E-14	14 AW139800.1	EST_HUMAN	UI-H-BI1-edw-e-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 31
170				TO C	A 00000014/A	144741.111 1-01	xc36f02.x1 NCI_CGAP_Co20 Homo saplens cDNA clone IMAGE:2586363 3' similar to contains MER1.t3
80		100/0		Z.UC-14	ANVOCAGO.	NEWOL CO	ואברו ופלפתונים
12536				2.0E-14	14 AF008191.1	Ļ	Homo saplens putative G6 protein (GR6) gene, complete cds
1045	13804		1.88	1.0E-14	14 AL163246.2	NT	Homo sapiens chromosome 21 segment HS210046
1385	14132		6.41	1.0E-14	14 AL163268.2	LN	Homo saplens chromosome 21 segment HS21C068
1385	14132			1.0E-14	14 AL163268.2	LN	Homo sapiens chromosome 21 segment HS21C068
	L						Homo saplens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase
1994			12.44	1.0E-14	14 L44140.1	LΝ	(G6PD) gene, complete cds's
2182		27643	4.55	1.0E-14	14 AL163303.2	LN	Homo sapiens chromosome 21 segment HS21C103
2409	15130			1.0E-14	14 AF001689.1	LΝ	Homo saplens ribosomal protein L23A (RPL23A) gene, complete cds
2945				1.0E-14	14 P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3165	1	[5.42	1.0E-14	14 BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3165	15928	28577	6.42	1.0E-14	14 BF33527.1	EST HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo saplens oDNA
3886	16616		1.67	1.0E-14	14 AA682994.1	EST_HUMAN	ae89c12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4440	17176	29802		1.0E-14	14 AW275852.1	EST_HUMAN	xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
							Bos faurus xenoblotic/medium-chain fatty acid: CoA ligase form XL-III mRNA, nuclear mRNA encoding
5719		31432	2.42	1.0E-14	14 AF126145.1	NT	mitochandrial protein, complete cds
9229	· '	32351	11.5	1.0E-14	11437150 NT	LN	Homo saplens prominin (mouse)-like 1 (PROML1), mRNA
9229				1.0E-14	11437150 NT	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
11818	15928	28576			14 BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo saplens cDNA
11818	15928			1.0E-14	14 BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-e09_1 CT0432 Homo sapiens cDNA
1570	14317	27002		9.0E-15	7427522 NT	LN	Homo saplens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
							Homo saplens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein,
							JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,
2170			1.43	9.0E-15	15/AF196779.1	NT	complete cds; and L-type calcium channel a>
7395	20074	33152	4.51	9.0E-15	15 P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
7915	20610		1.08	9.0E-15	15 BE903559.1	EST_HUMAN	601677750F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3960156 67
12718			2.36	9.0E-15		L	Homo saplens chromosome 21 segment HS21C047
2814	13253		0.91	8.0E-15	15 BE 261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo saplens cDNA clone IMAGE:3164023 5'
7081	19771	32836	1.14	7.0E-15	15 BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
10334	18666		3.07	7.0E-15	S AW241958.1	EST HUMAN	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR t2 THR repetitive element:
5 6		20400	200	2 10 0	Ī	100	Lama e saviene Xa ne cale and real saviene 20
0/8	-1	۱	600	0.05-10		N.	traine common the pocurioration is a first to the pocurioration of the p

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Top Hit Acession Top Hit Acession Database						5	gle Exori Pio	Single Exon Probes Expressed in Brain
18618 31549 1.02 6.0E-15 K73462.1 NT 1386 25834 6.63 5.0E-15 K73462.1 NT 15469 25834 6.63 5.0E-15 AL163208.2 NT 15469 28212 1.38 5.0E-15 AL163208.2 NT 16217 1.03 5.0E-15 AL163303.2 NT 12829 25442 2.85 4.0E-15 AL163303.2 NT 12829 25442 2.85 4.0E-15 AL163303.2 NT 20392 33505 3.08 4.0E-15 AL1330894.1 NT 20392 33506 3.08 4.0E-15 AL130894.1 NT 16633 3.2837 2.9 3.0E-15 AL30894.1 NT 17699 0.78 3.0E-15 AL30894.1 NT 18665 3.2836 3.08 4.0E-15 AL30894.1 NT 19665 3.2937 2.9 3.0E-15 AL30894.1 NT 22476 2.51 3.0E-15 AL20858.1 NT 23385 2.9 3.0E-15 AL2088.2 NT	Probe SEQ ID NO:		ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
18618 31550 1.02 6.0E-15 K73462.1 NT 13186 25834 6.63 5.0E-15 AL163208.2 NT 15469 28212 1.38 6.0E-15 AL73008.1 EST HUMAN 23269 2.4 5.0E-15 AV266817.1 EST HUMAN 23269 2.5 5.0E-15 AV266817.1 EST HUMAN 12822 25339 0.76 4.0E-15 AV266817.1 NT 20382 33506 3.0B 4.0E-15 AV26081.1 NT 20382 33506 3.0B 4.0E-15 AV30084.1 NT 20382 33506 3.0B 4.0E-15 AV30084.1 NT 16831 3.28 4.0E-15 AV30084.1 NT 17589 0.79 3.0E-15 AV30085.1 NT 19865 3.2937 2.9 3.0E-15 AV3085.1 NT 19865 3.2938 2.9 3.0E-15 AV3087214.1 EST HUMAN 23385 36625 2.47 3.0E-15 AV3087214.1 EST HUMAN 13062 25692 3.0E-15 AV223391.1 NT <td>5829</td> <td>ı</td> <td></td> <td></td> <td>6.0E-15</td> <td>X73462.1</td> <td>F</td> <td>O aries mRNA for hair keratin cystelne-rich protein</td>	5829	ı			6.0E-15	X73462.1	F	O aries mRNA for hair keratin cystelne-rich protein
13166 25834 6.63 5.0E-15 AL163208.2 NT 15469 28212 1.38 5.0E-15 AL163208.1 NT 16217 1.03 5.0E-15 AV73056.1 EST HUMAN 23289 2542 2.8 5.0E-15 AV73056.1 EST HUMAN 12829 25422 2.8 4.0E-15 AV73056.1 EST HUMAN 20392 33205 3.08 4.0E-15 AJ30894.1 NT 20392 33506 3.08 4.0E-15 AJ30894.1 NT 20392 33506 3.08 4.0E-15 AJ30894.1 NT 16833 7.06 3.0E-15 AJ30894.1 NT 17589 0.79 3.0E-15 AJ30894.1 NT 17895 3.2837 2.9 3.0E-15 AJ30894.1 NT 19855 3.2836 3.0E-15 AJ30894.1 NT 19859 2.29 3.0E-15 AJ30894.1 NT 19855 3.2837 2.51 3.0E-15 AR273391.1 NT 23385 3.2836 2.51 3.0E-15 AF223391.1 NT	5829				6.0E-15	X73462.1	LN	O aries mRNA for hair keratin cysteine-rich protein
15469 28212 1.38 5.0E-15 U91328.1 NT 16276 28212 1.38 5.0E-15 AW296817.1 EST_HUMAN 23269 25442 2.85 4.0E-15 AV730056.1 EST_HUMAN 12829 25442 2.85 4.0E-15 AV730056.1 EST_HUMAN 12829 33506 3.08 4.0E-15 AJ130894.1 NT NT 1589 0.79 3.0E-15 AJ130894.1 NT NT 1589 0.79 3.0E-15 AJ130894.1 NT NT 19855 32937 2.9 3.0E-15 AJ20894.1 NT NT 19855 32937 2.9 3.0E-15 AJ20896.1 NT NT 19855 32937 2.9 3.0E-15 AJ20896.1 NT NT 19855 32937 2.9 3.0E-15 AZ2885 NT EST_HUMAN 25056 1.35 3.0E-15 AZ2885.1 NT EST_HUMAN 13052 25692 3.6 2.0E-15 AZ23391.1 NT EST_HUMAN 13052 25692 3.6 2.0E-15 AZ23391.1 NT EST_HUMAN 13052 25699 3.99 2.0E-15 AZ23391.1 NT EST_HUMAN 16256 28910 0.71 2.0E-15 AZ23391.1 NT NT 16256 28911 0.71 2.0E-15 AZ23391.1 NT NT 16256 28911 0.71 2.0E-15 AZ23391.1 NT NT 16256 28911 0.71 2.0E-15 AZ23391.1 NT NT 16256 28911 0.71 2.0E-15 AZ23391.1 NT NT 16256 28911 0.71 2.0E-15 AZ23391.1 NT NT 16256 28911 0.71 2.0E-15 AZ23391.1 NT 16256 28911 0.71 2.0E-15 AZ23391.1 NT 16256 28911 0.71 2.0E-15 AZ23391.1 NT 16256 28911 0.71 2.0E-15 AZ23391.1 NT 16256 28911 0.71 2.0E-15 AZ23391.1 NT	401				5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
16277 1.03 5.0E-15 AW296817.1 EST_HUMAN 223269 25442 2.85 4.0E-15 AV730056.1 EST_HUMAN 12829 25442 2.85 4.0E-15 AL163303.2 NT 20392 33505 3.08 4.0E-15 AJ130894.1 NT 20392 33505 3.08 4.0E-15 AJ130894.1 NT 20392 33505 3.08 4.0E-15 AJ130894.1 NT 20392 33505 3.08 4.0E-15 AJ130894.1 NT 22476 22476 2.51 3.0E-15 AJ20898.1 NT 25956 3.2937 2.9 3.0E-15 AJ30898.1 NT 25056 1.35 3.0E-15 AJ30898.1 NT 25056 1.35 3.0E-15 AJ20393.1 NT 25056 1.35 3.0E-15 AJ20372 1.0885 3.0E-15 AJ207331.1 NT 25056 1.35 3.0E-15 AJ207331.1 NT 25056 1.35 3.0E-15 AJ207331.1 NT 25056 1.35 3.0E-15 AJ207331.1 NT 25056 1.35 3.0E-15 AJ207331.1 NT 25056 1.35 3.0E-15 AJ207331.1 NT 25056 1.35 3.0E-15 AJ207331.1 NT 25056 1.35 3.0E-15 AJ207331.1 NT 25056 1.35 3.0E-15 AJ207331.1 NT 25056 1.35 3.0E-15 AJ20331.1 NT 25056 1.35 3.99 2.0E-15 AJ203331.1 NT 16256 28911 0.77 2.0E-15 AJ203331.1 NT NT 16256 28911 0.77 2.0E-15 AJ203331.1 NT NT 16256 28911 0.77 2.0E-15 AJ203331.1 NT	2764		28212			U91328.1	I- N	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HIAAH) gene. RoRet gene and codium phosphate transporter (NDT3) was completed and
23269 2.4 5.0E-15 AV730056.1 EST_HUMAN 12829 25442 2.85 4.0E-15 AL163303.2 NT 19332 32339 0.76 4.0E-15 AL163303.2 NT 20392 33505 3.08 4.0E-15 AJ30894.1 NT 20392 33506 3.08 4.0E-15 AJ30894.1 NT 16533 7.06 3.0E-15 AJ30894.1 NT 17599 0.79 3.0E-15 P92485 SWISSPROT 19651 3.2937 2.9 3.0E-15 M27685.1 NT 19865 3.2937 2.9 3.0E-15 M27685.1 NT 22476 2.51 3.0E-15 M27685.1 NT 25365 2.547 3.0E-15 M27685.1 NT 2536 3.0E-15 M27685.1 NT 25376 1.35 3.0E-15 M27685.1 NT 2558 3.0E-15 M27688.1 NT 2578 3.0E-15 M2763391.1 NT 13157 25798 3.99 2.0E-15 M223391.1 NT 16256	3461			1.03	5.0E-15	AW296817.1		UI-H-BWO-alb-a-10-0-UI s1 NCI CGAP State Homo saniens cDNA chara NAACE 2734440 at
12829 25442 2.85 4.0E-15 AL168303.2 NT 19332 32339 0.76 4.0E-15 AB007970.1 NT 20392 33505 3.08 4.0E-15 AJ130894.1 NT 16933 7.06 3.0E-15 AJ130894.1 NT 17599 0.79 3.0E-15 AJ130894.1 NT 17599 0.79 3.0E-15 P92485 SWISSPROT 19651 1.33 3.0E-15 AJ30894.1 NT 19865 3.2937 2.9 3.0E-15 AJ30895.1 NT 22476 2.9 3.0E-15 MZ7685.1 NT 25365 2.9 3.0E-15 MZ7685.1 NT 25376 2.9 3.0E-15 MZ7685.1 NT 25385 2.9 3.0E-15 MZ7685.1 NT 25386 3.0E-15 MZ7685.1 NT 25316 1.81 3.0E-15 MZ7685.1 NT 25316 1.36 3.0E-15 AF223391.1 NT 13167 25798 3.96 2.0E-15 AF223391.1 NT 16256 28	10574	Ш		2.4	5.0E-15			AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
1932 32339 0.76 4.0E-16 AB007970.1 NT 20392 33505 3.08 4.0E-16 AJ30894.1 NT 16933 7.06 3.0E-15 AJ30894.1 NT 17599 0.79 3.0E-15 P92485 SWISSPROT 19651 3.2937 2.9 3.0E-15 M27685.1 NT 19865 3.2937 2.9 3.0E-15 M27685.1 NT 22476 2.51 3.0E-15 M27685.1 NT 23385 3.6625 2.47 3.0E-15 M27685.1 NT 25386 3.2938 2.9 3.0E-15 M27685.1 NT 25385 3.6625 2.47 3.0E-15 M27685.1 NT 25086 1.36 3.0E-15 M27685.1 NT 13052 25692 3.0E-15 AR23391.1 NT 13157 25798 3.9 2.0E-15 AF223391.1 NT 16256 28910 0.71 2.0E-15 AF223391.1 NT 16256 28911 0.71 2.0E-15 AF223391.1 NT	418				4.0E-15			Homo sapiens chromosome 21 segment HS21C103
20392 33506 3.08 4.0E-15 AJ30894.1 NT 20392 33506 3.08 4.0E-15 AJ30894.1 NT 16933 7.06 3.0E-15 NB9452.1 EST HUMAN 17599 0.79 3.0E-15 NB9452.1 EST HUMAN 19865 3.2937 2.9 3.0E-15 MZ7685.1 NT 19865 3.2937 2.9 3.0E-15 MZ7685.1 NT 23385 3.6625 2.47 3.0E-15 MZ7685.1 NT 25386 2.51 3.0E-15 MZ7685.1 NT 25386 2.54 3.0E-15 MZ7685.1 NT 25386 2.47 3.0E-15 MZ7685.1 NT 25386 1.31 3.0E-15 MZ7685.1 NT 13052 2.5692 3.0E-15 AF223391.1 NT 13157 25798 3.9 2.0E-15 AF223391.1 NT 16256 28910 0.71 2.0E-15 AF223391.1 NT 16256 28911 0.71 2.0E-15 AF223391.1 NT	6567				4.0E-15		LN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
20392 33506 3.08 4.0E-15 AJ30894.1 NT 16933 7.06 3.0E-15 NB9452.1 EST_HUMAN 17599 0.79 3.0E-15 P92485 SWISSPROT 19631 1.33 3.0E-15 D92485 SWISSPROT 19855 3.2937 2.9 3.0E-15 M27685.1 NT 19865 3.2938 2.9 3.0E-15 M27685.1 NT 22476 2.51 3.0E-15 M27685.1 NT 25385 36625 2.47 3.0E-15 AA807128.1 EST_HUMAN 25386 3.6625 2.47 3.0E-15 AA807128.1 NT 25086 1.36 3.0E-15 AA807128.1 NT 13052 2.5692 3.0E-15 AA807128.1 NT 13157 25798 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.77 2.0E-15 AF223391.1 NT 16256 28911 0.71 2.0E-15 AF223391.1 NT	10994		33505		4.0E-15		TN	Homo sapiens mRNA for transcription factor
16933 7.06 3.0E-15 N89452.1 EST_HUMAN 17599 0.79 3.0E-15 P92485 SWISSPROT 19631 1.33 3.0E-15 Q64625 SWISSPROT 19865 3.2937 2.9 3.0E-15 M27685.1 NT 19865 3.2937 2.9 3.0E-15 M27685.1 NT 22476 2.51 3.0E-15 M27685.1 NT 25385 3.6625 2.47 3.0E-15 A2608.1 NT 25066 1.81 3.0E-15 A271735.1 NT 13052 25692 3.0E-15 A223391.1 NT 13157 25798 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.77 2.0E-15 AF223391.1 NT 16256 28911 0.71 2.0E-15 AF223391.1 NT	10994		33506		4.0E-15		LN	Homo saplens mRNA for transcription factor
17599 0.79 3.0E-15 P92485 SWISSPROT 19631 1.33 3.0E-15 Q64625 SWISSPROT 19655 32937 2.9 3.0E-15 M27685.1 NT 19865 32937 2.9 3.0E-15 M27685.1 NT 22476 2.9 3.0E-15 M27685.1 NT 23385 36625 2.47 3.0E-15 M27685.1 NT 25056 2.47 3.0E-15 A807128.1 EST_HUMAN 25056 1.81 3.0E-15 A802898.1 NT 25056 1.36 3.0E-16 ANWITZ14.1 EST_HUMAN 13052 25692 3.6 2.0E-16 AF223391.1 NT 13157 25798 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.71 2.0E-15 AF223391.1 NT 16256 28911 0.71 2.0E-15 AF223391.1 NT	4192			7.06	3.0E-15	N89452 1	HEST HIMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo saplens cDNA clone LY1142 5' similar to ANFICARDIODII ATIN
19631 1.33 3.0E-15 G64625 SWISSPROT 19865 32937 2.9 3.0E-15 M27685.1 NT 19865 32937 2.9 3.0E-15 M27685.1 NT 22476 2.51 3.0E-15 M27685.1 NT 23385 36625 2.47 3.0E-15 M27685.1 NT 25016 1.81 3.0E-15 M27688.1 NT 25056 1.81 3.0E-15 AB026898.1 NT 25056 1.36 3.0E-15 AB026898.1 NT 13052 25692 3.0E-15 AV877214.1 EST_HUMAN 13052 25692 3.6 2.0E-15 AF223391.1 NT 13157 25798 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.71 2.0E-15 AF223391.1 NT 16256 28911 0.71 2.0E-15 AF223391.1 NT	4872	l		0.79	3.0E-15		SWISSPROT	NADH-UBIOUINONE OXIDOREDUCTASE CHAIN 5
19865 32937 2.9 3.0E-15 M27885.1 NT 19865 32938 2.9 3.0E-15 M27885.1 NT 22476 2.51 3.0E-15 M27885.1 NT 23385 36625 2.47 3.0E-15 A807128.1 EST_HUMAN 25056 1.81 3.0E-15 AB028898.1 NT 25056 1.36 3.0E-15 AB028898.1 NT 13052 25692 3.0E-15 AA271735.1 NT 13157 25798 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.771 2.0E-15 AF223391.1 NT 16256 28911 0.771 2.0E-15 AF223391.1 NT	6716			1.33	3.0E-15		SWISSPROT	GLUTATHIONE PEROXIDASE RYZD1 PRECURSOR (ODORANT-METARO) IZING PROTEIN PYSO1
19865 32938 2.9 3.0E-15 MZ7685.1 NT 22476 2.51 3.0E-15 A807128.1 EST_HUMAN 23385 38625 2.47 3.0E-15 A8026898.1 NT 25056 1.81 3.0E-15 AB026898.1 NT 25056 1.36 3.0E-15 AB026898.1 NT 13052 25692 3.6 2.0E-15 AF223391.1 NT 13157 25798 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.771 2.0E-15 AF223391.1 NT 16256 28911 0.771 2.0E-15 AF223391.1 NT	7179			2.9	3.0E-15		LN	Mus musculus ultra high sulfur keratin gene, complete cds
22476 2.51 3.0E-15 AA807128.1 EST_HUMAN 23385 36625 2.47 3.0E-15 AB026898.1 NT 25316 1.81 3.0E-15 AB026898.1 NT 25056 1.35 3.0E-15 AB0271735.1 NT 13052 25692 3.6 2.0E-15 AF223391.1 NT 13157 25798 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.771 2.0E-15 AF223391.1 NT 16256 28911 0.771 2.0E-15 AF223391.1 NT	7179		32938	2.9	3.0E-15		LN	Mus musculus ultra high sulfur Keratin gene, complete cds
23385 36625 2.47 3.0E-16 AB026898.1 NT 25316 1.81 3.0E-16 AJ271735.1 NT 25056 1.35 3.0E-16 AJ271735.1 NT 13052 25692 3.6 2.0E-15 AF223391.1 NT 13157 25798 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.71 2.0E-15 AF223391.1 NT 16256 28911 0.71 2.0E-15 AF223391.1 NT	9825			2.51	•		EST HUMAN	oc36e07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.t1 MER19 repetitive element:
25316 181 3.0E-15 AJ271735.1 NT 25056 1.35 3.0E-15 AW877214.1 EST_HUMAN 13052 25692 3.6 2.0E-15 AF223391.1 NT 13157 25798 3.99 2.0E-15 AF223391.1 NT 13157 25799 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.71 2.0E-15 AF223391.1 NT	10694				3.0E-15		Į.	Hamo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
25056 1.35 3.0E-15 AW877214.1 EST_HUMAN 13052 25692 3.6 2.0E-15 AF223391.1 NT 13157 25788 3.99 2.0E-15 AF223391.1 NT 13167 25789 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.71 2.0E-15 AF223391.1 NT 16256 28911 0.71 2.0E-15 AF223391.1 NT	12310			1.81	3.0E-15,	Γ	LN L	Homo sapiens Xq pseudoautosomal region: segment 1/2
13157 25788 3.99 2.0E-15 AF223391.1 NT 13157 25789 3.99 2.0E-15 AF223391.1 NT 13157 25789 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.71 2.0E-15 AF223391.1 NT	12814			1.35	3.0E-15		EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo saplens cDNA
13157 25788 3.99 2.0E-15 AF223391.1 NT 13157 25789 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.71 2.0E-15 AF223391.1 NT 16256 28911 0.71 2.0E-15 AF223391.1 NT	243	13052	25692	3.6			TN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
13157 25799 3.99 2.0E-15 AF223391.1 NT 16256 28910 0.71 2.0E-15 AF223391.1 NT 16256 28911 0.71 2.0E-15 AF223391.1 NT	359		25798	3.99			LN L	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
16256 28910 0.71 2.0E-15 AF223391.1 NT 16256 28911 0.71 2.0E-15 AF223391.1 NT	359	13157	25799	3.99		!		Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
18256 28911 0.71 2.0E-15 AF223391.1 NT	3500		28910	0.71			Į.	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
	3500	- 1	28911	0.71				Homo sapiens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	. Top Hit Descriptor
4049	16794	29423	1.08	20E-15	5 AW 238499.1	EST_HUMAN	xp28h01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMACE:2741521 3' similar to contains L1.t3 L1 repetitive element;
4580	17315		2.46	2.0E-15	5 Al806335.1	EST_HUMAN	wf07f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q81043 Q61043 NINEIN ;
6089			0.88	2.0E-15	5 BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877288 5'
6809	18867	31834	0.88	2.0E-15	15 BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Hamo sapiens cDNA clone IMAGE:3877288 5'
7014	19706		1.5	2.0E	AJ400877.1	TN	Homo saplens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7171	19857	32929	2.62	2.0E-15	-15 AA704195.1	EST_HUMAN	277e03.s1 Soares_fetal_liver_splean_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7294	19977	33054	5.18	2.0E-15	5 W05064.1	EST_HUMAN	za78d10.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:298675 5' sImilar to WP:F44F4'8 CE02227 TRANSPOSASE :
8804	21496	34642	2.86	2.0E-15	I5 D14547.1	LN LN	Human DNA, SINE repetitive element
8971	21661		1	2.0E-15	5 AA397758.1	EST_HUMAN	zt77g08.r1 Soares_testis_NHT Hamo saplens cDNA clone IMAGE;728414 5
8971	21661	34812	1	2.0E-15	5 AA397758.1	EST_HUMAN	zt77g08.r1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:728414 5'
9304	21971	35145	1.23	2.0E-15	2.0E-15 AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
9304	21971	35146	1.23	2.0E-15	5 AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
10742	23429		5.56	2.0E-15	5 AJ271735.1	LN	Homo sapiens Xq pseudoautosomal region; segment 1/2
12451	25338		2.04	2.0E-15	5 U82828.1	ΝΤ	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12653	16256	28910	3.34	2.0E-15	5 AF223391.1	-N	Homo seplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12853	16256	28911	3 34	2 OF-15	5 AE223301 1	FIX	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively
							bz8h05xt NCI_CGAP_Lu24 Hamo saplens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539
2777	15482		2.39	1.0E-15	5 AI689984.1	EST_HUMAN	MARINER TRANSPOSASE.;
3011	15777	28427	1.35	1.0E-15	5 BE043584.1		hk40e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2899162 51
3139	15903	28548	1.29	1.0E-15	5 P08547	Г	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5138	17856		0.97	1.0E-15	5 AW021431.1	EST_HUMAN	df23e06.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:24842025
							ye40e10.s1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains
6279	19052	32030	1.74	1.0E-15	5 T95763.1		MER6 repetitive element;
6069	19647		2.12	1.0E-15	5 BE074217.1	r HUMAN	QV3-BT0569-270100-074-g05 BT0569 Homo saplens cDNA
8131	20825	33961	0.86	1.0E-15	5 AL163280.2		Homo saplens chromosome 21 segment HS21C080
8319	21012	34149	4.56	1.0E-15			qf88h08.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1755227 3'
8319	21012	34150	4.56	1.0E-15		EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8937	21628	34770	0.67	1.0E-15	5 AL163207.2	Ę	Hamo saplans chromosame 21 segment HS21 C007

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Top Hit Descriptor	Homo sapiens spermidine synthase (SRM) mRNA	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM	oh37c03.s1 NCI_CGAP_Kid6 Homo saplens cDNA clone IMAGE:1459972 3' similar to contains L1.t3 L1	repetitive eteriterit,	Homo sapiens major nistocompatibility tocus class III region	tr31c05.x1 NCI_CGAP_Ov23 Homo saplens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive element;	Homo saplens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05	qi78a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element;	qi78a02x1 NCI_CGAP_Kid3 Homo saplens cDNA clone IMAGE:18653543' similar to contains MER10.t3	MER10 repetitive element;	Homo saplens chemokine (C-C motif) receptor 8 (CCR8) mRNA	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)	ye28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119082 5	EST384702 MAGE resequences, MAGL Homo saplens cDNA	Mus musculus offactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene	ot80c04.s1 Soares_total_fetus_Nb2HF8_9w Home sapiens cDNA clone IMAGE:1623078 3' similar to	contains element L1 repetitive element ;	Homo sapiens chromosome 21 segment HS21C046	601885734F1 NIH_MGC_57 Homo saplens cDNA clone IMAGE:4104129 5'	Homo saplens GTP binding protein 1 (GTPBP1), mRNA	Homo saplens gene for TMEM1 and PWP2, complete and partial cds	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA	Homo saplens chromosome 21 segment HS21C084
Top Hit Database Source	L	SWISSPROT	Π	HOMAN	N	EST_HUMAN	۲	EST_HUMAN	EST HUMAN	1	EST_HUMAN	NT		SWISSPROT	SWISSPROT	EST_HUMAN	П	۲Z		EST_HUMAN		EST_HUMAN	N	NT	EST_HUMAN	EST_HUMAN	SWISSPROT		T HUMAN	NT
Top Hit Acession No.	4507208 NT	15 Q39575	, 020,000	13 AA804033.1	15 AF044083.1	15 AI783944.1	4503168 NT	16 F08688.1	16 A1244341.1		16 A1244341.1	4885120 NT	,	16 088807	16 088807	18 194149.1	16 AW972611.1	16 AJ251154.1		16 AA992176.1	16 AL163246.2	16 BF217368.1	11418127 NT	18 AB001523.1	16 AW797168.1	68.1	16 Q16653	16 BE083875.1	IS BE083875.1	16 AL163284.2
Most Similar (Top) Hit BLAST E Value	1.0E-15	1.0E-15	L	1.0E-10	1.0E-15	1.0E-15	9.0E-16	9.0E-16	9.0E-16		9.0E-16	7.0E-16		7.0E-16	7.05-16	7.0E-18	6.0E-16	5.0E-16		5.0E-18	5.0E-16	5.0E-16	5.0E-16	4.0E-18	4.0E-18	4.0E-16	4.0E-16	4.0E-16	4.0E-18	4.0E-16
Expression Signal	1.78	0.87	3	300	3.6	4.72	86.0	2.04	1.46		1.46	0.71		1.49	1.49	1.98	8.38	1.08		2.17	0.54	3.6	14.19	1.81	1.77	1.77	3.58	5.02	5.02	46.62
ORF SEQ ID NO:	34774	35042			36651	30896	29830	36841	37615		37618	31324		33001	33002			26909		28134	35806	37418			27839		28856		29490	33386
Exon SEQ ID NO:	21631	i	l	_ { .	23409	25148	17204	23595	24291	1	24291	18411	l	19926	19926	25237	L	14223		15396	22602		25018	14961	15100	ı	16206			20278
Probe SEQ ID NO:	8940	9146		3037	10720	12722	4469	10915	11696		11696	5615		7241	7241	12675	2137	1476		2687	9954	11504	12757	2233	2378	2378	3450	4121	4121	7612

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9195	21865			4.0E-16	11423191 NT	LN	Homo saplens hypothetical protein FLJ10024 (FLJ10024), mRNA
11182	23847	37133		4.0E-16	-16 AV730030.1	EST_HUMAN	AV730030 HTF Homo saplens cDNA clone HTFAWA03 5
11851	24435	37778	1.44	4.0E-16	-16 Q62632	SWISSPROT	POLLISTATIN-RELATED PROTEIN PRECURSOR
12014	Ш		2.04		4.0E-16 P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12109	24605			4.0E-16	2456	ΕZ	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
130		25589	2.03	3.0E-16		EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
130				3.0E-16		EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5
453	13239		1.5	3.0E		EST_HUMAN	DKFZp434P037_r1 434 (synonym: htes3) Homo saplens cDNA clone DKFZp434P037 5'
463	13248		1.5	3.0E	-16 AF135446.1	Į,	Homo saplens TSX (TSX) pseudogene, exon 5
1435	14182	29867	1.38	3.0E-16	-16 Q 28983	SWISSPROT	ZONADHESIN PRECURSOR
200	i	00000		0	500000	7000001110	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN
2013	16663	20204	3.70	30.0 FOR	-10 PU3200	SWISSTROID	ESTD8060 Infant Brain Bento Scares Homo sablens cDNA clone HIRBA13 6' end
2000	ļ		000				Human BYBOO Care
3838	_1		0.85	3.05		L	Human bAP-20 gene
2186			0.99	3.0E-16	-16 AA077225.1	EST HOMAN	/b10F02 Chromosome / Feta Brain cDNA Library Homo sapiers cDNA clone /B10F02
9928	18327	31230	1.79	3.0E-16	-16 AF003529.1	LN	Homo saplens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
				-			am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains
8556	. I	34387	4.26	3.0E-16	-16 Al002836.1	EST_HUMAN	THR.b2 THR repetitive element;
9790			0.89	3.0E-16	-16 BF690617.1	EST_HUMAN	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10019		35883	5.57	3.0E-16	-16 L78810.1	LN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, сотпрієtе cds
951	13717		1.2	2.0E-16		LN	Homo sapiens chromosome 21 segment HS21C079
2385	15106		0.91	2.0E-16	-16 AA621761.1	EST_HUMAN	af06d04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2694	15403		1.06	2.0E-16	-16 J03061.1	Į.	Human SSAV-related endogenous retroviral LTR-like element
4157	16897	29526	1.16	2.0E-16	-16 X89211.1	NT	H.saplens DNA for endogenous retrovinal like element
							qg56f03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839197 3' similar to contains MER29.t3
4447				2.0E	-16 AI208733.1	EST_HUMAN	MER29 repetitive element ;
5104	17822			2.0E	-16 BE061178.1	EST_HUMAN	RC3-BT0046-131199-003-H12 BT0046 Homo seplens cDNA
6842	19404	32419	66.0	2.0E	-16 Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
							116e11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
7615	20281	33389	0.75	2.0E-16	-16 AI470723.1	EST_HUMAN	MER33 repetitive element ;
							nz47f06.x5 NCI_CGAP_Pr12 Homo saplens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849
7867	- 1	_ [20E	-16 AI732837.1	EST_HUMAN	HYPOTHETICAL 42.9 KD PROTEIN. [2] TR: 008905 ; contains MER7.t1 MER7 repetitive element ;
8028	20752	33883	0.57	2.0E-16	-16 BE858026.1	EST_HUMAN	7f82h09x1 NCI_CGAP_Pr28 Home sapiens cDNA clone IMAGE:3303521 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8058			0.57	2.0E-16	16 BE858026.1	EST_HUMAN	782h09x1 NCL CGAP_Pr28 Homo sapiens cDNA done IMAGE:3303521 3'
8425	21118	34256	0.81	2.0E-16	16 AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo saplens cDNA
8425	21118	34257	0.81	2.0E-16	16 AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
180	12992	25630	1.84	1.0E-16	16 AF200719.1	닐	Homo saplens pituitary tumor transforming gene protein (PTTG) gene, complete cds
373	13198		29.68	1.0E-16	16 AA628592.1	EST HUMAN	er39g11.s1 Soares_total_fetus_Nb2HFB_sw Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.t2 OFR repetitive element:
1963	14699	27414	2.37	1.0E-16	16 BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5635	18430		0.75	1.0E-16	16 AF163864.1	F	Homo saplens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6341	19111		27.85	1.0E-18	16 U45983.1	N	Homo saplens COR8 chemokine receptor (CMKBR8) gene, complete cds
6479	19246	32246	3.39	1.0E-16	16 Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7453	19111		7.15	1.0E-16	16 U45983.1	LN L	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
9183	21853	35018	1.07	1.0E-18	16 AW875651.1	EST HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo saplens cDNA
3722	16475	29112	2.11	9.0E-17	17 AW900048.1	EST_HUMAN	CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
6624	19386		2.2	9.0E-17	17 Al392964 1	EST HUMAN	1922c11x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28:12 MER28 repositive element:
							xg49g12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE.2830950 3' similar to contains OFR t2 OFR
8007	20702		4.75	9.0E-17	17 AW150257.1	EST_HUMAN	repotitive element;
10124	22772		2.47	9.0E-17	17 AF200719.1	LN	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
997	13757		1.77	8.0E-17	17 AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3872	16622		0.87	8.0E-17	17 AL163280.2	N	Homo sapiens chromosome 21 segment HS21C080
5498	25069	31193	3.7	8.0E-17	17 BE172081.1	EST_HUMAN	MR0-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7175	19861		1.94	8.0E-17	17 AV730759.1	EST HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1441	14188		3.44	7.0E-17	LN 2608929	LN	Mus musculus apolipoprofein B editing complex 2 (Apobec2), mRNA
5240	18046		3.3	7.0E-17	17 AF216650.1	LN	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6588	10351	37365	α α	7 05 47	7 A F020843 4	LN	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane
3	1,000	2000	33	יובקייי	T	- N	Contacted for against (CFTN) gains, section 1 of 2 of the complete cds, and unknown gene
3		20002	2	6.0E-17	17 AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo capiens cDNA
6221	18995	31971	1.64	6.0E-17	17 AW662772.1	EST_HUMAN	hi81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.22 L1 repetitive element ;
10190	22838	36053	0.46	6.0E-17	17 P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
412	12823	25436	2.97	5.0E-17			yc05h08.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
7486	20158	33250	2.09	5.0E-17	17 T81043.1	EST_HUMAN	yd26b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327.5'

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Table 4
Single Exon Probes Expressed in Brain

15153 15154 2.21 2.0E-17 028983 SWISSPROT 15167 28343 6.64 2.0E-17 M27685.1 NT 18097 30746 1.88 2.0E-17 M27685.1 NT
18948 2.04 2.0E-
19167 1.16 2.0E-17/AL134881.1 EST_HUMAN
338021 112
2067/ 33802 1.12 2.0E-17 Q95156 SWISSPROI

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Table 4
Single Exon Probes Expressed in Brain

	i			Most Similar			
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal		Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8356	1		1	2.0E-17	17 AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
9769		35628		2.0E-17	17 BE299888.1	EST_HUMAN	600944690F1 NIH_MCC_17 Homo sapiens cDNA clone IMAGE:2960615 5'
9804	. 1		3.22	2.0E-17	17 AL 163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9804		35658		2.0E-17	17 AL163247.2	N	Homo sapiens chromosome 21 segment HS21C047
10159	22807	38025	4.82	2.0E-17	17 D13391.1	LN	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10278	22926				17 P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10278	22926		0.73	2.0E-17	17 P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
3307	22954		0.49	2.0E-17	17 AI798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2348719 3'
10307	22954			2.0E-17	17 Al798902.1	EST_HUMAN	we94b04.x1 Scares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE;2348719 3'
733	13507	26164		1.0E-17	17 P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1703	14446				17 AJ271736.1	LN	Homo sapiens Xq pseudoautosomal region; segment 2/2
761	14503		2.73	1.0E-17	17 AL163207.2	L	Homo sapiens chromosome 21 segment HS21 C007
2109	14840	27571			17 P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
335	15059		2.06	1.0E-17	17 U79410.1	LN	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3554	16309		6	1.05-17	17 AF224669 1	1	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) nenes complete cds
4116	16858		7.37			T HUMAN	y80e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'
							he38e05.x1 NCI_CGAP_CML1 Homo sepiens cDNA clone IMAGE:2921312.3' similar to contains Alu
9366	19136		0.69		-		repetitive element;contains LTR8.t1 LTR8 repetitive element;
200	19320			1.0E-17			qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
9555	19320		2.04	1.0E-17	2.1	EST_HUMAN	qe55b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:17438253'
8	19682			1.0E-17			URIDINE PHOSPHORYLASE (UDRPASE)
8490	21182			1.0E-17	17 BE062744.1		QV0-BT0263-101299-072-d07 BT0263 Homo sapiens cDNA
8	22556			1.0E-17	17 AW996538.1	EST_HUMAN	QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA
11394	24000	37304	2.09	1.0E-17	17 Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
11732	24325	37649	2.47	1.0E-17	17 AA453647.1	EST HUMAN	2x48f05.s1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:7954893' similar to TR:G1263081 G1283081 MARINER TRANSPOSASE
2474	15192			9.0E-18	18 AA174078.1	EST HUMAN	2p18g12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3'
8686	22060		3.31	9.0E-18		Г	ti86d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2148389 3'
3766	16518	29156	1.62	8.0E-18	4758977 NT		Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
339	13140	25776	16.92	7.0E-18	8 AW316976.1	EST HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Home sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
١							

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						-:	
Probe SEQ (D NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
339	13140	25777	16.92	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
7343	L	33100	1.33	7.0E-18	AW887542.1	EST HUMAN	RC3-OT0091-170300-011-d03 OT0091 Homo saplens cDNA
12492	13140	25776	3.41	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
12492						EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Home sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3289	16050			6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived nexin/protease nexin I, enhancer region
4698			3.02		P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8148	L		284	6.0E-18	11428155 NT	FZ	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8246	1	34077		6.0E-18	AL1632	LN-	Homo sapiens chromosome 21 segment HS21 C010
11079	23749			6.0E-18	AL163246.2	LN	Homo saplens chromosome 21 segment HS21C046
41300	l	37260	1 74		X87344 1	FZ	H.sapiens DWA, DWB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 denss
12241	L			6.0E-18		NT	Human aconitate hydratase (ACO2) gene, exon 4
1125	1	١			Ai280214.1	EST_HUMAN	qm65g11x1 Soares_placenta_8tp9weeks_2NbHP8tb9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element.
5047	l			5.0E-18	D61517.1	EST_HUMAN	HUM411F05B Ciontech human fetal brein polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-411F05 S
5191	1			5.0E-18	AF087913.1	LN LN	Human endogenous retrovirus HERV-P-T47D
8820	1		5.25	5.0E-18	BE143312.1	EST_HUMAN	MR0-HT0161-221099-002-c06 HT0161 Homo saplens cDNA
10899	23579				10242378 NT	LN L	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
10899	23579	ĺ	3.47		10242378 NT	닐	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12368	1		3.4	5.0E-18	AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo saplens cDNA
12895	١.		4.18		AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'
121	L.	25580	1.37	4.0E-18	BE044076.1	EST_HUMAN	ho36h04.x1 NCI_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
121	<u>L</u>	١.		L	BE044076.1	EST_HUMAN	ho38h04.x1 NCLCGAP_Ut1 Homo sepiens cDNA clone IMAGE:3039511.3' similar to contains MER29.b3 MER29 repetitive element;
1711	1.		1.19	4.0E-18	AA621814.1	EST_HUMAN	nq24f11.s1 NCI_CGAP_CG10 Homo sepiens oDNA clone INAGE:1144845 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1882	1			4.0E-18	AI738592.1	EST_HUMAN	w/33h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2198	14927	27662	1.33	4.0E-	18 006430	SWISSPROT	N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N- ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) /IGNT)
2198	14927	27863	1.33	4.0E-	18 006430	SWISSPROT	N-AGETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (N-ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING EN YME) (1901)
3772		29162	0.68	4.0E-	18 Al581586.1	EST HUMAN	er93b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alurebetiline element:
5279	1 1			4.0E	18 A/017565.1	EST HUMAN	ou23e06.x1 Soares NFL T GBC S1 Homo saplens cDNA clone IMAGE-1627138.3"
5279			2.24	4.0E-	18 AI017565.1	EST_HUMAN	ou23e08.x1 Soares_NPL_T_GBC_S1 Homo septens cDNA clone IMAGE:1627138.3'
7745	20441		0.63	4.0E-	18 AA746811.1	EST_HUMAN	nx64a08.s1 NCI_CGAP_AIv1 Homo sapiens cDNA clone IMAGE:1266998 similar to contains L1.t2 L1 repetitive element;
10927	23607	36858	8.76	4.0E-1	B AA371807.1	EST_HUMAN	EST88633 Pituitary gland, subtracted (protactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
829		26270	1.68	3.0E-18	8 AA814196.1	EST_HUMAN	ob23h11.s1 NCI_CGAP_Kid5 Homo saplens cDNA clone IMAGE:1324581 3' similer to SW:RS5_HUMAN P46782 40S RIBOSOMAL PROTEIN S5.:
606			3.47	3.0E-18	8 BE088634.1	EST HUMAN	CM0-BT0690-210300-298-q07 BT0690 Homo sapiens cDNA
3931				3.0E-18	I8 AL 163247.2	N	Homo sapiens chromosome 21 segment HS21C047
6730				3.0E-18		EST_HUMAN	PM0-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
10844	23526			3.0E-18		Г	601884858F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 57
12497			6.14	3.0E-18	18 AW022015.1	HUMAN	d/31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
244	١,	25693	4.42	2.0E-18	8 AW836820.1	EST_HUMAN	QV1-LT0036-150200-070-e07 LT0036 Homo saplens cDNA
1130	13886		62.93	2.0E-18	I 8 BE 256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3355044 5'
5326	18129		3.19	2.0E-18	8 AA868610.1	EST_HUMAN	ak63a07.s1 Soares_lestis_NHT Homo saplens cDNA clone IMAGE:1409652 3' similar to TR:014577 014577 BAC CLONE RG114A06 FROM 7031. COMPLETE SEQUENCE
5419	- 1		3.68	2.0E-18		NT	Human DNA, SINE repetitive element
5419	- 1	30928	3.68	2.0E-1	8 D14547.1	TN	Human DNA, SINE repetitive element
5788	- 1		1.68	2.0E-1	8 BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4156670 5
8073	18852			2.0E-1		LN FN	Human IFNAR gene for Interferon alpha/beta receptor
6073		31818		2.0E-18		N _T	Human IFNAR gene for interferon alpha/beta receptor
6185	18962		1.04	2.0E-18	8 BF352940.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
6226	19000	31977	5.18	2.0E-18	8 AW665853.1	EST_HUMAN	hi94g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984.3' similar to contains MER19.t2 MER19 repetitive element;
7336		33096	0.81	2.0E-18	8 AA457619.1	EST HUMAN	aa89d11.r1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:838485 5' similar to TR:G61634 G61634 POLYPEPTIDE PR77
8047	20741		0.47	2.0E-18		Т	HTM1-160F1 HTM1 Home sapiens cDNA
					l	Ŧ	

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Top Hit Descriptor	xf67e10.x1 NCL CGAP. Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element ;	x/67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element;	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2876499 3' similar to contains THR.b3 THR repetitive element ;	xg47e09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element;	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 6' similar to contains L1 repetitive element	AV653405 GLC Homo sapiens cDNA clone GLCDKE11 3'	Homo saplens mRNA for Na,K-ATPase alpha-subunit, complete cds	Homo sepiens mRNA for Na,K-ATPase alphe-subunit, complete cds	Hamo sapiens chromosome 21 segment HS21C080	oz69409.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone iMAGE:1680593 3' similar to contains L1.t1 L1 repetitive element;	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gane, and sodium phosphate transporter (NPT3) gene, complete cds	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element;	211d06.r1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MFR19 condition element:	HSC23F051 normalized infant brain cDNA Homo sabiens cDNA clone c-23f05	Homo saciens chromosome 21 segment HS21C003	Homo saplens chromosome 21 segment HS21C003	Homo sapiens mRNA for KIAA1143 protein, partial cds	zd1406.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element:	EST387007 MAGE resequences, MAGN Homo saplens cDNA	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	MR0-HT0404-210200-001-g06 HT0404 Homo sapiens cDNA
Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	Γ	EST HUMAN	Г	П	١	LZ	EST_HUMAN		LN	EST_HUMAN	HIMAN	Т	Т		LN	EST HUMAN	Т	П	EST_HUMAN
Top Hit Acession No.	-18 AW151673.1	18 AW 151673.1	18 AW470791.1	-18 AW 151299.1	-18 BE256097.1	-18 T95406.1	-18 AV653405.1	1.0E-18 D00099.1	-18 D00099.1	1.0E-18 AL163280.2	-18 AI148288.1	.18 U91328.1	1.0E-18 AF003529.1	-19 AA281961.1	10 4 5 28 1061 1	19 F08688.1	19 At 163203.2	19 AL 163203.2	19 AB032969.1	.19 AA281961.1	8.0E-19 AW974902.1	19 P08548	19 BE158936.1
Most Similar (Top) Hit BLAST E Value	2.0E-18	2.0E-18	2.0E-18	2.0E-18	2.0E-18	1.0E-18	1.0E-18	1.0E-18	1.0E-18	1.0E-18	1.0E-18	1.0E-18	1.0E-18	9.0E-19	0.05_40	9 OF-19	9.0E-19	9.0E-19	9.0E-19	9.0E-19	8.0E-19	8.0E-19	8.0E-19
Expression Signal	1.66	1.66	2	3.91	1.45	1.02	3.63	2.94	2.94	1.53	1.43	4.22	4.23	5.34	40.6	4 47	2.54	2.54	4.82	1.88	1.25	1.04	0.92
ORF SEQ ID NO:	35798	35799	36824	37653			30707	31180	31181	32128	34171	35653	31092	25952	25052		34419	34420				П	33874
Exan SEQ ID NO:	22595	22595	23574	24329	l	17119	18077	18282	18282	19133	21034	22450	1	13316	13318	20443		1	ı	13316	1	ı	20742
Probe SEQ IO NO:	9947	8947	10894	11736	12174	4382	5271	5483	5483	6363	8341	9789	12130	532	533	7747	8588	8688	11072	11901	1026	4372	8048

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2242	14970	27708	1.51	7.0E-19	4758139 NT	۲	Homo saplens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helinase 54kh) vintxs mpNa
6364		32129	2.34	7.0E-19	-19 AF092090.1	NT.	Rattus nonegicus cp151 mRNA, partial cds
7199	19885		6.0	7.0E-19	-19 P26444	SWISSPROT	BETA CRYSTALLIN A2
9911		35756	0.51	7.0E-19	19 Al344951.1	EST_HUMAN	tb01c08.x1 NCI_CGAP_Lu26 Homo saplens cDNA clone IMAGE:2052302.3'
12036			2.05	7.0E-19	·19 AA705684.1	EST_HUMAN	260b01.s1 Soares fetal liver spleen 1NFLS S1 Homo saplens cDNA clone IMAGE 435145 31
3761			1.34	6.0E-19	-19 AW852930.1	EST HUMAN	PM0-CT0248-131099-001-g01 CT0248 Homo saplens cDNA
4430		29795	1.36	6.0E-19	19 P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4430			1.36	6.0E-19	19 P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4747			1.3	6.0E-19	19 AJ271735.1	L	Homo sapiens Xq pseudoautosomal region: segment 1/2
4967	17692	30301	1.04	6.0E-19	19 AL120817.1	EST_HUMAN	DKFZp762F192_r1 762 (synonym: hmel2) Homo saplens cDNA clone DKFZp762F192 5'
5767	18558	31485	5.36	5.0E-19	19 000193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
10324	22971	36191	1.03	5.0E-19	19 AJ297699.1	IN	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11526	24125	37431	7.45	5.0E-19	19 AW183725.1	EST HUMAN	x/87b02.x1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2684171 3' similar to contains element MSR1 repetitive element:
541		25956	1.68	4.0E-19	19 AB007970.1	N-I	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2689	15398		1.02	4.0E-19	19 BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4287674 5
F344	107		0	10.	, 000, 000	1	Homo saplens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
360	1		78.0 78.0	4.0E-18	19 AF 224669.1	Z	(UBEZU3) genes, complete cds
3	-	81282	1.04	3.0E-19	19 028997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3833		29220	1.04	3.0E-19	19 0 28897	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4253	_ 1		0.99	3.0E-19	19 043900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4253		29623	0.99	3.0E-19	19 043900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4413		29777	1.12	3.0E-19	19 AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5
5198	18006		0.64	3.0E-19	19 AF223467.1	TN	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
, 7283	19966		2.79	3.0E-19	11432214 NT	LΝ	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9329		33548	1.15	3.0E-19	19 X89685.1	NT.	M.musculus mRNA for TPCR33 protein
12264	24709		23.34	3.0E-19	19 AF165520.1	TN	Homo sapiens phorbolin I protein (PBI) mRNA, complete cds
2565	15279	28017	21.33	2.0E-19	19 AL163201.2	L	Homo sapiens chromosome 21 segment HS21C001
4411	17148		1.03	2.0E-19	19 Al311783.1	EST HUMAN	qo91e02x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POL/ENV GENE ;
5963	18745	31706	0.57	2.0E-19	19 AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5"

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Тор Hit Descriptor
7238	19923	32998	0.93	2.0E-19	7657286 NT	LN	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8228	ı			2.0E-19	19 AA012854.1	EST_HUMAN	ze34c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
6086	i		0.68	2.0E-19	19 095155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
11828	I		1.33	2.0E-19	19 BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-f04 BT0333 Homo saplens cDNA
11829	l		1.33	2.0E-19	19 BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-f04 BT0333 Homo saplens cDNA
469			1.87	1.0E-19	1.0E-19 BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
							yo79g07.r1 Soares adult brain N2b4HB55Y Homo septens cDNA clone IMAGE:184188 5' similar to contains
2161		27626		1.0E-19	19 H30795.1	EST_HUMAN	MER10 repetitive element;
2723	15430		2.37	1.0E-19	19 D38044.1	ΝΤ	Human gene for Ah-receptor, exon 7-9
2851	15619		4.95	1.0E-19	TN 288574	TN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
000				70,		1407 E G L	aj49b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.2. MED37 constitue clonest:
DASS SASS	1			1.0E-19	-	ביין	MENO) repetitive destructs,
5983	18764	31/28	2.38	1.0E-19	19 012186.1	Z	Oryciolagus cuniculus socium/dicarpoxylate coudinsporter micryt, partial cos
						1	nh22d03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE;953093 similar to contains L1.t1 L1
6114	25419		25.02	1.0E	19 AA5955Z/.1	ES L FICIMAIN	ובספתוואם בומווסור
7528	20199		0.86	1.0E-	19 U08813.1	LN	Oryctolagus cuniculus Na≁/glucose cotransporter-related protein mRNA, complete cds
7528	20199	33294		1.0E	19 U08813.1	LN⊤	Oryctolagus cuniculus Na+/glucose cofransporter-related protein mRNA, complete cds
7695	25118		0.93	1.0E-19	19 AF200719.1	TN	Homo sapiens pitultary tumor transforming gene protein (PTTG) gene, complete cds
8349	21042	34179	1.75	1.0E-19	19 M64657.1	L	Rabbit phosphorylase kinase beta subunit mRNA, complete ods
		١.					ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains
8640			2.64	1.0E-19	19 T99920.1	EST_HUMAN	OFR repetitive element;
9849	22301		0.48	1.0E-19	19 U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10087	22735	35950	23.03	1.0E-19	19 AW812259.1	EST_HUMAN	RC0-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA
10097	22745	35960		1.0E-19	19 N44631.1	EST_HUMAN	yy31e09.r1 Soares melancoyis 2NbHM Homo sapiens cDNA clone IMAGE:272872 5'
							Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1
11760	24351	37683	1.55	1.0E-19	19 U93163.1	LN	(MAGE-B1) genes, complete cds
6949	19314	32319	2.58	8.0E-20	7657286 NT	LN	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6249				8.0E-20	7657286 NT	LΝ	Mus musculus keratin-associated protein 8-1 (Krtap9-1), mRNA
7418	<u>L</u>		1.34	8.0E-20	-20 AI221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7418	20095		1.34	8.0E-20	-20 A1221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3270	16031	28682	1.41	7.0E-20	.20 BF326455.1	EST_HUMAN	PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA
9689	17972			7.0E-20	-20 AL138120.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: hfbr1) Homo sepiens cDNA clone DKFZp547D092 5'
						HOL	n/46c04.s1 NCI_CGAP_Pr4 Homo septens cDNA clone IMAGE:1043718 similar to contains MER29.b2
8394	21087	34222	12.48). U	-ZU AA35/65/.1	מאוסט"ו פש	ווובוזכם וקבמות אם מפורבות י

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Single Exon Probes Expressed in Brain	Top Hit Acession Top Hit Descriptor No. Source	nl46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 7.0E-20 AA557657.1 EST_HUMAN MER29 repetitive element:	6912633 NT	SWISSPROT	34.1 EST_HUMAN	AV725123.1 EST_HUMAN AV725123 HTC Homo sapiens cDNA clone HTCBTA01 5	EST HUMAN	2h78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;	TST HIMAN	1 EST HUMAN	IN	LN	SWISSPROT		SWISSPROT	A1874352.1 EST_HUMAN 1264g03.x1 NCI_CGAP_Ov35 Homo saplens cDNA clone IMAGE:2293396 31	EST_HUMAN QV3-DT0043-090200-080-c04 DT0043 Homo saplens cDNA	TN	P23273 SWISSPROT OLFACTORY RECEPTOR-LIKE PROTEIN 114	H	3.0E-201A403701.1 EST FUNIAN CARRENTS ELIS ET PEPUNG SINE PEPUNG S	14 FST HIMAN	SWISSPROT	EST_HUMAN	gj70d02x1 NCLCGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive	EST HIMAN	EST_HUMAN	1
	Most Similar (Top) Hit BLAST E Value	7.0E-20 AA6	7.0E-20	6.0E-20 P39188	6.0E-20 BE	5.0E-20 AV7	5.0E-20 AFC	6.0E-20 W90525.1	5 0F-20 W90525 1	5.0E-20 BE1	5.0E-20 ABC	6.0E-20 AB028174.1	5.0E-20 O60809	4.0E-20 AL1	4.0E-20 Q99880	4.0E-20 AI874352.1	4.0E-20 AW	3.0E-20 U03888.1	3.0E-20 P23273	20 10 0	3.0E-20 AA03/616	3 0E-20 BF185264 1	3 0E-20 P11369	3.0E-20 AI284244.1	2 05 30 4 284244	3.0E-20 AIZ	2.0E-20 AW	
	Expression ('Signal B	12.48	1.95	3.52	3.33	1.18	1.07	6.28	5.28	0.7	2.54	2.54	0.94	1.34	8.0	5.15	1.33	1.02	1.29	200	7.05	0 63	1.87	1.5	4	2.65	3.12	
ŀ	ORF SEQ ID NO:	34223		28949	29605	_	32763	33668	33669	33825	34572	34573		27054			36259	27595	29557	,,,	73244	36078		37408	97400	31118		
	SEQ ID NO:	21087	24308	16298	16980	17291	19707	20541	20541	20697	21426	21426	20416		18359	20521	23042	14865	16926	20027	24525	22867	23257	24097	24007	24569	13582	
	Probe SEQ ID NO:	8394	11714	3543	4239	4556	7015	7846	7848	8002	8734	8734	9345	1616	5562	7826	10396	2135	4185	0007	4502	10219	10561	11496	11,408	12051	811	

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Probe		ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit	Islan Top Hit
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	SEO SO O	Ö Q	Signal	BLAST E Value	o Z	Source	i op mit Descriptor
1089	13847	28505	3.37	2.0E-20	2.0E-20 AA516335.1	EST_HUMAN	ng89h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224069 ORF2: FUNCTION UNKNOWN.;
900					2 0F-20 AA518335 1	EST HUMAN	ng89h09.s1 NCI_CGAP_LIp2 Homo sapiens cDNA clone IMAGE:940097 similer to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN. ;
2820	J					EST HUMAN	x24e10.x1 NCI_CGAP_Ut4 Homo septiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN SS.;
4883	L	30238	4.97		2.0E-20 Q28983	SWISSPROT	ZÖNADHESIN PRECURSOR
4893	17620					SWISSPROT	ZONADHESIN PRECURSOR
5067					5174538 NT	TN	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
8017	20712	33843	0.81		7.1	EST HUMAN	EST180328 Liver III Homo sapiens cDNA 5' end
9089	1					NT	Homo sapiens RGH1 gene, retrovirus-lika element
6806	ı	34943	8.8			LN	Homo sapiens RGH1 gene, retrovirus-like element
12426	ł				2.0E-20 H55371.1	EST_HUMAN	CHR220310 Chromosome 22 exan Homo sapiens cDNA clone C22_391 5'
12815			1.39	L	11437152 NT	TN	Homo sapiens heparin-binding growth factor binding protein (HBP17), mRNA
	l						z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2
2007	15525	27468	3.71		1.0E-20 AA281961.1	EST_HUMAN	MER19 repetitive element ;
	l						hr84b08.x1 NCI_CGAP_Kld11 Hamo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.t2 L1
4406	17143	29772	<u>-</u>	1.0E-20	1.0E-20 BF115158.1		repetitive element ;
6794	19538	32566	0.75		1.0E-20 AF049567.1	EST_HUMAN	AF048567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
9061	Į		2.04		11418491 NT	FZ	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
	L						Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively
11541	24141	37450	2.62		1.0E-20 AF223391.1	LN	spliced
							nc60g08.r1 NCL_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.t3 L1
12171	24651		1.73		1.0E-20 AA420453.1	EST_HUMAN	repetitive element :
2913	15679		0.98		9.0E-21 AJ003514.1	EST_HUMAN	AJ003514 Selected chramosome 21 cDNA library Homo sapiens cDNA clone MPIp112-8J21
11804	24469		2.62		AW898189.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
0711	<u> </u>		л. c		8 0E-21 AW674891 1	EST HUMAN	bb30a02.71 NIH_MGC_10 Home sapiens cDNA clone IMAGE:2984714 5' similar te SW:NIAM_HUMAN 095169 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR ;
11.00	L	27.700			A A BODA11 1	ENT HIMAN	ob7100 s1 NCI CGAP GCB1 Home sertiens cDNA clone IMAGE:1336835 3'
1000	L				0 OE 24 C2430	TORRESIME	ATP SYNTHASE A CHAIN (PROTEIN 6)
20021	L				D15800	TOGENIA	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
1007	- }	1	70.1		1,000	TOUR DE LA COMP	AMININ BETA 2 CHAIN DESCRIPTION (I AMININ CHAIN RS)
2061	ı				F15800	SWISSPRO	DAWNING DELATE CITATIVE CITATIVE CANONICATIVE
3689	- 1	29083			7.0E-21 AL163300.2	I N	ndrio septera un università dell'accionatora della consiste della MANDE AGREGIE.
4228	16969		5.58		7.0E-21 AA046502.1	ES - HOMAIN	CASTROOT I SOMES DIRECT LINETICS INDITION SQUEETS COLAN CIONE INTOCE ASSOCIATION OF THE COLON OF

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Probe SEQ (D NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Açesslon No.	Top Hit Database Source	Top Hit Descriptor
6340	19110	32100	0.79	7.0E-21	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
8287		34121	1.53	7.0E-	21 AJ277557.1	Ę	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxymibonucleotidase (dNT-2 gene), exons 1-5
8576		34407	10.76	7.0E-	21 D14718.1	FN	Human chromosomal protein HMG1 related gene
10013	1		0.86	7.0E-	21 AW856922.1	EST_HUMAN	RC0-CT0301-271199-031-F03 CT0301 Homo sapiens cDNA
10594	23288	36525	2.19	7.0E-	21 AA723404.1	EST HUMAN	zg73d03.s1 Soares_fetal_heart_NbHH19W Homo sepiens cDNA clone IMAGE:398981 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.t3 OFR repetitive element :
11234	23897	37184	1.75	7.0E-	7706668 NT	N ₁	Homo saplens PTD013 protein (PTD013), mRNA
4083	16827	29454	0.83	6.0E-21	21 BE408611.1	EST HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5
9034	21724			6.0E-	21 BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
903	13670	26334		5.0E-21	5902031 NT	N	Homo saplens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4330		29697	,	5.0E-	BE968839.1	EST_HUMAN	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMACE:3833880 5'
4749	17481	30112	5.56	5.0E-21	4885474	N	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
6665	19582		0.9	5.0E-	21 AW440864.1	EST_HUMAN	he05e10.x1 NCI_CGAP_CML1 Homo saplens cDNA clone IMAGE:2318154 3'
6917	19654	32700	0.86	5.0E-21	BF856505 1	FST HIMAN	7/83411.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3303573.3' similar to contains OFR.t1 OFR repetitive element
10474	23120		4.0	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLH (GLH)
10474	1	36350	0.44	5.0E-21	091690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
11986			2.83	5.0E-21	5.0E-21 AA393574.1	EST_HUMAN	zf72c04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5
1727	14469	27168	1.81	4.0E-21	AA970713.1	EST HUMAN	0086608.s1 NCI_CGAP_Kid5 Homo saplens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;contains OFR.t1 OFR repetitive element;
6772	19516	32544	3.27	4.0E-21	4.0E-21 AB019576.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
9680	22332	35527	0.63	4.0E-21		NŤ	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9705	22356	35552	0.7	4.0E-21		Z-N	Homo saplens chromosome 21 segment HS21 C002
1829	14568		0.94			HUMAN	zq15d06.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:6297713'
2272	14998	27736	1.24				Homo sapiens chromosome 21 segment HS21C001
3078	15843	28485	4.31		3.0E-21 AJ007973.1	TN	Homo sapiens LGMD2B gene
5412	18211	30919	0.68	3.0E-21	3.0E-21 AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonuclectidase (dNT-2 gene), exons 1-5
5412	18211	30920	0.68	3.0E-21	3.0E-21 AJ277557.1	ΤN	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyrlbonucleotidase (dNT-2 gene), exons 1-5

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					Š	מום באחוו ליו	Single Explication of the state
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ (D NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
5652	18447		0.65	3.0E-21	21 AV661044.1	EST_HUMAN	AV661044 GLC Homo sapiens cDNA clone GLCGOA10 3'
9809	18864		2.3	3.0E-21		EST_HUMAN	601844465F1 NIH_MGC_54 Homo sepiens cDNA clone IMAGE:4064945 5'
6969	19451	32469	7.69	3.0E-21	21 BF361093.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
9592	22245	35429	1.15	3.0E-21	_	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
12533	L	l	2.88	3.0E-21	21 AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
141	L.		17.18	2.0E-21	21 BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
914			1.85	2.0E-21	21 AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
914	13681	26343	1.85	2.0E-21	21 AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1192	13944				21 BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
2644	15354	28098	1.98	2.0E-21	21 028983	SWISSPROT	ZONADHESIN PRECURSOR
2844	15354	28099	1.98	2.0E-21	21 028983	SWISSPROT	ZONADHESIN PRECURSOR
				100			ts30f03.x1 NO_CCAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR.Q99854 Q99854
5396	- 1	ŀ		2.0E-21		ES TOWAN	TITOTHE ICAL SIT NO PROTEIN;
5489	1			2.0E-21		EST_HUMAN	ze97a12.r1 Soares_fetal_heart_NbHH19W Home sapiens cDNA clone IMAGE:366910 5/
5489	18288		0.68	2.0E-21	21 AA027211.1	EST_HUMAN	ze97a12.r1 Soares_fetal_heart_NbHH19W Home sapiens cDNA clone IMAGE:366910 5
8170	20864	33996	9.0	2.0E-21	21 AJ010770.1	LN	Homo sapiens hyperion gene, exons 1-50
8261	20955	34094	6.16	2.0E-21	21 BE141785.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
8722	21414	34557	3.74	2.0E-21	21 AU136779.1	EST_HUMAN	AU136779 PLACE1 Homo sepiens cDNA clone PLACE1005052 5'
							ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
10991			1.55	2.0E-21	21 BE350127.1	EST HUMAN	MER29 repetitive element ;
11289			1.3	2.0E-21	21 BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo saplens cDNA clone IMAGE:3951008 5'
11289	23950	37247	1.3	2.0E-21	21 BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
12272	24712		28.6	2.0E-21	21 AF176815.1	LN	Hono sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
							n46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA done IMAGE:1043718 similar to contains MER29.b2
1233		26652	1.6	1.0E-		EST_HUMAN	MER29 repetitive element ;
1381	14128		2.62	1.0E-21		EST_HUMAN	ar88d12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE::2152343 3'
9629	19165		2.74	1.0E-21	21 AL079752.1	EST_HUMAN	DKFZp434l0830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434l0830 5'
	l						qg47e05x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1838338 3' similar to gb:M64241 QM
7092	19781	32847	6.6	1.0E-21	AI223104	EST_HUMAN	PROTEIN (HUMAN);
10484	23130		1.07	1.0E-21	5730038 NT	L	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
4377	47414	17/200	20.00	9 OF-22	22 AI702438 1	FST HUMAN	t294a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE;2296204 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT :
8502	П			9 0F-22	22 Al 163201 2	L	Homo saplens chromosome 21 segment HS21C001
2000	1			0 OF 22	22 AI 183201 2	LN	Homo seplens chromosome 21 segment HS21C001
2000	ı			0.00	711000011		

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Top Hit Descriptor	AV781874 MDS Homo septens cDNA clone MDSCCG05 5'	AU140358 PLACE2 Homo saniens cDNA clone PLACE2nnn394 5	CM0-HT0179-281099-076-h05 HT0179 Homo saniens cDNA	2k67a08.r1 Soares pregnant uterus NhHPLI Home saniens CONA clone IMAGE: 497959 5'	Homo saplens chromosome 21 segment HS21C048	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)	Homo sabiens gene for activin receptor the IIB, complete cds	Homo sapiens HSPC220 mRNA, complete ads	EST00738 Fetal brain, Stratagene (cattl936206) Homo saniens cDNA clone HERCE07	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	Zu65d10.r1 Soares, testis NHT Homo sapiens cDNA clone IMAGE 742867 5	wx05g07.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE-2542812.3	Homo saplens chromosome 21 segment HS21C103	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds	naa27b06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Atu	Homo saniens Xii bsa idoa ifosomal rodion: sommat 472	AV703223 ADB Home seniens cDNA clane ADRAI IE12 5	Homo sapiens chromosome 21 segment HS21Cn02	601882813F1 NIH MGC 57 Home saniens cDNA clone IMAGE:4005424 F	Homo sapiens chromosome 21 segment HS210009	tm14h10.x1 NCI_CGAP_C014 Homo saplens cDNA clone INAGE:2156611 3' similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN):contains 1.1 transfitting along to	wi68b04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN	Himan chromosomal protein LWC4 related accept	2/2007 V. Scarge, precipant inferire NAHDI Home analyses CON Alexa 1110 C. 2007 C.	ontains MER12.t2 MER12 repetitive element:	QV0-HT0368-090200-099-f12 HT0368 Homo sapiens cDNA	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA	R. rattus RY2G5 mRNA for a potential ligand-binding protein	R.rattus RY2G5 mRNA for a potential ligand-binding protein	yx73d05.s1 Soares melanocyte ZNbHM Homo sapiens cDNA clone IMAGE 267369.3'	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
Top Hit Database Source	EST HUMAN	Г		Г		ISSPROT	Г		EST HUMAN E	Г	EST HUMAN 2			N FN	L V	T	T HUMAN	Г	Т	LN L	EST HUMAN A		NAMOUL - PA		EST_HUMAN 6	EST HUMAN C	EST_HUMAN R	Г	NT NT	1	SWISSPROT
Top Hit Acession No.	AV761874.1	AU140358.1	-22 BE144748.1	-22 AA046502.1	AL163246.2		.22 AB008681.1	-22 AF151054.1		.22 AF009660.1	.22 AA405040.1		.22 AL163303.2	22 U60822.1	.22 RE476511 1						-22 AI469679.1				22 A1090125.1	.22 BE156613.1	22 BE089841.1	22 X60660.1			
Most Similar (Top) Hit BLAST E Value	9.0E-22	Ŋ	8.0E-22	8.0E-22	7.0E-22	នុ	7.0E-22	7.0E-22	7.0E-22	7.0E-22	6.0E-22		5.0E-22	5.0E-22	5 OF-22	4.0E-22	4.0E-22	4.0E-22	4.0E-22	4.0E-22	3.0E-22	3 05 32			3.0E-22	3.0E-22	3.0E-22	3.0E-22	3.0E-22	2.0E-22	2.0E-22
Expression Signal	2.63	1.34	5.55	3.72	5.92	2.21	66'0	1.38	3.56	2.04	0.98	1.33	3.78	7.83	2.22	0.85	0.45	3.11	2.47	2.06	1.58	0 0	1.46		2.6	0.8	2.48	0.97	0.97	2.29	2.15
ORF SEQ ID NO:	36622				26067	29616	30307		34568	35335	29413	-	32188	36077			33827		36556			28028		-	30111		33963	34088	34089		27981
Exon SEQ ID NO:	Ц		13698	20492									19192	22865	24854		L	25428	23316	24957	13706	1528Q			17480	20823	20828	20952	20952	14681	15242
Probe SEQ ID NO:	10691	11707	678	7797	620	4250	4977	8590	8731	9502	4038	8140	6424	10217	12499	3627	8004	8312	10823	12657	939	2575	3662		4748	8129	8134	8258	8258	1946	2526

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Probe SEQ ID NO:	Exon SEQ ID NO:	S S S	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3414	16172	28821	15.41	2.0E-22	8394043 NT	TN	Homo saplens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4200	16941	29567	1.17	2.0E-22	2.0E-22 AW817794.1	EST_HUMAN	PM1-ST0282-261199-001-d12 ST0262 Homo saplens cDNA
5761	25075	31476	1.18	2.0E-22	W39456.1	EST HUMAN	zc20f01.r1 Soares_senescent_fibroblasts_NbHSF Homo sepiens cDNA clone IMAGE:322873 5' similar to qb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
6084	L			2.0E-22	2.0E-22 BF092116.1	EST_HUMAN	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
9602	22255	35440	1.53	2.0E-22	2.0E-22 A(276522.1	EST HUMAN	qi76h06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains MER29:3 MER29 repetitive element;
9696	l	İ	0.69	2.0E-22	2.0E-22 AA715315,1	EST HUMAN	nv04h11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219289 3'
9696	22347	35541	69.0	2.0E-22	AA715315.1	EST HUMAN	nv04h11.s1 NCI_CGAP_Pr22 Home sapiens cDNA clone IMAGE:1219269 3'
11781	24352	37684	1.88	2.0E-22	AW418960.1	EST_HUMAN	ha24f04x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
11872	24946	30983	3.71	2.0E-22	2.0E-22 AL163280.2	NT	Homo saplens chromosome 21 segment HS21C080
1871	14609	27320	1.79	1.0E-22	1.0E-22 AW865517.1	EST_HUMAN	PM4-SN0020-010400-009-h02 SN0020 Homo saplens cDNA
2588	15302	28038		1.0E-22	1.0E-22 U50871.1	NT	Human familial Alzhelmer's disease (STM2) gene, complete cds
3405	16163	28814		1.0E-22	1.0E-22 D14547.1	NT	Human DNA, SINE repetitive element
7841	20306		68.0	1.0E-22	1.0E-22 BE084667.1	EST_HUMAN	MR0-BT0659-220200-002-h07 BT0659 Homo saplens cDNA
							qz09b07 x1 NCL_OGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2
10451	23097	36328	0.79	1.0E-22	1.0E-22 Al365435.1	EST HUMAN	MERZ9 repetitive element :
							q209b07.X1 NCI_CGAP_CL11 Homo saplens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2
10451	23097	36329		1.0E-22	1.0E-22 Al365435.1	EST HOMAN	MER29 repetitive element ;
12704	24984		5.89	9.0E-23	AW802801.1	EST_HUMAN	L2-UM0076-070400-061-F11 UM0076 Home sapiens cDNA
3557		28959	62.0		8.0E-23 AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3305	16065		2.55		AV647246.1	EST_HUMAN	AV647246 GLC Hano sapiens cDNA clone GLCAWC07 3'
10966	23642	36895	4.16	7.0E-23	7.0E-23 5031952 NT	NT	Homo saplens Not56 (D. melanogaster)-like protein (NOT56L) mRNA
3427	16184		1.72	6.0E-23	6.0E-23 AF199333.1	NT	Rettus norvegicus RIM1B (RIm1B) mRNA, complete cds
4235	16976	29601	1.39	6.0E-23	6.0E-23 AL163249.2	NT	Homo saplens chromosome 21 segment HS21C049
							Homo saplens mannosidase, beta A, Iysosomal (MANBA) gene, and ublquitin-conjugating enzyme E2D 3
12005	24540	31105	1.6	6.0E-23	6.0E-23 AF224669.1	NT	(UBE2D3) genes, complete cds
							Homo saplens mannosidase, beta A, Ivsosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12005	24540	31106	1.5	6.0E-23	6.0E-23 AF224669.1	NT	(UBE2D3) genes, complete cds
12192	24663	31067	3.28	6.0E-23	6.0E-23 AI209130.1	EST_HUMAN	qg59c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to SW:MV10_MOUSE P23249 PROTEIN MOV-10. ;
	_			1			Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A3 (MAGEA3), caltractin
2328	18160	30844	4.09	5.0E-23	5.05-23 0826/1.2	2	(CALI), NAU(P)'H denyaragenase-like promin (NaUHL), and LIP

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United Extending and The State of the State	Top Hit Descriptor	Pongo pygmaeus offactory receptor (PPY116) gene, partial cds	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds	Homo saplens chromosome 21 segment HS21C027	Homo sapiens chromosome 21 segment HS21 C027	zl35g09.r1 Soares, pregnant_uterus_NbHPU Homo saplens cDNA clone IMAGE:503968 5' similar to contains MER29.t2 MER29 repetitive element;	Human endogenous retroviral element HC2	Human endogenous retroviral element HC2	RC3-NN0066-270400-011-h01 NN0066 Hamo sapiens cDNA	Homo saplens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	Human matrix Gla protein (MGP) gene, complete cds	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)	qs/34/1.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.	MR3-HT0487-150200-113-g01 HT0487 Homo saplens cDNA	yr16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'	yr16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'	Homo sapiens cytochrome P450 polypeptide 43 (CYP3443) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450	polypeptide 5 (CYP3AS) gene, partial cds	Homo sapiens chromosome 21 segment HS21C103	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1	Homo saplens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	Homo saplens chromosome 21 segment HS21C052	Hamo saplens chromosome 21 segment HS21C010	601236455F1 NIH_MGC_44 Hamo sapiens cDNA clone IMAGE:3608653 5'	zw82c06.r1 Sogres_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.t2	PTR5 repetitive element;	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'	ab75a08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE;852758 3' similar to TR:E19822 E19822 CA PROTEIN :	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
אופ ראסוו ב וסופ	Top Hit Database Source	TN TN	LN TN	I	I	EST HUMAN 0		I	HUMAN	I L	H	SWISSPROT	SWISSPROT T	EST HUMAN N	Г	Г	Г	Ι 4	ă L	H L		NT	H LN	H ⊢N	EST_HUMAN 6				EST_HUMAN 6	EST HUMAN T	
115	Top Hit Acession No.			-23 AL163227.2		23 AA130165.1			23 AW897927.1	23 AJ289880.1	23 M55270.1			23 AI201458.1		23 H59931.1	23 H59931.1		23 AF280107.1	.2		23 AF009660.1	23 AL163252.2		23 BE378471.1				23 BE409643.1		-24 11422027 NT
	Most Similar (Top) Hit BLAST E Value	5.0E-23	5.0E-23	3.0E-23	3.0E-23	3.0E-23	3.0E-23	3.0E-23	3.0E-23	2.0E-23	2.0E-23	2.0E-23	2.0E-23	2.0E-23	2.0E-23	2.0E-23	2.0E-23		2.0E-23	2.0E-23	2.0E-23	2.0E-23	1.0E-23	1.0E-23	1.0E-23		1.0E-23	1,0E-23	1.0E-23	9.0E-24	8.0E-24
	Expression Signal	3.93	3.37	1.34	1.34	4.1	2.96	2.98	1.18	4.25	3.87	1.98	1.98	1,46	3.35	3.65	3,65		4.3	1.21	2.45	2.87	1.1	5.56	3.28		4.6	2.05	. 2.05	1.84	1.53
	ORF SEQ ID NO:	31893	31893	32106			35045	35048		26068			28244				29347			34579			29857						36504		32121
	Exon SEQ ID NO:	25086	25086	19117	19117	20434	21879	21879	22863			15503	15503	16123	16458	16707	16707		20468				17228		19382				23265	13322	
	Probe SEQ ID NO:	6145	7337	6347	6347	7738	9148	9148	10215	199	1120	2798	2798	3364	3705	3958	3958		7772	8742	11991	12508	4492	4714	6620		8254	10570	10570	539	6357

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	Top Hit Descriptor	QV0-DT0047-170200-122-a06 DT0047 Homo saplens cDNA	DKFZp434A2311_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A2311 5'	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element;contains MER19.t2 MER19 repetitive element;	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds	Homo sapiens chromosome 21 segment HS21C049	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively	Spliced	hd24b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910413 3' similar to TR:O94851 O94851 KIAA0750 PROTEIN. ;	m31h05.s1 NOI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN ;	RC3-ST0197-130100-014-f06 ST0197 Homo sapiens cDNA	601078812F1 NIH_MGC_12 Homo sepiens cDNA clone IMAGE:3464498 5'	Homo sapiens mRNA for KIAA1093 protein, partial cds	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA	hh68c08.x1 NCI_CGAP_GU1 Homo septens cDNA clone IMAGE:2967950 3' similar to contains MER29.b2 MER20 condition element	FST374149 MAGE resentences. MAGG Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C052	601810449F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5'	zp11f09.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPlp112-5H13	DKFZp761L1712_r1 761 (synonym: hamy2) Homo saplens cDNA clone DKFZp761L1712 5'	yr92b09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains	MER28 repetitive element ;	ii77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'	ti77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'	MR1-SN0063-040500-001-a06 SN0063 Homo sapiens cDNA	MR1-SN0063-040500-001-a06 SN0063 Homo sapiens cDNA	Human O family dispersed repeat element
. (Top Hit Acession No.	-24 AW937954.1	-24 AL039498.1	-24 AW303317.1	-24 AB001421.1	-24 AL 163249.2	-24 AJ229043.1		24 AF223391.1	-24 AW514229.1	-24 AA594178.1	-24 AW813711.1	-24 BE544822.1	-24 AB029016.1	11418318 NT	04 018/644074 4	24 AW062076 1	24 At 163252 2	-24 BF127762.1	-24 AA167539.1	-24 AW898189.1	-24 AF086824.1	-24 AJ003536.1	-24 AL119158.1		-24 H69214.1	-24 AI521759.1	-24 AI521759.1	-24 AW868552.1	-24 AW868552.1	-24 M28877.1
	Most Similar (Top) Hit BLAST E Value	7.0E-24	7.0E-24	7.0E-24	6.0E-24	6.0E-24	5.0E-24		5.0E-24	5.0E-24	4.0E-24	4.0E-24	4.0E-24	4.0E-24	4.0E-24	20.00	3.0E-24	3.0F-24	3.0E-24	2.0E-24	2.0E-24	2.0E-24	2.0E-24	2.0E-24		2.0E-24	2.0E-24	2.0E-24	2.0E-24	2.0E-24	2.0E-24
	Expression Signal	1.49	0.95	1.33	2.72	11.74	7.9		0.58	1.45	3.85	1.35	1.95	4.89	1.77	200	7 4 4	4.33	1.41	2.72	1.01	0.81	0.65	3.28		0.98	0.94	0.94	1.31	1.31	7.44
	ORF SEQ ID NO:					28256	ľ		33430	37513	31563			ļ				35114				33135		34476			11936	35612	L	37745	
	Exon SEQ ID NO:	16803		23233			1_		20321	24194		L	23801	L	L	<u> </u>	61012	ı	1		16531	20054	_	21331	Ŀ		22405	22405	ı	24409	25377
	Probe SEQ ID NO:	3853	5087	10536	089	818	3953		7657	11595	5840	8581	11133	12361	12595	6	2222	9365	12438	2346	3779	7374	7379	8639		8676	9754	9754	11825	11825	12281

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	Top Hit Descriptor	Homo sapiens CGI-127 protein (LOC51646). mRNA	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA	Mus musculus mRNA for HGT keratin, partial cds	Homo sapiens PTEN (PTEN) gene, exan 2	Homo saplens chromosome 21 segment HS21C103	MR0-HT0166-271199-005-d09 HT0166 Homo sapiens cDNA	CM0-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA	Homo sapiens putative secreted protein (SIG11), mRNA	ne92e10.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2 MER1 repetitive element :	ne06a09.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element :	n/25h06.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST Pagnas PROBABILE for BIBOSOMAI DEOTERN 14.54	2h65h07.1 Soares fetal liver spiece 1NFIS S1 Homo saniens cDNA close MACE 446080 F	Mus musculus otogelin (Otog), mRNA	IL3-CT0219-161199-031-D04 CT0219 Homo sapiens cDNA	EST391217 MAGE resequences, MAGP Homo sapiens cDNA	ye56h04.rl Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:121783.5	PM3-OT0093-280200-001-g07 OT0093 Homo saptens cDNA	QV3-HT0543-140400-148-e11 HT0543 Homo saplens cDNA	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)	np27b02.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gb:M61866 ZINC FINGER PROTEIN 85 (HUMAN):	Homo sapiens chromosome 21 segment HS21C010	nf30h10.s1 NCI_CGAP_Pr1 Homo saplens cDNA clone IMAGE:915331 similar to contains L1.f1 L1	repetitive element;	Homo saplens transducin (beta)-like 1 (TBL1) mRNA	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5	40S RIBOSOMAL PROTEIN S16	40S RIBOSOMAL PROTEIN S16	40S RIBOSOMAL PROTEIN S16
מסי וייייייייייייייייייייייייייייייייייי	Top Hit Database Source		EST HUMAN Q				T HUMAN	Γ		EST_HUMAN M	EST HUMAN re		Т		EST HUMAN	Т	Г	Г	EST_HUMAN Q			/ISSPROT	EST HUMAN FI	T	Г	T_HUMAN		EST_HUMAN 60	SWISSPROT 40	SWISSPROT 40	
	Top Hit Acession No.	7706340 NT	-24 AW820194.1		-24 AF143313.1				6707	-25 AA483944.1	-25 AA468646.1			305360	5.0E-25 AW850271.1	Γ	.25 T98107.1	25 AW887671.1	.25 BE170957.1	8923321 NT	8923321 NT	25 P29622	25 AA603590.1			-25 AA579013.1	2158	16.1			25 P17008
	Most Similar (Top) Hit BLAST E Value	1.0E-24	1.0E-24	1.0E-24	1.0E-24	1.0E-24	1.0E-24	1.0E-24	9.0E-25	7.0E-25	7.0E-25	7.0E-25	6.0E-25	6.0E-25	5.0E-25	5.0E-25	4.0E-25			3.0E-25	3.0E-25	3.0E-25	3.0E-25	3.0E-25		3.0E-25/	2.0E-25	2.0E-25	2.0E-25	2.0E-25 F	2.0E-25 F
	Expression Signal	2.69	1.83	1.49	1.71	4.32	0.81	2.09	1.31	2.33	6.59	3,28	4.9	8.34	1.18	2.44	2.25	3.04	2.93	3.98	3.98	0.75	0.6	4.86		1.99	2.94	6.42	3.67	1.76	1.76
	ORF SEQ ID NO:	27131		28433			33404		37619	30275	33946			33397		l						30190	32288	34065		١				29535	29536
	Exon SEQ ID NO:	14435	15388	15786	16978		20296		24294	17667	20811	24296	17969	20288	14393	23947	14176	16155	17021	16074	16074	17568	19284	20928		23635		- 1		16907	16907
	Probe SEQ ID NO:	1691	2679	3020	4237	7447	7630	7845	11699	4939	8117	11701	6893	7622	1647	11286	1429	3397	4282	3314	3314	4837	6518	8235		10959	1326	5306	2835	4167	4167

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Single Exultrices Explassed in prain	Top Hit Descriptor	AL 49573 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA	DKFZp434H0313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5'	Human endogenous retrovirus, complete genome	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA	zq45b06.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to	contains Alu repetitive element;	nn54h11.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:10877493'	z/96g04,s1 Soares_fetal_heart_NbHH19W Hono sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.t3 PTR5 repetitive element;	R. rattus RY2G5 mRNA for a potential ligand-binding protein	R. rattus RY2G5 mRNA for a potential ligand-binding protein	Homo saplens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1	(MAGE-B1) genes, complete cds	Human lambda-Immunoglobulin constant region complex (germline)	Homo sapiens chromosome 21 segment HS21C018	Human DNA, SINE repetitive element	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	H.saplens DNA for endogenous retroviral like element	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908366 3'	Homo sapiens chromosome 21 segment HS21C002	zn30d08.r1 Shatagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA cione IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);	EST386629 MAGE resequences, MAGC Homo sapiens cDNA	Homo sepiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families	zq52h04.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'	Homo sapiens chromosome 21 segment HS21C002	Homo sapiens chromosome 21 segment HS21C002	Homo sapiens chromosome 21 segment HS21C010	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319619 3' similar to WP:F49C12.11 CE03371;
ie Exuli Prube	Top Hit Database Source	EST_HUMAN A	EST_HUMAN DI		SWISSPROT A	EST_HUMAN P		コ	EST_HUMAN nr		NT R	Т		NT (A	H LN	H	NT	Į S	N F	EST_HUMAN ho	H	EST_HUMAN si		Ŧ	EST_HUMAN 20	Ĭ	H LN	NT	BST_HUMAN W
SIIIC	Top Hit Ácessíon No.		E-25 AL040229.1	5487		-25 BE162737.1			-25 AA582690.1	-25 AA709079.1	1.0E-25 X60660.1			1.0E-25 U93163.1	-25 X51755.1	-26 AL163218.2	-26 D14547.1						7.0E-26 AW954559.1		-26 AA206131.1	6.0E-26 AL163202.2	6.0E-26 AL163202.2	26 AL163210.2	-26 AI708235.1
	Most Similar (Top) Hit BLAST E Value	2.0E-25	1.0E-25	1.0E-25	1.0E-25	1.0E-25		1.0E-25	1.0E-25	1.0E-25	1.0E-25	1.0E-25		1.0E-25	1.0E-25	9.0E-26	8.0E-26	7.0E-26	7.0E-26	7.0E-26	7.0E-26	7.0E-26	7,0E-26	6.0E-26	6.0E-26	6.0E-26	6.0E-28	6.0E-26	5.0E-26
	Expression Signal	1.94	1.03	2.02	1.03	2.84		0.79	3.14	4.03	0.75	0.75		3.06	2.18	1.41	1.99	1.72	1.23	2.27	0.62	8.45	1.64	2.04	0.95	0.68	99'0	2.03	3.61
	ORF SEQ ID NO:	35514	25794		27890	30160			32657	33633	35302	35303		36821		27945		27003		29508				27689	28752	36301			26572
	SEQ ID NO:	22317	13153	13976	15158	17537			25100	20509	22123	ı	1	23570	25024	15204	18403	14318	16711	16880	18348	24264	24885	14950	16100	23078	23078	24278	13909
	Probe SEQ ID NO:	9665	355	1226	2435	4806		6472	6899	7814	9446	9448		10890	12768	2487	2992	1571	3962	4138	5551	11669	12547	2222	3341	10432	10432	11683	1154

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					115	TO LINE SIE	Single Exell Tibbes Expressed in plain
Probe SEQ (D NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
154	13909	26573	3.61	5.0E-26	-26 AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo saplens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;
1535	14282		1.4	4.0E-26	4.0E-26 AA329548.1	EST_HUMAN	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' end
9312	21979		3.72		T857670 NT	LNT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10558			2.75		7.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:3535210 5'
1753	14495		1.21	3.0E-26	3.0E-26 D14547.1	IN	Human DNA, SINE repetitive element
1996	14732	27454	1.31	3.0E-26	3.0E-26 AL045855.2	EST_HUMAN	DKFZp4341066_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4341066 51
2025	14760		3.15		3.0E-26 AA115895.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3760	16512	29148	1.04		3.0E-26 AA152464.1	EST_HUMAN	zo30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR;
3760	16512		1.04		3.0F-26 AA152464 1	EST HUMAN	zo30f10.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR:
6811	1	32495	1.78	L	3.0E-26 BF245458.1	EST HUMAN	601864963F1 NIH MGC 57 Homo saptens cDNA clone IMAGE:4083278 51
10626	L		1.42	3.0E-26	-26 AF036405.1	LN	Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds
11559		37468	1.83	3.0E-26	-26 AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11659	24168			3.0E-26	-26 AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11602	24201	37523	6.56		3.0E-26 AA583173.1	EST_HUMAN	nn37d05.s1 NCLCGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.t1 OFR repetitive element ;
11858	<u></u>		1.36			L	Mus musculus harmonin Isoform b3 (Ush1c) mRNA, complete cds, alternatively spliced
12724	24995		2.52		3.0E-26 AW073434.1	EST HUMAN	xa57b09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2570873 3' similar to contains MER30.t1 MER30 repetitive element;
999	1	26083	6.76	1	2.0E-26 AL163282.2	F	Homo sapiens chromosome 21 segment HS21 C082
1861	14599		3.07		AL038099.2	EST_HUMAN	DKFZp566L171_s1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566L171 3'
3225	15988	28642	5.89		X86694.1	ΝΤ	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
5147	17866		1.09	30.2	-26 AF073482.1	LN	Homo sapiens myotubularin related protein 7 mRNA, partial cds
10653	23344		2.7	2.0E	:-26 D87675.1	۲	Homo sapiens DNA for amyloid precursor protein, complete ods
	}					1 1 1 1	to89a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE.2185416.3' similar to contains Alu
11180	١	37132	50		2.0E-26 AI801412.1	ES HOMAN	repeative element contains element interact interactive element;
1383	- }		2.43		Z.UE-Z0 Arussubb.1	- I	Tiorno sapiens with crass I region
12106	- }		1.57		AB037859.1	Į.	Homo sapiens mKNA for KIAA1438 protein, partial cds
133	- }	25591	5.18		1.0E-26 BE170371.1	EST_HUMAN	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
2040	- }		1.37		1.0E-26 AL039363.2	EST HUMAN	UKFZp434H1910_r1 434 (synonym: htes3) Homo sapiens cDNA cione UKFZp434H1910 5
2693	15402		9.04	-	-26 AF261085.1	Ł	Homo sapiens glyceraidehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds

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Single Exon Propes Expressed in Brain	Top Hit Descriptor	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA	DKFZp566C2148_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566C2146 5'	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22 45 5'	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1	(WAGE-61) genes, complete cas	nad03007.X1 NCI_CGAP_PT2B Homo sapiens cDNA clone IMAGE;3253644.31 similar to contains OFR.t1 OFR repetitive element ;	w/49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA cione IMAGE:2408150 3' similar to contains THR.b2 THR repetitive element	Homo sapiens chromosome 21 seament HS21C027	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00568	IOBULIN ALPHA-1 CHAIN (HUMAN);	au87h08.x1 Schnelder fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN):	PM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA	ADP ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSI OCATOR 3) (ANT 3)	Homo caniene WRN (WRN) years complete cole	AV732214 HTF Homo sapiens cDNA clone HTFBCB06 51	MR4-BT0398-250800-204-d06 BT0398 Homo sapiens cDNA	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1761 5' similar to	REPETITIVE ELEMENT L1	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA	Human endogenous retroviral element HC2	hi51h12.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2975879 3' similar to TR:O76040	O76040 ORF2 FUNCTION UNKNOWN.;	Human mRNA for KIAA0231 gene, partial cds	Homo sapiens Xq pseudoautosomal region; segment 1/2	AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5'	Human nucleolar protein (B23) mRNA, complete cds	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
Je Exon Propes	Top Hit Database Source	EST_HUMAN MF	EST_HUMAN DK	EST_HUMAN CH	EST_HUMAN RC		N I	EST_HUMAN OF	wj4 EST HUMAN TH	T		ESI_HUMAN IIO	EST HUMAN TU	Т	SWISSPROT NU	Т	T HUMAN	Τ	1		EST_HUMAN CM		NT TO		T_HUMAN	NT Hu		T HUMAN	NT Hur	Hor (MA
Žijo	Top Hit Acession No.	1.0E-26 BE165980.1		1.0E-26 H55093.1	27 BF371227.1		27 093103.1	.27 BF445556.1	27 AI831462.1			2/ AW162/3/.1	27 AW 162737.1		27 P12236	1,70	Γ	T				1.6.	27 270664.1		2.1		7.0E-27 AJ271735.1		27 M26697.1	27 U93163.1 P
	Most Similar (Top) Hit BLAST E Value	1.0E-26	1.0E-26	1.0E-26	9.0E-27		9.0E-2/	9.0E-27	8.0E-27	8.0E-27	100	8.05-27	8.0E-27	8.0E-27	8.0E-27	8 OF-27	8.0E-27	8.0E-27		8.0E-27	8.0E-27	8.0E-27	7.0E-27	-0.20	7.0E-27	7.0E-27	7.0E-27	7.0E-27	6.0E-27	6.0E-27
	Expression Signal	3.05	2.24	3.53	1.11		1	5.72	3.83	4.33	9	85.88	59.39	1.37	1.81	0 84	1.02	2.53		2.29	1.51	1.51	1.23		2.25	1.19	4.26	2.12	2.75	1.57
	ORF SEQ ID NO:						-		25450		0,000	81.007	26820	27629	28594	28762	31317			32444	34961	34962							36558	37728
	SEQ ID NO:	19574	23492	25395	20156		70077	24454	12837	13327	,	7414	14142	14893	15943	18107	18404	17957		19429	21797	21797	13444		17750	21448	23341	24843	23320	24394
	Probe SEQ ID NO:	6740	10809	12348	7484	0000	2078	11875	6	\$	1204	CAC	1395	2164	3180	3348	9099	888		6947	9109	9	999	-	9030	8756	10650	12484	10627	11804

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Probe SEQ ID NO:	Exon SEQ ID NQ:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10137	22785	35996		5.0E-27	BF666614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5
10137		35997	2.82	5.0E-27	E-27 BF666614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Home sapiens cDNA clone IMAGE:4278527 5
6645	19407	32421	1.65	4.0E-27	9910569 NT	LN.	Mus musculus sperm tail associated protein (Stap), mRNA
7840	t I		1.07	4.0E-27	4.0E-27 AL163209.2	L _Z	Homo sapiens chromosome 21 segment HS21C009
7883			1.54	4.0E-27	AF078779.1	LN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9644		35491	7.0	4.0E-27	-27 AW880859.1	EST_HUMAN	QV0-OT0033-070300-152-b10 OT0033 Homo sapiens cDNA
11604		37525	1.98	4.0E	-27 X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2034		27499	4.61	3.0E-27	-27 X60658.1	TN	R.rattus RYA3 mRNA for a potential ligand-binding protein
4238		29604	1.06	3.0E-27	-27 BE071924.1	EST_HUMAN	PM0-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
5262		30697	6.24	3.0E-27	-27 AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
7698	20361	33475	0.63	3.0E-27	-27 BE670351.1	EST_HUMAN	7e33f02.xf NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284283 3'
9205		35256	2.93	3.0E-27	-27 BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
40	12868	25487	14.84	2.0E-27	-27 AF054187.1	FZ	Homo sapiens alpha NAC mRNA, complete cds
							nk01b10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000689 similar to gb:M17886 60S
1888	14625		5.12	2.0E-27	-27 AA565345.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
3107	15872	_	10.39	2.0E-27	27 AW629172.1	EST HUMAN	hi51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:076040 O76040 ORF2: FUNCTION UNKNOWN.;
3218	15981	28632	1.96	2.0E-27	-27 AF111167.2	, F	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3218	15981	28633	1.96	2.0E-27	-27 AF111167.2	IN	Homo sapiens jun dimerization protein gene, partial cds: cfos gene, complete cds: and unknown gene
4009	16755	29385	1.36	2.0E-27	-27 AF000368.1	LZ	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
6577	19340	32353	0.64	2 0F-27	H02655 1	NAMI IH TRE	y36e01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 6' similar to SP HMGC MOLISE CORSOL HOMEOROX PROTEIN
7989	20684	33810	1.65	2.0E-27	-27 AI866347.1	EST HUMAN	W28g07.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426268 3
9,5	040			L			nh08h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.t3 L1
8 6		25520	2.3	2.0E-2/	27 X6051527.1	ESI_HUMAN	rependive element;
200	1	00000	0/5			Z	A cause N to S mixing for a potential ligano-pinging protein
CSSS	- 1	35/82	1.28	2.05-27	27 M78590.1	EST_HUMAN	ES I 00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
9935	22583	35783	1.28	2.0E-27	27 M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
10875	23555	36802	4.11	2.0E-27	27 AU121685.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5
11469	14625		3.31	2.0E-27	27 AA565345.1	EST HUMAN	nk01b10.s1 NC_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
426	13212		1.51		27 AL163246.2	П	Homo saplens chromosome 21 segment HS21C046

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Similar Top Hit Acession Detabase Top Hit Acession Detabase Source		1.0E-27 AB026898.1 NT complete cds)	ht09g01 x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3	7 6005855 NT	7 F30158.1	F30158.1 EST_HUMAN	AB007923.1 NT	1.1 EST_HUMAN	1.0E-27 D87449.1 NT Human mRNA for KIAA0260 gene, partial cds	1.0E-27[AF111083.1 NT Bos taurus letrophilin 3 splice varient bbah mRNA, complete cds	9.0E-28 BE348399.1 EST HUMAN SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313 ;	Γ	9.0E-28 AA174078.1 EST_HUMAN Zp18912.s1 Stratagene felal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3'	EST_HUMAN	8.0E-28 AW157571.1 EST HUMAN TR:080302 O60302 KIAA0555 PROTEIN ; contains element MER22 repetitive element;	EST_HUMAN	7866 NT	T_HUMAN		6.0E-28 AA504562.1 EST HUMAN repetitive element contains element PTR5 repetitive element;		5.0E-28 A1921003.1 EST_HUMAN THR repetitive element:	6.0E-28 R79762.1 EST_HUMAN ly89710.r1 Scares placenta Nb2HP Homo saplens cDNA clone IMAGE:146443 5'	A DE-28 AW 195066 1 EST HUMAN Q08379 GOLGIN-95 :		EST_HUMAN	
單半四	Value	1.0E-27 AB	1.0E-27 BE	1.0E-27	1.0E-27 F3	1.0E-27 F3	1.0E-27 AE	1.0E-27 BE	1.0E-27 D8	1.0E-27 AF	9.0E-28 BE	9.0E-28 AL	9.0E-28 AA	9.0E-28 BF	8.0E-28 AV	7.0E-28 AL	7.0E-28	7.0E-28 AV	6.0E-28 AF	6.0E-28 AA		5.0E-28 AI	5.0E-28 R7	4 0F-28 AV	4.0E-28	4.0E-28 BE	
Expression Signal		1.34	0.98	6.26	1.96	1.96	0.98	2.28	2.65	3.51	2.94	3.31	0.63	4.85	2.46	7.89	3.36	2.78	76.0	2.35		4.19	4.1	88	0.78	2.52	
ORF SEQ ID NO:		26404		32215						37625			36150			L	37089					٠.	29372	28087			
Probe Exon SEQ ID SEQ ID	L	13741	16806	1	L	l	ı	1		24299	12951	13107	l	24504	25245	L	L	L	21509		ı	13114	L	15343			L
		976	4061	6449	6771	6771	8	8884	9622	11704	137	303	10289	11951	12286	1158	11142	15	8817	12526		310	3990	2831	2976	3106	1^{-}

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10774	23457		3.08		4.0E-28 AF029308.1	TN	Homo saplens chromosome 9 duplication of the T cell receptor beta loous and trypsinogen gene families
10928	23608		17.24		4.0E-28 AB038241.1	TN	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
10950	19915	32988	4.75		4.0E-28 AI198941.1	EST_HUMAN	qf86f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12312	24734		1.84		4.0E-28 AW854244.1	EST_HUMAN	RC3-CT0254-240400-210-f12 CT0254 Homo sapiens cDNA
1260	14009		2.88		3.0E-28 AF155382.1	LN TN	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
-	17770		1.05		3.0E-28 AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8726	21418	34562			BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-f09 HT0713 Homo sapiens cDNA
-	23533	36778			3.0E-28 U53588.1		Homo sapiens MHC class 1 region
12344	24751		3.62		3.0E-28 AI831991.1	EST_HUMAN	wj98f07.x1 NCI_CGAP_Lym12 Homo saplens cDNA clone IMAGE:2410895 3' similar to contains Alu repetitive element; contains element HGR repetitive element;
87	12913	25551	10.6	l	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-005 BT0254 Homo saplens cDNA
1023	13783	26444	0.86		2.0E-28 4501912 NT	NT	Homo saplens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
1142	13897	26558	16.03		Y11107.3	L	Homo saplens ITGB4 gene for Integrin beta 4 subunit, exons 3-41
2481	15199	27939	2.1		2.0E-28 Al348634.1	EST_HUMAN	qo35b06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element;
6215	18989	31966	1.33		2.0E-28 BF224402.1	EST_HUMAN	hr76c03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element;
6238	19012		5.07		2.0E-28 BF212905.1	EST HUMAN	601814196F1 NIH_MGC_54 Hamo sapiens cDNA clone IMAGE:4048751 5'
7943	20638	33766			2.0E-28 AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
9484	22137		5.54		AW972305.1	EST_HUMAN	EST384394 MÅGE resequences, MÅGL Homo sapiens cDNA
11614	24212	37536	1.84			TN	Homo saptens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12322	24741		2.22	L	2.0E-28 H06376.1	EST_HUMAN	y/79c09.r1 Scares Infant brain 1NIB Homo sapiens cDNA clone IMAGE: 44300 5'
1461	14208	26895	2.84		ŀ	, LN	Human gene for Ah-receptor, exon 7-9
2217	14945	27685	2.37			EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
_	20455		3.2		11429885 NT	LN	Homo saplens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
L	20612		3.3	1.0E-28	8922793 NT	L	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
	21848	35014	48.84	·	1.0E-28 AA308744.1	EST HUMAN	EST 179615 HCC cell line (matastasts to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
9776	22427	35633	8.73		4758431 NT	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1). mRNA
9776	22427	35634	8.73	1.0E-28	4758431 NT	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
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Probe NO: 10422 11815 12749 12749 12749 12749 12749 12749 12779 8830 8830 8830 8844 4381 4684 4381 8631 8632 8631 8631 8631 8632 8631 8631 8631 8631 8631 8631 8631 8631	Exan SEC ID NO: NO: 23088 24478 25145 25144 25045 14324 24324 24806 143361 2323 24717 21328 18629 221336 177118 17118 17118 17118 18629 22109 22509	ORF SEQ ID NO: 27034 27034 33797 33797 33798 34480 29751 30054 3465 3465 3465	Expression Signal Signal Signal 0.63 7.79 7.79 7.13 7.13 7.13 7.13 7.13 7.13 7.13 7.13	Most Similar (Top) Hit BLAST E Value 1.06-28 1.06-28 1.06-29 7.06-29 8.06-29 8.06-29 6.06-29 4.06-29 4.06-29 3	st Similar Top) Hit LAST E Value 1.0E-28 AU149356.1 1.0E-28 AU149356.1 1.0E-28 AU149356.1 1.0E-29 AV653987.1 8.0E-29 AV653987.1 6.0E-29 AV663987.1 6.0E-29 BE940438.1 6.0E-29 BE940438.1 6.0E-29 BE940438.1 6.0E-29 BE940438.1 6.0E-29 AV887541.1 4.0E-29 AV887541.1 4.0E-29 AV887541.1 3.0E-29 AV876317.1 3.0E-29 AV876377.1	Top Hit Database Source EST HUMAN ES	TOP HIS Descriptor TOP HIS Descriptor EST HUMAN AU146958 NT2R/M Home sapiens a DNA clone NT2R/M4002146 3' EST HUMAN AU146958 NT2R/M Home sapiens a DNA clone NT2R/M4002146 3' EST HUMAN AU146958 NT2R/M Home sapiens and sap
11235	23898	37185	1.47	3.0E-29	AA403053.1	EST_HUMAN	zt62b01.r1 Sceres_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769 G1335769 GAG-POL POLYPROTEIN.;
12102	24600			3.0E-29 3.0E-29	3.0E-29 D63882.1 3.0E-29 AA016177.1	NT EST_HUMAN	Human HSLIM15 mRNA for HSLIm15, complete cds zs32e09.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360712 3'
480	13265	25900	1.72	2.0E-29	AF084869.1	۲	Homo sapiens envelope protein RIC-6 (env) gene, complete cds

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Top Hit Descriptor	Homo sapiens envelope protein RIC-6 (env) gene, complete cds	wr85d10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN	wr85d10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O16546 O15546 HERV-E ENVELOPE GLYCOPROTEN:	Homo saplens chromosome 21 segment HS21C068	os71e04.x1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.t2 L1 repetitive element;	w/27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3¹ similar to contains element MER6 repetitive element :	wf27g07x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' sImilar to contains element.	601442206F1 NIH MGC 65 Homo sapiens cDNA clone IMAGE:3846648 5'	Homo saplens DNA-binding protein (LOC56242), mRNA	Homo sapiens DNA-binding protein (LOC56242), mRNA	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens chromosome 21 segment HS21 C048	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens chromosome 21 segment HS21C048	601669934F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3952833 5'	Homo sapiens splicing factor similar to dnaJ (SPF31), mRNA	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA	R.rattus RYA3 mRNA for a potential ligand-binding protein	nz20c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1	Homo saniens zinclion ramidad transmoter like (2001) DNA	HSC23F051 normalized infant brain cDNA Homo sabiens cDNA clone c-23fn5	EST97317 Thymus I Homo saplens cDNA 5' end similar to EST containing O family repeat	PT2.1_13_B11.r tumor2 Homo sapiens cDNA 3'	PM4-BT0724-150400-004-d11 BT0724 Homo saplens cDNA	Human mRNA for integrin alpha subunit, complete cds	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA	Homo sapiens CTCL tumor antigen se20-10 mRNA, partial cds
Top Hit Database Source	TN	EST_HUMAN	EST HUMAN	Т	EST HUMAN	EST HUMAN		Г			Į.				HOMAN		EST_HUMAN	T HUMAN	LN	NAMI III TOD	2000	T HUMAN	Т	EST HUMAN	EST HUMAN			TZ.
Top Hit Acession No.	29 AF084869.1	29 A1963604.1	29 Al963604.1		2.0E-29 Al082459.1	2.0E-29 AI806418.1	29 AI806418.1		37821	10567821 NT	29 AL163248.2			29 AL 163248.2	29 BF025947.1	11425108 NT	29 AW880701.1	30.1	29 X60658.1	0 0F.30. A A 781215 1	27745		8.0E-30 AA383873.1	Γ				6.0E-30 AF177227.1
Most Similar (Top) Hit BLAST E Value	2.0E-29	2.0E-29 A	2.0E-29 A	2.0E-29 A	2.0E-29 A	2.0E-29 A	2.0E-29 A	2.0E-29 B	2.0E-29	2.0E-29	2.0E-29 A	2.0E-29 A	2.0E-29 A	2.0E-29 A	2.0E-29 B	2.0E-29	2.0E-29 A	1.0E-29 A	1.0E-29 X	A 05,30 0	9.0F-30	8.0E-30 F	8.0E-30 A	8.0E-30 AI557072.1	7.0E-30 BE091133.1	6.0E-30 D	6.0E-30 B	6.0E-30 A
Expression Signal	1.72	6.62	6.62	1.63	0.99	1.48	1.36	1.16	0.63	0.63	3.61	3.61	3.61	3.61	1.31	2.04	1.73	7.37	0.85	2 0 7	176	8.94	3.72	3.1	1.03	1.73	2.3	0.48
ORF SEQ ID NO:	25901	26955	26926	29610	31449	31830	31830	33698	34313	34314	35241	35242	35999	36000	36804			34527	36391	32255			33994	34412		27209	28598	36310
Exen SEQ ID NO:	13265	14270	14270	16987	18527	18865	18865	20571	21169	ı	22070		22787	22787	23557	24063	24100	21383	23164	19254	24531	19001	20862	21275	14251	14508	15948	23083
Probe SEQ ID NO:	480	1523	1523	4246	5735	6087	7459	7878	8477	8477	9408	9408	10139	10139	10877	11459	11499	8691	10518	6487	11992	6227	8168	8283	1505	1766	3185	10437

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12769	17897		3.38	6.0E-	30 X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3	. 67.42	27,000			E OC 30 (300002 4	Note:	tg92g03.x1 NCI_CGAP_CLL1 Home saplens cDNA clone IMAGE:2116276 3' similar to contains Alu
500	_			1	110704 4	1000	Limon accomplete but reference (ACO2) cana aven 7
6169	\perp		5,44	5.0E	30 08/931.1	Z	Furnan accinicios nyol acase (ACCZ) gene, excit
10802			1.95		30 AL163278.2	L	Homo sapiens chromosome 21 segment HS21C078
11103	23773	37047	2.47	5.0E-	5.0E-30 AL163210.2	NT	Homo sapiens chromosame 21 segment HS21C010
11103	23773			5.0E-		LN	Homo sapiens chromosome 21 segment HS21C010
2139	14869			4.0E-	30 AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2139	14869			4.0E-	30 AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
6756	17925	30560	0.63	4.0E	30 P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8803	1		2.82	4.0E-	30 AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-f08 ST0181 Homo saplens cDNA
	l				1		qq83c05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to
1129	- [3.0E-	30 AI338551.1	EST HOMAN	contains Mickel of Mickel repetitive element
3740		29128		3.0E-	30 AF128893.1	ŁZ	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
7852	20547		0.58	≻30'E	30 AF078779.1	TN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8385	21078		0.48	3.0E-	30 AF078779.1	FZ	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
	Ĺ.,						ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3
10333	22980		1.7	3.0E-	30 BE350127.1	EST_HUMAN	MER29 repetitive element ;
10465	23111	36342	0.53	3.0E-	30 AB032969.1	LN	Homo sapiens mRNA for KIAA1143 protein, partial cds
10465	23111		0.53	3.0E-	30 AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11168	Ĺ	37116	2.48	3.0E-	30 P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
099	13436	26077	0.92	2.0E-	30 AW857315.1	EST_HUMAN	CM0-CT0307-310100-156-h03 CT0307 Homo saplens cDNA
1062	13820		3.11	2.0E-	30 F08688.1	EST_HUMAN	HSC23F051 normalized Infant brain cDNA Homo saplens cDNA clone c-23f05
1462	14209	26896		2.0E-	30 BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo saplens dDNA
2720	15427		8	2.0E-	30 BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2920	1		6:39	2.0E-	30 AF114156.1	TN	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3769	16521			2.0E-	30 AW 206581.1	EST_HUMAN	UI-H-BI1-afo-c-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4727	17459			2.0E-	30 BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4727	17459	30096	1.51	2.0E-	30 BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Home sapiens cDNA clone IMAGE:3029438 5
0999	19420	32435		2.0E-		EST_HUMAN	601893208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138983 5'
8375				2.0E-	7.	EST_HUMAN	zs58c10.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363186 5
8435	21128	34265	4.68	2.0E-	30 C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-570C01 5

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													_						_					_			
Single Exon Probes Expressed in Brain	Top Hit Descriptor	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR :	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE (UBIQUINONE) EI AVOPROTEIN SI IRI INIT PRECI IPSOR	EST383657 MAGE resequences, MAGL Homo sapiens cDNA	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repositive element:	C18939 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-570C01 5'	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2910991 3' similar to contains MER1.t3 MER1 tabelitive element:	Homo sapiens chromosome 21 segment HS21C003	ac77b08.s1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:868599.31	802022560F1 NCI CGAP Bru67 Homo sapiens cDNA done IMAGE:4157991 5'	EST186868 HCC cell line (matastasis to liver in mouse) II Homo saciens cDNA 5' end	601809932F1 NIH MGC 18 Homo sapiens cDNA clone IMAGE 4040694 5	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22 728 5	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'	y/99b08.r1 Scares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);	ytggb08.r1 Scares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS RELATED PROTEIN RAB-2 (HI IMAN):	HSC05F032 normalized infant brain cDNA Homo saniens cDNA clone conserva 3:	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA	Homo sapiens chromosome 21 segment HS21C008	OLFACTORY RECEPTOR 15 (OR3)	OLFACTORY RECEPTOR 15 (OR3)	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial eds
gie Exon Pro	Top Hit Database Source	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	FN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	LN	FZ	LN	SWISSPROT	SWISSPROT	EST_HUMAN	EST_HUMAN	NT	LN
 	Top Hit Acession No.	-30 BE670617.1	BE670617.1	2.0E-30 AW971568.1	2.0E-30 AW 470791.1	-30 C18939.1	1.0E-30 AW 468897.1	-30 AL163203.2	-30 AA664377.1	1.0E-30 BF347728.1		1.0E-30 BF183230.1		9.0E-31 T73025.1		-31 R18214.1	31 R18214.1	31 Z38293.1	-31 AF078779.1	TN 68523389 NT	-31 AL163208.2			İ			7.0E-31 AF208541.1
	Most Similar (Top) Hit BLAST E Value	2.0E-30	2.0E-30	2.0E-30	2.0E-30	1.0E-30	1.0E-30	1.0E-30 /	1.0E-30 /	1.0E-30	1.0E-30	1.0E-30	1.0E-30	9.0E-31	9.0E-31	9.0E-31	9.0E-31	9.0E-31	9.0E-31/	8.0E-31	8.0E-31/	8.0E-31	8.0E-31 P23275	7.0E-31	7.0E-31 E	7.0E-31 /	7.0E-31 A
	Expression Signal	3.61	3.61	3.62	7.37	16.33	2.34	2.62	7.16	2.01	0.94	2.46	6.95	0.81	0.81	0.81	0.81	1.63	0.48	2.41	4.6	1.43	1.43	3.29	3.29	96'0	0.96
-	ORF SEQ ID NO:	34366	34367	35741	35839	25729	25942	26122	27675	27921	28461	33399		29135	29136	34053	34054		34359	26473		30213	30214	28123	28124	34130	34131
	Exon SEQ ID NO:	21225	21225	22547	22630	13087	13309	13474	14937	15182	15816	20290	25268	16501	16501	20917	20917	21214	21216	13813	15135	17590	17590	15383	15383	20994	20994
	Probe SEQ ID NO:	8533	8533	2882	2866	280	525	669	5209	2464	3050	7624	12581	3748	3748	8223	8223	8522	8524	1054	2414	4861	4861	2674	2674	8300	8300

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9166	21836		0.94	7.0E-31	31 BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5
12434	24805	31044	2.26	7.0E-31	31 X51755.1	LN.	Human lambda-Immunoglobulin constant region complex (germline)
	ı						Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively
3667	16420		2.66	6.0E-31	31 AF223391.1	NT	spliced
8053	20747		4.37	6.0E-31	31 AF055066.1	TN	Homo saplens MHC class 1 region
	<u> </u>	ļ					ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
828	. 1	34062		6.0E-31		ESI HUMAN	MEK-29 repetute element
12169	25195		1.96	6.0E-31	31 BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo saplens cDNA clone IMAGE:3918524 5
187	13000	25640	3.58	5.0E-31	31 M60694.1	LΝ	Homo saplens type I DNA topoisomerase gene, exon 8
187	13000			5.0E-31	31 M60694.1	ΙN	Homo saplens type I DNA topolsomerase gene, exon 8
3			0	10 U	4 0 4 9 9 9	IAALU III FOR	7k06f04.x1 NCI_CGAP_GC6 Homo saplens cDNA clone IMAGE:3443479.3' similar to TR:Q13537 Q13537 Q13137 CMM AD TO DOCO ELEMENT contains 1.14.1.1 condition alament.
3	1		0.73	3.0E-3.1		ESI DOMEN	
585	13362		5.18	4.0E-31	31 AJ271735.1	L Z	Homo saplens Xq pseudoautosomal region; segment 1/2
							POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
							ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-
1606	14352	27040	0.91	4.0E-31	31 Q10473	SWISSPROT	ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
1810	14550		1.57	4.0E-31	31 AL163280.2	LN	Homo sapiens chromosome 21 segment HS21C080
2792	15497		1.23	4.0E-31	LN 8600673	LN	Homo saplens SET domain and mariner transposase fusion gene (SETMAR) mRNA
12205	24672		1.86	4.0E-31	AJ230125.1	LΝ	Homo saplens GGT1 gene, exon 1
12457	1_		1.86	4.0E-31	11430273 NT	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
	L						
7239			_	3.0E-31	4826853 NT	L	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI) (NDU-EB) mKNA
7393	20072	33151	1.26	3.0E-31	3.0E-31 11420329 NT	۲N	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8081	20755		2	3.0E-31		NT	Homo sapiens chromosome 21 segment HS21C006
9479	22132	35312	3.7	3.0E-31	3.0E-31 D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
10498	23144	36371	0.54	3.0E-31	31 AA421242.1	EST_HUMAN	zu08d04,r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731047 5'
10527	ı			3.05-31	31 P11174	SWISSPROT	40S RIBOSOWAL PROTEIN \$15 (RIG PROTEIN)
11101	ı			3.0E-31	31 BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3862086 5'
12819	25059		1.66	3.0E-31	31 AB037763.1	N	Homo sapiens mRNA for KIAA1342 protein, partial cds
1910		27358		2.0E-31	31 AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-f03 LT0051 Homo saplens cDNA
2211				2.0E-31	2.0E-31 Al393388.1	EST_HUMAN	tg44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672.3'
2339	15062		1.89	20E-31	31 AL119245,1	EST_HUMAN	DKFZp761G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
2772	15121	27808	20.4	2 OF-34	31 44458824 1	EST HIMAN	ae88f11.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:838413 3' similar to contains THR.t2 THR repetitive element :
7447	1			50F-21	T-Somethy.		

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						· · · · · · · · · · · · · · · · · ·	Chigh Chord Tobas Children III Bigill
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5193	18001	30624	0.81	2.0E-31	2.0E-31 AW 444496.1	EST_HUMAN	UI-H-Bi3-akb-f-09-0-UI.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE-2733833 31
5624	18421	31334	3.57	2.0E-31	31 BE350127.1	EST_HUMAN	ht08g01.x1 NCI_CGAP_Kid13 Home sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
8975	21665		2.05	2.0E-31	31 AA877764.1	EST HUMAN	nr06f04.s1 NCI_CGAP_Co10 Homo saplens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE FIFMENT COMPLETE CONSENSUS SECULENCE.
9107	1	34959	3.64	2.0E-31	7661535 NT	NT TN	Homo sapiens B9 protein (B9), mRNA
986				2.0E-	31 AV710948.1	EST HUMAN	AV710948 Cu Hamo sapiens cDNA clane CuAALB07 5
9806		35662	0.94	2.0E-	31 AV710948.1	EST HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
9975				2.0E-	31 BE408611.1	EST HUMAN	601304125F1 NIH MGC 21 Homo sabiens cDNA clone IMAGE:383310 5
8975		35830	2.35	2.0E-31	31 BE408611.1	EST HUMAN	601304125F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3638310 5
12144			1.58	2.0E-31	31 AF148512.1	FZ	Homo sapiens hexokinase II gene, promoter region
12279	25413		1.75	2.0E-31	31 AI114527.1	EST HUMAN	HA1110 Human fetal liver cDNA library Homo sabiens cDNA
<u>ل</u> 50	12842	25456	11.09	1.05-31	31 U93163 1	Į.	Homo sapiens WAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1
1658	14404	27092		1.0E-31	31 095371	SWISSPROT	OLFACTORY RECEPTOR 201
1658	14404	27093	1.35	1.0E-31	31 095371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1658	14404	27094	1.35	1.0E-31	095371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4592	17327	29952	1.15	1.0E-31	1.0E-31 AL134376.1	EST HUMAN	DKFZp5478235 r1 547 (synonym: hfbr1) Homo saniens cDNA class DKE725478235 g
4592	17327	29953	1.15	1.0E-31	AL134376.1	EST HUMAN	DKFZp547B235 r1 547 (synonym: hfbr1) Home sapiens cDNA clone DKFZp547B235 g
5210		30640	3.79	1.0E-31	31 AW391679.1	EST HUMAN	MR3-ST0220-151299-028-a08 1 ST0220 Homo septems cDNA
6042	18822	31782	2.2	1.0E-31	31 AF048727.1	LN	Homo saplens minisatellite ceb1 repeat region
7189	19875	32948	1	1.0E-31	1.0E-31 AF126145.1	FX	Bos taurus xenobiotid/medtum-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
10136	22784	35995	0.51	1.0E-31	1.0E-31 U93163.1	IN	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
10833	23515	36757	2.7	1.0E-31	1.0E-31 A1086434.1	EST HUMAN	qf21h03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRATAXIN. :
11830	24414	37752	1.48	1.0E-31	1.0E-31 (166081,1	L Z	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV19S1P, TCRBV19S1P, TCRBV14S1, TCRBV14S1, TCRBV14S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY7, TRY5, TRY5, TRY5, TRY5, TRY5, TRY6, TRY5, TRY5, TRY6, TRY7, TRY6, TRY7, TRY6, TRY7, TRY6, TRY7, TRY6, TRY7, TRY6, TRY7, TRY6, TRY7, TRY6, TRY7, TRY6, TRY7, TRY8, TRY7, TRY8, TRY7, TRY8,
6542	19307	32312	2.38	9.0E-32	2.	T HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAACA1 5
7492	20164		99'0	9.0E-32	11430822		Homo sapiens hypothetical protein FL/11294 (FL/11294) mRNA
2070	14802	27530	2.48	8.0E-32	8.0E-32 Al056770.1	EST_HUMAN	oz15a09.x1 Soares_feta_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:16763843'

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Top Hit Descriptor	AV736449 CB Homo saplens cDNA clone CBFBIA08 5'	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'	Homo sapiens chromosome 11open reading frame 9 (C110RF9), mRNA	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR renefitive element	TO TOTAL TOTAL	nwo robext NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:088539 088539 WW DOMAIN BINDING PROTEIN 11.;	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156970 5'	Homo sapiens chromosome 21 segment HS21C080	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA	tof 2b09.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR	repetitive element;	AV730056 HTF Homo saplens cDNA clone HTFAVE06 5'	EST383396 MAGE resequences, MAGL Homo sapiens cDNA	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5	EST383657 MAGE resequences, MAGL Homo sapiens cDNA	no16h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.t1 L1 repetitive element;	Homo sapiens chromosome 21 segment HS21C085	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06	HSPD21201 HM3 Homo saplens cDNA clone s4000107H06	Human glyceraldehyde-3-phosphate dehydrogenase (CAPDH) gene, complete cds	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA	Mus musculus SRY-box containing gene 6 (Sox6), mRNA	Mus musculus SRY-box containing gene 6 (Sox6), mRNA	QV1-FT0169-100700-271-a02 FT0169 Homo sapiens cDNA	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA	Homo sapiens spermidine synthase (SRM) mRNA	Homo sapiens spermidine synthase (SRM) mRNA
Top Hit Database Source	EST HUMAN	Г		H IMAN	T	EST_HUMAN	Ł	EST HUMAN	П	Ę	F			EST_HUMAN	П	LN.	EST HUMAN		EST HUMAN	1	EST_HUMAN	Г	Г				EST_HUMAN			
Top Hit Acession No.	NV736449.1		1.0E-32 11439789 NT	32 44720574 1	1	33 BE327112.1	33 AF223391.1	33 BF347229.1	33 AL163280.2	5031736 NT	5031736 NT	The state of the s	33 AI590115.1	33 AV730056.1	33 AW971307.1	-33 X54890.1	33 BF347229.1	33 AW971568.1	33 AA601416.1		33 F30631.1	33 F30631.1	33 J04038.1	11429198 NT	EV 6092529	TN 6095529	33 BF373515.1	11141884 NT	4507208 NT	4507208 NT
Most Similar (Top) Hit BLAST E Value	2.0E-32	1.0E-32	1.0E-32	4 OF 32	20101	9.0E-33	9.0E-33	9.0E-33	9.0E-33 /	7.0E-33	7.0E-33		7.0E-33 /	7.0E-33	7.0E-33	7.0E-33	7.0E-33	7.0E-33	7.05-33/	6.0E-33	6.0E-33	6.0E-33	6.0E-33	6.0E-33	6.0E-33	6.0E-33	5.0E-33	5.0E-33	5.0E-33	5.0E-33
Expression Signal	2.42	1.67	7.02	80 8	2	4.58	4.05	1.95	5.22	3.14	3.14		2.28	6.45	9.3	1.56	2.41	1.93	4.34	0.94	96.0	96'0	9.33	3.09	1.12	1.12	1.46	1.19	1.43	1,43
ORF SEQ ID NO:	30962		32453	34320				34523		25517	25518		27622				36660	37162	31090		31720	31721	34315		35754	35755			27337	
Exon SEQ ID NO:	25022	15855	19437	21186	Ł	16230	19098	21379	23392	12887	12887				15998	21537	23419	23876	24619	16473	18758	18758		21295	22559	22559	14512	14612	14628	14628
Probe SEQ ID NO:	12763	3090	6955	8494		3474	6326	2898	10701	58	58		2158	2655	3236	8845	10732	11213	12127	3720	5976	5976	8478	8603	9910	9910	1770	1874	1891	1891

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ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ; nt09g01x1 NCI_CGAP_Kid13 Homo septens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to ab51g11.r1 Stratagene lung cardinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to ab51b11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to ak32b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR:Q13579 2x48f05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795489 3' similar to TR:G1263081 G1263081 MARINER TRANSPOSASE.; qb67g03.x1 Soares, fetal_heart_NbHH19W Homo sapiens cDNA done IMAGE:1705204.3' similar to contains OFR.t1 OFR repetitive element; zl71a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5 similar to UI-H-BI2-ahl-c-03-0-UI.s1 NCI_CGAP_Sub4 Homo saplens cDNA clone IMAGE:2727149 3' gb:X12871_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); gb:M29638 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN); Homo saplens hypothetical protein SIRP-b2 (SIRP-b2), mRNA d96d01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3 contains Alu repetitive element; contains MER28.b2 MER28 repetitive element; xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 xq33f11x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 oncogene family (RAB1) mRNA Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA Homo saplens polymerase (DNA directed), alpha (POLA), mRNA Top Hit Descriptor Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA MR0-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA AV647851 GLC Homo sapiens cDNA clone GLCBCF09 3 gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN); Jomo sapiens hypothetical protein SIRP-b2 (SIRP-b2), Homo sapiens chromosome 21 segment HS21C085 Homo sapiens chromosome 21 segment HS21C00 Homo sapiens chromosome 21 segment HS2: Q13579 MARINER TRANSPOSASE Homo sapiens RAB1, member RAS MER29 repetitive element EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN EST_HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** Top Hit Database Source 11421332 NT 8393994 11421332 11421332 11421332 8393994 Top Hit Acession 5.0E-33 AL163285.2 5.0E-33 AW264679.1 5.0E-33 AW264679.1 BE350127.1 AV647851.1 4.0E-33 AL163210.2 4.0E-33 AW293349.1 2.0E-33 AA453647.1 4.0E-33 AA626621.1 AA053053.1 3.0E-33 BE350127.1 3.0E-33 AA861510.1 2.0E-33 BE159039.1 4.0E-33 AL163207.2 2.0E-33 AA626683.1 2.0E-33 AI277492.1 ġ 2.0E-33 AI160189.1 AI052256.1 4.0E-33/ 3.0E-33 E 4.0E-33 4.0E-33 2.0E-33 2.0E-33 2.0E-33 2.0E-33 2.0E-33 (Top) Hit BLAST E Most Similar 1,28 2.18 2.02 2.15 24.73 5.5 3.89 1.04 48 1.29 9.0 2.16 4.15 0.8 3.21 28.91 2.75 4.8 0.87 8 Expression Signal 36384 36985 36010 30779 30265 30366 27999 32057 36203 36011 27581 29811 32058 32087 ORF SEQ 36385 ÖZQ SEQ ID 18122 23716 13825 22985 21688 23159 15140 13825 17653 13863 19072 12843 19099 15595 17122 Ž ÿ 1907 10148 2547 10148 1106 6299 10338 102 10513 11048 5318 1068 6329 SEQ ID 2270 4450 1087 4925 5033 5033 8998 628 4385 2451 ÿ

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sion Top Hit Database Top Hit Descriptor Source	Homo sepiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat NT regions	4502556 NT Homo sapiens calcium/calimodulin-dependent protein kinase IV (CAMK4) mRNA	NT Homo sepiens F-box protein FBL4 (FBL4) mRNA, complete cds	NT Homo sapiens protein knase C beit-ii type (PRKCB1) mRNA, complete cds	-	EST HUMAN QV3-BN0047-230200-102-b03 BN0047 Homo saplens cDNA	П	т		EST_HUMAN AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'	NT Homo sapiens Xq pseudoautosomal region; segment 1/2	8922751 NT Home seplens hypothetical protein FL/10900 (FL/10900), mRNA	EST_HUMAN MR4-BT0399-200100-001-h03 BT0399 Homo sapiens cDNA	EST_HUMAN [vd15e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5		EST_HUMAN 1/14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5	NT Human G2 protein mRNA, partial ods	NT Human G2 protein mRNA, partial ods	NT Mus musculus DAB/2J hair-specific (haci-1) gene	7706500 NT Homo sapiens Npw38-binding protein NpwBP (LOC61729), mRNA	NT Human splicing factor SRp56-1 (SRp-55) mRNA, complete cds				Г	Г	THUMAN	NT Human Ig germline H-chain D-region genes, partial cds	EST_HUMAN 601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' sImilar to contains
Top Hit Acession No.	-33 AF003528.1	4502	-33 AF199420.1	-33 M13975.1	-33 U60822:1	-33 AW996818.1	-33 U60822.1	-33 AI927191.1	33 AF003528.1	33 AV727809.1	9.0E-34 AJ271735.1	8922	34 BE069882.1	7.0E-34 T70845.1	T70845.1	34 H12866.1	34 U10991.1	34 U10991.1	34 U03686.1	. 7706	34 U30883.1	5.0E-34 AF078779.1	5.0E-34 AB037856.1	5.0E-34 AL163209.2	A1804667.1	4.0E-34 AA861773.1	3F209778.1	34 M37277.1	34 BF035327.1	
Most Similar (Top) Hit BLAST E Value	1.0E-33	1.0E-33	1.0E-33	1.0E-33	1.0E-33	1.0E-33	1.0E-33	1.0E-33	1.0E-33	1.0E-33	9.0E-34	8.0E-34	8.0E-34	7.0E-34	7.0E-34	7.0E-34	6.0E-34	6.0E-34	6.0E-34	5.0E-34	5.0E-34	5.0E-34	5.0E-34	5.0E-34	4.0E-34	4.0E-34	4.0E-34		3.0E-34	100
Expression Signal	1.16	2.46	0.58	1,04	0.84	1.83	3.32	2.21	4.07	1.41	1.61	96.0	99.0	2.27	0.56	3.05	2.3	2.3	2.13	2.9	3.61	1.37	2.24	1.79	1.64	0.64	1.26	0.78	3.14	9
ORF SEQ ID NO:		30485	31198	33067		37251	37581			31005		27631	33468	26858	26858		25884	25885	31107		30328	34607	36482		27449	31488	34769	31886		70070
Exon SEQ ID NO:	12835	17873	18299		25432	23953	24259	24790	12835	24914	- 1		20353	14173	14173		ĺ	- 1	- 1	14611	17725	21457	- 1	- 1		18561	21627	18916	23770	2,0
Probe SEQ ID NO:	ω	5156	5501	7307	9920	11292	11663	12407	12570	12602	12780	2168	7689	1426	0066	12191	458	458	12011	1873	2002	8765	10550	11219	1991	5770	8936	6138	1110	a a

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		_	_					_	-		_											1	-1		_	_	-т	_	\neg
Top Hit Descriptor	wd35g08.xf Soeres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.t2 MER29 repetitive element ;	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)	ADP ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)	Homo sapiens X-linked anhidrotite ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds	RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone iMAGE:3886899 5'	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'	OLFACTORY RECEPTOR-LIKE PROTEIN F5	DKFZp564A1563_r1 564 (syncnym: hfbr2) Homo sapiens cDNA clone DKFZp564A1563 5'	601470592F1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:3873478 5'	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'	Homo sapiens nucleobindin 2 (NUCB2), mRNA	oc31c11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);	Homo saplens chromosome 21 segment HS21C010	hh77b06.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'	Homo sapiens prohibitin (PHB) mRNA	naa33808.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912 075912 DIACYLGLYCEROL KINASE IOTA. ;	nag33g08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912	075912 DIACYLGLYCEROL KINASE IOTA.;	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'	601236468F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3608513 5	602184624T1 NIH_MGC_42 Homo seplens cDNA clone IMAGE:4300660 3'	Homo saplens phosphatidylinositol glycan, class L (PIGL), mRNA	ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'	Homo sapiens zinc finger protein 208 (ZNF208), mRNA	UFH-BW0-ejd-d-09-0-UI,s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
Top Hit Database Source	EST_HUMAN	SWISSPROT	SWISSPROT	SWISSPROT	FZ	Ę	ΓN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	EST HUMAN	Ŋ	EST_HUMAN	۲	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	l i	EST_HUMAN	FN	EST HUMAN
Top Hit Acession No.	2.0E-34 AI678101.1	P51805	P51805	P12236	1.0E-34 AF003528.1	1.0E-34 AY009397.1	1.0E-34 AY009397.1	1.0E-34 BE071414.1	1.0E-34 BE874052.1	1.0E-34 BE874052.1	P23266	1.0E-34 AL036635.1	1.0E-34 BE781790.1	1.0E-34 BE781790.1	11439599 NT	1.0E-34 AA807097.1	1.0E-34 AL163210.2	AW 663302.1	8.0E-35 6031190 NT	8.0E-35 BF589937.1		BF589937.1	8.0E-35 BF183195.1	8.0E-35 BE378480.1	8.0E-35 BF569282.1	11425417 NT	8.0E-35 AA757115.1	FN 5765009	6.0E-35 AW 297191.1
Most Similar (Top) Hit BLAST E Value	2.0E-34	2.0E-34 P51805	2.0E-34 P51805	1.0E-34 P12236	1.0E-34	1.0E-34	1.0E-34	1.0E-34	1.0E-34	1.0E-34	1.0E-34 P23266	1.0E-34	1.0E-34	1.0E-34	1.0E-34	1.0E-34	1.0E-34	9.0E-35	8.0E-35	8.0E-35		8.0E-35	8.0E-35	8.0E-35	8.0E-35	7.0E-35	8.0E-35	8.0E-35	8.0E-35
Expression Signal	1.16	1.34	1.34	6.53	1.32	78.0	76.0	3.44	2.05	2.05	0.45	7.1	1.39	1.39	1.82	1.65	422	1.2	7.71	3.43		3.43	2.69	2.42	3.95	2.05	1.83		0.84
ORF SEQ ID NO:	34688	37057					29426		31788	31789								29029		27171		_				32163		27409	
Exon SEQ ID NO:	21541	23783	23783	1		16796	16796	17182	18827	18827	21904	L	L.	23805	23820	Ι.		1	ı	l	L_{-}	14472	17545	23283	L.	19162	L	14696	!!
Probe SEQ ID NO:	8850	11113	11113	1494	3663	4051	4051	4446	6047	6047	9225	9598	11138	11138	11153	12372	12593	3636	218	1730		1730	4814	10589	12119	6383	1391	1960	4030

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Single Exon Probes Expressed in Brain	SEQ Expression (Top) Hit Acession (Top) Hit Descriptor Signal BLAST E No. Source	Homo saplens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	35939 1.12 3.0E-35 AW003063.1 EST_HUMAN P10268 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE	25667 1.88 2.0E-35 N88965.1 EST HUMAN REPETITIVE ELEMENT	1.55 2.0E-35 T11909.1	2.0E-35 AB018413.1 NT	1.12	2.0E-35 6912459 NT		TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo saplens 0.78 2.0E-35 BE247575.1 EST_HUMAN cDNA done TCBAP4328	29280 0.78 2.0E-35 BE247575.1 EST HUMAN GDNA clone TCBAP4328	2.67 2.0E-35 H49239.1 EST HUMAN yq19a12.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:274079 5'	31192 2.7 2.0E-35 BF332417.1 EST_HUMAN (QV0-BT0701-210400-199-b04 BT0701 Home saplens cDNA	32749 0.95 2.0E-35 BEB32838.1 EST_HUMAN CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA	0.95 2.0E-35 BE832636.1 EST_HUMAN		0.45 2.0E-36 AV723718.1 EST_HUMAN	2.24 2.0E-35[X59417.1 NT	2.0E-35 BF332417.1 EST_HUMAN	1.72 2.0E-35 6912459 NT	459 NT	1.36 2.0E-35 BE904978.1 [EST_HUMAN	2.0E-35 BE904978.1	5.98 2.0E-35 AL163210.2 NT Homo sapiens chromosome 21 segment HS21C010	25567 1.56 2.0E-35 N88965.1 EST_HUMAN REPETITIVE ELEMENT	1.0E-35 AA631949.1 EST_HUMAN	6.81 1.0E-36 AA631949.1 EST_HUMAN	29165 19.5 1.0E-35 AW389473.1 EST_HUMAN I.2.ST0162-131099-006-d12 ST0162 Homo saplens cDNA
		4.1							6.0			2.5												5.9			·	
	ORF SEQ ID NO:	22050	22722 35936	15535 25567		14943 2768			16300	16640 29275		356	L	19696 32749		L								900				
	be Exon 1 ID SEQ ID NO:	9388 220	10074 227	106 155				3306 160		3890 166	3890 16640	321 17356	5495 18294		i	7775 20471			11817 18294		11889 16066		362 24577	12572 24900	12689 15535			735 13509
. [Probe SEQ ID NO:	Ö	101	Ĺ	-	7	ဗ်	લ	ဗိ	ਲ ਲ		4	, p	_		7	7.	10697	11	11	4	12(12	12	126			

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
735	13509	26166	19.5	1.0E	-35 AW389473.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
889	13658		1.3	1.06	-35 T87947.1	EST_HUMAN	yd93a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN ;
2544	15258	27996	1.68	1.0E-35	7705994 NT	TN	Homo sapiens hypothetical protein (LOC51233), mRNA
2770	15475	28217	1.09	1.0E	-35 BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo saplens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
2770	1	28218	1.09	1.05		EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
3140	15904	28549	1.81	1.0E-35	E006030 NT	L	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
3161	15924	28570	3.3	1.0E	-35 AV650422.1	EST_HUMAN	AV650422 GLC Home sapiens cDNA clone GLCCEF063'
3161	15924	28571	3.3	1.0	E-35 AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEF063'
4388	17125	29756	3.93	1.0	7656905 NT	TN	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4388	17125	29757	3.93	1.0E-35	7656905 NT	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5423	18222	30934	1.41	1.0E-35	11526236 NT	LN	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7383	20063	33141	0.86	1.0	E-35 AB033105.1	LN	Homo sapiens mRNA for KIAA1279 protein, partial cds
7541	20211	33311	1.18	1.0	3002	LN	Homo sapiens KIAA0645 gene product (KIAA0645), mRNA
9442	25125	35297	2.16	1.0E	-35 AU158595.1	EST_HUMAN	AU168695 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
9442	25125	35298	2.16	1.0E	-35 AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
10477	23123	36352	0.7	1.0E	-35 BF589594.1	EST HUMAN	naa08d06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA done IMAGE:3254051 3' sImilar to TR:031341 031341 BETA-GALACTOSIDASE :
							naa06d06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA done IMAGE:3254051 3' similar to TR:031341
10477	23123	36353	0.7	1.0E		EST_HUMAN	031341 BETA-GALACTOSIDASE;
11758	24349	37680	1.46	1.0E	-35 AB028980.1	LN	Homo sapiens mRNA for KIAA1057 protein, partial cds
11758	24349	37681	1.46	1.0E	_	TN	Homo sapiens mRNA for KIAA1057 protein, partial cds
11768	24359		1.91	1.0E	-35 AI525119.1	EST_HUMAN	promma-7.D01.r bytumor Homo sapiens cDNA 5'
11917	25313		1.37	L	11418274 NT	LN	Homo sapiens fibulin 1 (FBLN1), mRNA
12121	24613		1.63	1.0E	11418110 NT	NT	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
12471	24837		2.13	1.0E	-35 BE792832.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5'
9129	21817	34983	0.56	805	-36 AA348480 1	EST HUMAN	EST54938 Hippocampus II Homo saplens cDNA 5' end similar to similar to endocembus retrovirus 9 5' LTR
2931		28344	1.1	7.0E	-36 AW857579.1	EST HUMAN	CM1-CT0315-091289-063-d07 CT0315 Homo saplens cDNA
3116	15881		3.84	7.0E	4557498 NT	LN	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7554	20224	33327		7.0E		LΝ	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N
7564	20224	33328	5.92	7.0E	-36 U06672.1	LN	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N

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Top Hit Descriptor	Hamo sapiens ninjurin 2 (NINJ2), mRNA	Hamo sapiens TCL6 gene, exon 12	UI-H-BW1-env-c-12-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA done IMAGE:3083542 3'	#93b06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' cimilar to gb:M/1949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);	ho06h02xt NCI_CGAP_Co14 Homo sepiens cDNA clone IMAGE:3038627 3' similar to SW:IMA2_HUMAN DESSON MADODTIN ALDIA 2 SLIBITITE.	Homo saplens syncytin precursor, mRNA, complete cds	C16927 Clontech human aorta polyA+ mRNA (#6572) Homo saplens cDNA clone GEN-535C11 5	#85009.xt NCI_CGAP_CLL1 Homo sepiens oDNA done IMAGE:2107024 3' similar to contains MER9.b2 MER9 repetitive element :	Homo sapiens Xq pseudoautosomal region; segment 1/2	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'	Homo sapiens chromosome 21 segment HS21C009	Homo sapiens API5-like 1 (API5L1), mRNA	Homo sapiens APIS-like 1 (APISL1), mRNA	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASEI	601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 57	601282286F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5	y19705.r1 Soares placenta Nb2HP Homo saplens cDNA clone IMAGE:139713 5'	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), trancript variant 3, mRNA	Human platelet Glycoprotein Ilb (GPIIb) gene, exons 2-29	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens DNA for amylold precursor protein, complete cds	zu89c10,r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'	Homo sepiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA	AV753629 TP Homo sapiens cDNA clone TPGABH01 5'
Top Hit Database Source		- LN	EST_HUMAN	EST_HUMAN	INVESTIGATION AND ADDRESS OF THE PARTY OF TH	T	T HUMAN	EST HUMAN	Г	EST_HUMAN	Г				NT		EST_HUMAN	SWISSPROT	Τ		HUMAN	Γ.	EST HUMAN	NT		L		T_HUMAN		EST_HUMAN
Top Hit Acessian No.	7706622 NT		6.0E-36 BF515101.1			T		36 AI380499.1			Г	5729729 NT	5729729 NT	3227		5.0E-36 11417862 NT			74.1					97041				4.0E-36 AA400370.1	9218	36 AV753629.1
Most Similar (Top) Hit BLAST E Value	6.0E-36	8.0E-38	6.0E-38	6.0E-36	0	8.0F-38	6.0E-36	8.0E-38	5.0E-38	5.0E-36	5.0E-36	5.0E-38	5.0E-38	5.0E-38	5.0E-36	5.0E-36	4.0E-38	4.0F-36	4.0E-36	4.0E-38	4.0E-38	4.0E-36	4.0E-36 R64023.1	4.0E-38	4.0E-38	4.0E-36	4.0E-36	4.0E-36	4.0E-36	4.0E-36/
Expression Signal	2	5.58	0.71	3.54	22.0	2.33	0.51	3.11	10.74	5.75	1.45	2,15	2.15	0.61	3.53	3.45	1.69	1.03	1.61	2.13	0.82	0.82	0.84	2.33	1.63	1.62	1.62	2.84	2.09	7.3
ORF SEQ ID NO:	27458		29023	30682		34385		37443			28991		30105		25592			26856	27074		28783			31707				36835		
Exan SEQ ID NO:	14734	15139	16383	18054	1			24136	L.		16352	i	17468	L	12949	24650	13955	14170	L	14947	16108		18425		\mathbf{l}_{-}					25199
Probe SEQ ID NO:	1888	2418	3830	5248	2002	8550	10125	11636	134	2755	3599	4736	4736	7686	11887	12168	1203	1423	1640	2219	3349	3349	5629	5964	7653	8453	8453	10909	12183	12227

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Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
25047		1.44	4.0E-36		NT	Homo saplens mRNA for KIAA0027 protein, partial cds
13455	26100	2.58	3.0E		L	Homo sapiens neurexin III-alpha gene, partial cds
14231	26917	1.32	3.0E-		NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
14231	26918	1.32	3.0E-36		NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
15022	27757	1.21	3.0E-36		TN	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
17203	29829	88.3	3.0E-36		NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
23720	36991	1.59	3.0E-36		EST HUMAN	601458531F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3862086 5'
15930	28579	2.38	2.0E-36		EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
17631	30246	5.45	2.0E-36		EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo saplens cDNA
18198	30892	1.6	2.0E-36		NT	Mus musqulus p47-phax gene, complete cds
18550	31471		2.0∈		EST HUMAN	EST06648 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBJ28 5' end
19248	32248		2.0E		EST_HUMAN	yc44a07.r1 Stratagene liver (#937224) Homo saplens cDNA clone IMAGE:83508 5'
21955			2.0E		EST_HUMAN	UI-H-BW1-amu-a-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
21999		62'0	2.0E-36		NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
21999		0.79	2.0E	4507848	L	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
13634	26304	1.8.1	1.0E-36		EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
14871	27603	1	1.0E-36	BE146523.1	EST_HUMAN	RC1+HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
14871	27604	-	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo saplens cDNA
14928	27664	1.36	1.0E-36		EST_HUMAN	602136483F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5
16099		1.16	1.0E		IN	Homo sapiens human endogenous retrovirus W proC6-19 protease (pro) gene, partial cds
18599	31527	1.29	1.0E		IN	Homo saplens zInc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
						wb37c12x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu
18868		4.19	- -	AI867714.1	EST HUMAN	repetitive element;
19069		1.21	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Scares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34529 5' sImilar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
			1.05-36	R25012.1	EST HUMAN	Vg36g10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
			1.0E		EST HUMAN	DKFZp761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
١_			1.0E	11426108	7	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
20009	33088				TN	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
			1.0E	AA148034.1	EST_HUMAN	zo51a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
			1.0E	AA148034.1	EST HUMAN	zo51a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE;590398 5'
Probe EO ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:		Exen SEQ ID ID ID ID ID ID ID ID ID ID ID ID ID	Exon ORF SEQ Express NO:	Exon SEQ ID ID NO: Expression Signal ID NO: Most Simal Signal Si	Exon DRF SEQ Expression Signal Most Similar Top Hit Accession No. NO: 10 NO: Signal Top Hit Accession No. 13466 26100 2.58 3.0E-36 AF10239.1 14231 26917 1.32 3.0E-36 AF10239.1 17203 29829 5.88 3.0E-36 AF10239.1 17203 29829 5.88 3.0E-36 AF10239.1 17203 29829 5.88 3.0E-36 AF10239.1 17203 28529 5.88 3.0E-36 AF10239.1 17203 28691 1.21 3.0E-36 AF10239.1 17631 30246 5.45 2.0E-36 BF527747.1 18560 31471 3.95 2.0E-36 BF527747.1 18560 31471 3.95 2.0E-36 AF507747.1 18560 31471 3.95 2.0E-36 BF627747.1 18560 31471 3.95 2.0E-36 AF50774.1 18560 3172 0.79 2.0E-36	Exon No.: CRF SEQ Expression Signal Most Similar (Top) Hit Accession ID No.: Top Hit Accession Signal PLAST E No.: Top Hit Accession Double Signal PLAST E No.: Top Hit Accession Signal PLAST E No.: Top Hit Accession Double Signal PLAST E No.: Top Hit Accession Double Signal PLAST E No.: Top Hit Accession No.: <th< td=""></th<>

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	nc60e08,11 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745670	nc60e08,r1 NCI_CGAP_Pr1 Homo saplens cDNA clone IMAGE:745670	AU141688 THYRO1 Homo saplens cDNA clone THYRO1001033 5'	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'	xe82b07.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2614357 3'	QV3-NN1023-010600-199-h01 NN1023 Homo saplens cDNA	RC3-CT0279-040500-017-a10 GT0279 Homo sapiens cDNA	RC3-CT0279-040500-017-a10 CT0279 Homo saplens cDNA	CM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA	UI-HF-BNO-ale-c-03-0-UI.11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5	RC-BT091-210199-110 BT091 Homo sapiens cDNA	RC-BT091-210199-110 BT091 Homo sapiens cDNA	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo sapiens chromosome 21 segment HS21C013	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds	ws80b07.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:25042453'	ws80b07.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'	73D4 Human retina cDNA Tsp509l-cleaved sublibrary Homo sapiens cDNA not directional	Homo sapiens chimerin (chimaerin) 2 (CHN2) mRNA	CM0-UT0003-050800-503-409 UT0003 Homo sapiens cDNA	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element :	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 resettitve element:	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14	genes	DKFZp434E0422_f1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5	Homo saplens Jun dimerization protein gene, partlal cds; cfos gene, complete cds; and unknown gene	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	wk25b11.x1 NC_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.t2 PTR5 repetitive element ;
gle Exon Probe	Top Hit Database Source	EST_HUMAN no	EST_HUMAN no	EST_HUMAN A			EST_HUMAN Q						Г		NT TN	NT	EST_HUMAN W	EST_HUMAN w	T_HUMAN		EST_HUMAN C	EST HUMAN M	_	EST HUMAN R			EST_HUMAN DI	NT H	Ĭ	EST_HUMAN P
Sin	Top Hit Acession No.	E-36 AA420487.1	1.0E-36 AA420467.1	1.0E-38 AU141688.1	E-36 AU141688.1	E-36 AW 103658.1	E-36 BF364169.1	E-36 AW855868.1	E-36 AW855868.1	E-36 AW897636.1	E-36 AW504143.1	E-36 AI905536.1	E-36 A 1905536.1	11418177 NT	E-36 AL163213.2	E-36 AF202723.1	9.0E-37 AW009277.1	9.0E-37 AW009277.1	9.0E-37 W22618.1	4757979 NT	E-37 BE698077.1	8.0E-37 BE350127.1	8.0E-37 BE350127 1				7.0E-37 AL042800.1	7.0E-37 AF111167.2	7.0E-37 AF111167.2	7.0E-37 AI817700.1
	Most Similar (Top) Hit BLAST E Value	1.0E-38	1.0E-36	1.0E-38	1.0E-36	1.0E-36	1,0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-36	9.0E-37	9.0E-37	9.0E-37	8.0E-37	8.0E-37	8.0E-37	8.0F-37	8.0E-37		8.0E-37	7.0E-37	7.0E-37	7.0E-37	7.0E-37
	Expression Signal	1.34	1.34	0.61	0.61	2.71	3.88	0.56	0.56	3.3	4.17	1.45	1.45	3.81	3.03	3.23	2.12	2.12	1.35	66.0	1.58	3.75	3.75	8.24		6.22	3.03	0.97	76.0	8.69
	ORF SEQ ID NO:	33770	33771	33902	33903	34762	35878	36086	36087	36795	37347	37302	37303				33042	33043		28765		31451	31452	31507		33604		27179	27180	36585
	Exon SEQ ID NO:	20647			20773		. 1	22874						24575	24855	25011	19965	19965	24733	16109	17977	18530	18530	18578		20479	14011	14480	14480	23348
	Probe SEQ ID NO:	7952	7952	8079	8079	8927	10014	10226	10228	10867	11354	11393	11393	12060	12501	12747	7281	7281	12309	3350	5168	5738	5738	5787		7784	1262	1738	1738	10657

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						200	
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10811	23494	36729	2.25	7.0E-37	-37 AI536702.1	EST_HUMAN	tm87g03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element ;
8338	21031	34168	1.34	6.0E-37	-37 AF169689.1	LN L	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
12624	24929		2.94	6.0E-37	-37 AF202723.1	TN	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6002				5.0E-37	-37 AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo saplens cDNA 5' end
6002				5.0E-37	-37 AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8654	21346	34490	6.0	5.0E-37	5.0E-37 AV750211.1	EST_HUMAN	AV750211 NPC Homo saplens cDNA clone NPCBGH09 5'
10837	23519		4	5.0E-37	7657117 NT	. TN	Homo saplens glycine C-acetyftransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
12055	24572		6.86	5.0E-37	-37 AF149773.1	TN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2423	15144			4.0E		EST_HUMAN	290504.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4480153'
6194	18970			4.0E		EST_HUMAN	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9228	21935	35109		4.0E	-37 AA843806.1	EST_HUMAN	ak09c02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:14054423'
2010	14745		3.2	3.0E-37	-37 AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2010			3.2	3.0E-37		EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2965	15731		3.15	3.0E-37	1	EST_HUMAN	EST373222 MAGE resequences, MAGF Homo saplens cDNA
5774	18565	31494	76'0	3.0E-37	-37 AL138274.1	EST_HUMAN	DKFZp547G067_r1 547 (synonym: hfbr1) Homo sapiens cDNA done DKFZp547G067 5'
7455	20,700	22004	F2 0	2 05 27	37 01740062 4	ECT LINAN	at34c05.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373896 3' similar to TR:Q13537
3	1		5 6	0.000	D002004	ביים ביים	Home and SMA for AMIL and a second
3/2			0.08	2.0E-3/	2.0E-3/ D89/90.1	Z	Tromo sapiens mistra for AML1, complete dos
3/2	- 1			2.0E-3/	-37 D89790.1	I N	nome sapiens mikiwa jer Amili, complete cas
1058	- 1	26477		2.0E-37	2.0E-37 AU131202.1	EST_HUMAN	AU131202 N 12KF3 Homo sapiens cDNA clone N 12KF33002166 5
1058			2.64	2.0E-37	2.0E-37 AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1956	14692	27405		2.0E-37	AL163247.2	۲N	Homo sapiens chromosome 21 segment HS21C047
			Ę	L	1100000	1	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous
2/05		10767	4.70	2.05-37	Z.OE-37 4303Z 10	1	Aguinoratosis, pulypeptus i (CTCZ/ATIO) in No.
4968			0.83	2.0E-3/	AL163284.2	z	nomo sapiens criromosome 21 segment HSZTCU84
5304				2.0E-37	2.0E-37 BF035327.1	EST_HUMAN	601456531F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3862086 5
6561				2.0E-37	2.0E-37 AA346720.1	EST_HUMAN	EST52931 Fetal heart II Homo saplens cDNA 5' end
7895			0.46	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA cione IMAGE:3453657 5
7895	20590			2.0E-37	2.0E-37 BE537764.1	EST_HUMAN	601087534F1 NIH_MGC_10 Homo sapiens cDNA cione IMAGE:3453657 5'
7937				2.0E-37	2.0E-37 BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4111406 5'
11549		37459		2.0E-37	2.0E-37 AF176013.1	닏	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
12784				2.0E-37	11417972 NT	NT	Homo saplens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
2081	14813	27546		1.0E-37	1.0E-37 AL163281.2	٦	Homo sapiens chromosome 21 segment HS21C081

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| Top Hit Descriptor | RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA | Homo sapiens ribonuclease III (RN3) mRNA, complete cds | QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA | Mus musculus otogelin (Otog), mRNA | 601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5 | क्य1602.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to
contains L1 t2 L1 recetitive element : | Human somatic cytochrome c (HC1) processed pseudogene, complete cds | CM3-FT0096-140700-243-d07 FT0096 Homo saplens cDNA | Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA | Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA | 602018401F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153992 5' | Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
 | yn51f07.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:171973 5' | Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds | 601455722F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3859348 5' | Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA | Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA | Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA | Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
 | Homo sapiens DNA for Human P2XM, complete cds | Homo sapiens adenylosuccinate lyase (ADSL), mRNA

 | EST383908 MAGE resequences, MAGL Homo sapiens cDNA | Homo sapiens RIBIIR gene (partial), exon 8 | Homo sapiens deiodinase, lodothyronine, type II (DIO2), transcript variant 2, mKNA | yd40h07.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:110749 5' similar to SP:0LF3_MOUSE P23275 OLFACTORY RECEPTOR; | yd40h07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110749 5' similar to
SP:OLF3_MOUSE P23275 OLFACTORY:RECEPTOR; | 601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5
 | B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS | B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions | Homo sapiens HIRA interacting protein 4 (dnaJ-like) (HiRIP4), mKNA
 |
| Top Hit
Database
Source | EST_HUMAN | TN | EST_HUMAN | | | NAMIN TOR | NT | EST_HUMAN | TN | NT | EST HUMAN | TN
 | EST_HUMAN | TN | EST_HUMAN | ΤN | H | TN | TN
 | LN | TN

 | EST_HUMAN | LZ. | Ä | EST_HUMAN | EST HUMAN | EST_HUMAN
 | ΝΤ | L | LN | L
 |
| Top Hit Acession
No. | 1 | | | 5360 | | | | | 10048482 | 11436955 | | 36955
 | | | | 11425114 | 11425114 | 8923130 | 11435947
 | | 11418164

 | 4W971819.1 | 4J237740.1 | 7549804 | TB3107.1 | T83107.1 | BE871610.1
 | 725466.1 | 225466.1 | AF003530.1 | 7549807 NT
 |
| Most Similar
(Top) Hit
BLAST E
Value | 1.0E-37 | 1.0E-37 | 1.0E-37 | 1.0E-37 | 1.0E-37 | 4 05 37 | 1.0E-37 | 1.0E-37 | 9.0E-38 | 8.0E-38 | 8.0E-38 | 8.0E-38
 | 7.0E-38 | 7.0E-38 | 6.0E-38 | 6.0E-38 | 8.0E-38 | 8.0E-38 | 8.0E-38
 | 6.0E-38 | 6.0€-38

 | 5.0E-38 | 5.0E-38 | 5.0E-38 | 5.0E-38 | 5.0E-38 | 5.0E-38
 | 4.0E-38 | 4.0E-38 | 3.0E-38 | 3.0E-38
 |
| Expression
Signal | 1.08 | 0.72 | 2.35 | 0.94 | 1.25 | 73.0 | 2.98 | 2.81 | 2 | 2.02 | 4.8 | 1.6
 | 0.73 | 1.31 | 1.2 | 1.6 | 1.8 | 0.57 | 2.57
 | 12.79 | 1.7

 | 1.38 | 66'0 | 0.85 | 0.92 | 0.92 | 1.48
 | 4.59 | 4.59 | 5.25 | 2.19
 |
| ORF SEQ
ID NO: | | | | | 33940 | | | | | | |
 | | | 28450 | | | 32986 |
 | 31038 | 30900

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NO: | 15955 | 16633 | 17615 | 18699 | 20807 | 200 | 23291 | 24766 | 18483 | 13952 | 15219 | ı
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 | 13484 | | <u> </u> | | | 1
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 |
| Probe
SEQ ID
NO: | 3192 | 3943 | 4888 | 5914 | 8113 | 3 | 10597 | 12363 | 2690 | 1200 | 2502 | 12420
 | 4197 | 5039 | 3037 | 5502 | 5502 | 7228 | 11918
 | 12395 | 12767

 | 710 | 2455 | 3840 | 3917 | 3917 | 6930
 | 116 | 116 | 2093 | 3684
 |
| | Exon ORF SEQ Expression (Top) Hit Top Hit Acession Signal BLASTE No. Source | Exon ORF SEQ ID NO: Expression Signal No: Most Similar Signal No: Top Hit Acession No. Top Hit Acession Database Source Top Hit Acession Signal No. Top Hit Acession No. Database Source No. Source Source No. Source No. Source No. r>SEQ ID
NO: ORF SEQ
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Source No: Avge2082.1 EST_HUMAN RC3-CT0347-210400-016-h03 CT0347 Hom
Homo sapiens ribonuclease III (RN3) mRNA, | Exon NO:- SEQ ID NO:- NO:- Signal NO:- Signal NO:- Signal NO:- Signal NO:- NO:- Signal NO:- NO:- NO:- NO:- NO:- NO:- NO:- NO:- | Exon SEQ ID NO: ORF SEQ ID NO: Expression Signal No: Most Similar Value No. Top Hit Acession No. Top Hit Acession No. Top Hit Acession No. Top Hit Acession No. Top Hit Acession No. Top Hit Acession No. Database Source Nation No. Database Source Nation No. Source Nation No. No. Source Nation No. No. Source Nation No. No. Source Nation No. No. No. No. No. No. No. No. No. No. No. No. No. No. No. HUMAN No. O:- SEQ ID NO:- Signal NO:- SEQ ID NO:- Signal NO | Exon SEQ ID NO: ORF SEQ Signal Signal Signal NO: Top Hit Top Hit Acession Signal No: Top Hit Top Hit Acession No: Top Hit Top Hit Acession Signal No: Top Hit Top Hit Acession No: Acession No: Acession No: Acession No: Acession No: Acession No: Acession No: Acession No: Acession No: | Exon SEQ ID NO: CRF SEQ Signal Signal Signal NO: Top Hit Top Hit Top Hit Top Hit 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Signal No: No: Signal No: No: Signal No: No: Signal No: No: No: No: No: No: No: No: No: No: | Exon ORF SEQ Expression Signal Top Hit Top Hit Top Hit Top Hit Acession No. Top Hit Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Top Hit Acession No. Top Hit Top Hit Top Hit Top Hit Acession No. Top Hit Top Hit Top Hit Top Hit Acession No. Top Hit Top Hit Top Hit Acession No. Top Hit Top Hit Top Hit Acession No. Top Hit Top Hit Top Hit Acession No. Top Hit Top Hit Top Hit Acession No. Top Hit Top | Exon No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: Signal No: No: No: Signal No: No: No: Signal No: No: No: Signal No: No: No: Signal No: No: No: Signal No: No: No: Signal No: No: No: No: No: No: No: No: No: No: | Exon No: Signal ORF SEQ ID No: Signal ORF SEQ ID No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signal No: Signa | Exon ORF SEQ Expression Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Acession Signal Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Hit Hit Top Hit Top Hit Top Hit Hit Hit Top | Exon ORF SEQ Expression Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit Top Hit Acession Signal Top Hit Top Hit 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11436956 NT EST HUMAN 1636 1.31 7.06-38 BF34922.1.1 EST HUMAN 1633 1.1436956 NT EST HUMAN 1630 31199 1.6 6.06-38 BF34923.1.1 EST HUMAN | Exon No.: ORF SEQ ID No.: Expression Signal No.: Top Hit Top Hit Top Hit Top Hit Top Hit No.: Top Hit Source Source No.: Top Hit Top Hit Top Hit Top Hit Top Hit No.: Top Hit Source Source No.: Top Hit Top Hit Top Hit Top Hit No.: Top Hit Source Source No.: Top Hit Top Hit Top Hit Top Hit No.: Top Hit Source Source No.: Top Hit Top Hit Top Hit Top Hit No.: Top Hit Top Hit Top Hit Top Hit Top Hit No.: Top Hit | Exon ORF SEQ Expression Signal Top Hit Top Hit Top Hit Top Hit Top Hit Top Hit No. Top Hit Source Top Hit Top Hit Top Hit Top Hit No. Top Hit Source 16965 26932 1.06 1.0E-37 Aw862082.1 EST HUMAN 16863 26932 0.72 1.0E-37 AF189011.1 NT 16864 30234 2.35 1.0E-37 AF189011.1 NT 17615 30234 2.35 1.0E-37 AF189011.1 EST HUMAN 20807 33940 1.25 1.0E-37 BE548032.1 EST HUMAN 21328 34468 2.57 1.0E-37 BE71814.1 EST HUMAN 24768 2.81 1.0E-37 BE71814.1 EST HUMAN 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Figures 275 of 536 Table 4 Single Exon Probes Expressed in Brain

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Top Hit Descriptor		SSU72 PROTEIN	SSU72 PROTEIN	601157633F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3504272 5'	Homo saplens chromosome 21 segment HS21C100	xw04d01.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2827009 3'	CM3-FT0181-140700-241-f07 FT0181 Homo saplens cDNA	yv88b04.r1 Soares melanocyte 2NbHM Homo saplens cDNA clone IMAGE:249775 5'	yv88b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'	Homo saplens chromosome 21 segment HS21C048	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA	zw30d01.r1 Scares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' sImilar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE;	zw30d01.r1 Scares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW::MA12 RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE;	zd66g09.r1 Soares_feta heart_NbHH19W Homo saplens cDNA clone IMAGE:345664 5'	Homo sapiens mRNA for ankyrin B (440 kDa)	Homo sapiens mRNA for ankyrin B (440 kDa)	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA	HSC18F031 normalized infant brain cDNA Homo saplens cDNA clone c-18f03	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds	hu09g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:002710 002710 GAG POLYPROTEIN ;	Homo sapiens mRNA for KIAA0145 protein, partial cds	no34g03.s1 NCI_CGAP_Pr23 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316 E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE.;	no34g03.s1 NCI_CGAP_Pr23 Homo sapiens cDNA clone IMAGE:1102612 3 similar to TR:E212316	EZIZS IO NACIONES ENDEM L'ECONO INCINE DE 12411 DINOMINATE DE 1241	QV2-HT0698-080800-293-a05 HT0698 Homo sapiens cDNA	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds	
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Expression Signal		1.76	1.76	1.47	8,11	0.56	8.26	2.1	2.1	2.24	1.65	1.4	2.99	2.21	2.21	1.45	0.69	69.0	1.46	4.38	0.56	2.04	1.06	1.71	1.37		1.37	5.79	3.52	
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Page 276 of 536 Table 4 Single Exon Probes Expressed in Brain

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טווקים ראטון וספס ראף פססם וויסיים	Top Hit Descriptor	Homo sapiens leucine-rich repeat-containing G protoin-coupled receptor 6 (LGR6) mRNA, partial cds	AV726988 HTC Homo sapiens cDNA clone HTCAXH07 5'	Homo sapiens gene for kinesin-like protein, complete cds	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'	E1 bata≕pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA	zu62b02.r1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element;	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA	Homo sepiens KIAA0173 gene product (KIAA0173), mRNA	Homo sapiens cyclin K (CCNK) gene, exon 7	Hamo septens chromosome 21 segment HS21C003	Homo sapiens chromosome 21 segment HS21C003	Homo septens hypothetical protein FLJ10600 (FLJ10600), mRNA	Mus musculus otogelin (Otog), mRNA	Mus musculus otogelin (Otog), mRNA	Homo sapiens mRNA for KIAA0612 protein, partial cds	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similer to contains MER29.b3 MER29 repetitive element;	yf96b08.r1 Soares infant brain 1NIB Homo saplens cDNA clone IMAGE:30486 5'	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA	wh53f10.x1 NCI_CGAP_Kid11 Homo sapiens oDNA clone (MAGE:2384491 3' sImilar to TR:P87890 P87890 PPCL PROTEIN ;	Homo saplens chromosome 21 segment HS21C027	QV/1-BT0631-040900-357-f02 BT0631 Homo saplens cDNA	7e34c03.x1 NCI_CGAP_Lu24 Horno sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6 CE00828 ;	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flenking repeat regions
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	Top Hit Acession No.	,			2.0E-38 H55641.1		11418248 NT	1.0E-38 AA401570.1	4885288 NT	7661969 NT	1.0E-38 AF270831.1	1.0E-38 AL163203.2	1.0E-38 AL163203.2	8922543	7305360 NT	7305360 NT	1.0E-38 AB014512.1	11422250 NT	1.0E-38 BE350127.1	38 R18512.1	7662109 NT	1.0E-38 AL163284.2	4502312 NT	4758229 NT	8.0E-39 AI823404.1		6.0E-39 BF331829.1	6.0E-39 BE670394.1	5.0E-39 AF003528.1
	Most Similar (Top) Hit BLAST E Value	2.0E-38	2.0E-38 /	2.0E-38	2.0E-38 h	2.0E-38	2.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38 /	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	8.0E-39	8.0E-39	8.0E-39	7.0E-39	6.0E-39	6.0E-39	5.0E-39
	Expression Signal	3.52	3.05	2.06	6.45	1.43	3.76	2.55	2.53	1.11	2.34	1.23	1.23	-	4.71	4.71	3.15	0.71	5.13	0.58	1.28	2.2	15.3	1.45	1.27	5.79	2.24	1.66	1.57
	ORF SEQ ID NO:	37558			31081				27450		27960					31678		34898			l		25510			27650			26412
	SEQ ID	24235	24517	24518	24705	24742	25031	1	14728	14747	l		ı	1	l	18719		21740	l	L	24187	25140	12882	14121	14580	14819	23400		
	Probe SEQ ID NO:	11638	11971	11973	12260	12323	12777	1071	1992	2012	2489	4290	4280	4558	5937	5937	7304	9051	9310	10301	11588	12118	53	1373	1821	2087	10711	12696	987

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2984	15750	28397	8.62	5.05-39	-39 AI750154.1	EST_HUMAN	at36b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;contains LTR7.t1 LTR7 repetitive element ;
12410			2.04	5.0E-39	11420289 NT	NT	Homo saplens hypothetical protein FLJ10803 (FLJ10803), mRNA
537		25954		4.0E-39	-39 AB015610.1	NT	Chlorocebus aethlops mRNA for ribosomal protein S4X, complete cds
3559	16314	28961	26'0	4.0E-39	-39 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7974		33791	1.27	4.0E-39	-39 AA682949.1	EST HUMAN	ae92g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains OFR.b1 OFR repetitive element;
9228	21907			4.0E-39	-39 D84116.1	N	Homo sapiens DNA for prostacyclin synthase, exon 2
9228	21907	35079	92.0	4.0E-39	-39 D84116.1	N	Homo sapiens DNA for prostacyclin synthase, exon 2
12427	24802		4.47	4.0E-39	11418177 NT	L	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12534			2.71	4.0E-39	-39 BE836452.1	EST_HUMAN	QV0-FN0063-260600-278-c06 FN0063 Homo sapiens cDNA
46		25498		3.0E-39	-39 AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
46	12875	25499	14.86	3.0E-39	-39 AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
46	12875	25500	14.86	3.0E-39	-39 AA631949.1	EST_HUMAN	firifc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
11963	24511	37257	4.35	3.0E-39	-39 Al084557.1	EST_HUMAN	ox3a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
11963	24511	37258	4.35	3.0E-39	AI084557.1	EST_HUMAN	ox83a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;
12006	24541		5.82	3.0E-39		EST_HUMAN	yp51c06.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:1909543'
877			5.8	2.0E-39		EST_HUMAN	601301607F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3636289 5'
892			14.08	2.0E	-39 AI525119.1	EST_HUMAN	promma-7.D01.r bytumor Homo sapiens cDNA 5'
1009	13769		4.2	2.0E-39	-39 AF000573.1	NT	Home saplens homogentisate 1,2-dioxygenase gene, complete cds
1520	14267		11.91	2.0E-39	-39 AW372318.1	EST_HUMAN	PM0-BT0340-211299-003-d02 BT0340 Homo saplens cDNA
1966	14702	27419	3.28	2.0E-39	-39 AA720574.1	EST HUMAN	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element :
2634	15346	28089	1.84	2.0E-39	-39 AL163248.2	LN	Homo sapiens chromosome 21 segment HS21C048
4370	17108	29743	1.48	2.0E-39	-39 BF370207.1	EST_HUMAN	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA
5403		30907	4.21	2.0E-39	-39 AA508880.11	EST_HUMAN	ng86f03.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:941693
7269				2.0E-39	-39 AA080867.1	EST_HUMAN	Zn06f02.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
7431				2.0E-39	-39 AL163202.2	NT	Homo saplens chromosome 21 segment HS21C002
7431		33196		2.0E-39	-39 AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8209		34038		2.0E-39	-39 AF078779.1	LN	Rettus norvegicus putative four repeat ion channel mRNA, complete cds
9394	22056		0.55	2.0E-39	-39 AA984531.1	EST HUMAN	am88c11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630196 3'

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SEQ ID NO: 1408 11408 11503 11	"	ORF SEQ ID NO: 10 NO: 26836 2884 2884 2884 28881 30735 30735 31287 31287 31287 34287 28855 2885	Signa Signa	Most Sin (Top) H (Albert Correction of the Corre	Top Hit Acession No. No. No. No. No. No. No. No. No. No.		Lu55ec3.x1 NCI_CGAP_P728 Home sapiens cDNA done IMAGE:22530523' Human mRNA for KIAA0209 gens, partial cds Home sapiens KVLQT1 gene Home sapiens KVLQT1 gene Home sapiens KVLQT1 gene Home sapiens KVLQT1 gene Home sapiens KVLQT1 gene Home sapiens KVLQT1 gene Home sapiens KVLQT1 gene Home sapiens Catelon (Cadderlin-associated protein), alpha 2 (CTNNA2), mRNA Home sapiens Catelon (Cadderlin-associated protein), alpha 2 (CTNNA2), mRNA Home sapiens CATELONA22, mRNA Home sapiens CATELONA22, mRNA Home sapiens CATELONA22, mRNA Home sapiens DKFZA43P211 protein (DKFZP434P211), mRNA Home sapiens DKFZA43P211 protein (DKFZP434P211), mRNA Home sapiens DKFZA43P211 protein (DKFZP434P211), mRNA Home sapiens DKFZA43P211 protein (DKFZP434P211), mRNA Home sapiens GATELONA220 Harden sapiens cDNA Home sapiens GATELONA220 Harden sapiens CDNA Home sapiens Edal liver spien NH25 Home sapiens cDNA Home sapiens Edal liver spien NH25 Home sapiens cDNA Home sapiens Edal liver spien NH25 Home sapiens CNNA Home sapiens mRNA for neuronal Interacting factor X ((NIX1) (NIX1 gene) Home sapiens tubby Interacting factor X ((NIX1) (NIX1 gene) Home sapiens tubby Interacting factor X ((NIX1) (NIX1 gene) Home sapiens tubby Interacting factor X ((NIX1) (NIX1 gene) Home sapiens AE-binding protein 1 (AEBP1) mRNA Home sapiens AE-binding protein 1 (AEBP1) mRNA Home sapiens AE-binding protein 1 (AEBP1) mRNA Home sapiens AE-binding protein 1 (AEBP1) mRNA Home sapiens fagile X mental retardation 1 (FMR1) mRNA Home sapiens fagile X mental retardation 1 (FMR1) mRNA Home sapiens FRANA (FMLAY124 protein) and the protein of the pattern of the
3038	15802		3.35	Ш	8.0E-40 AA078155.1 8.0E-40 BE396541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Home saplens cDNA clone IMAGE:3819168 6
7616	20282	33390	2.03	7.0E	40 U60325.1	FZ	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complets cds

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Origie Exor Probes Expressed in Drain	Top Hit Descriptor	xr24e10.x1 NCI_CGAP_Ut4 Homo seplens cDNA clone IMAGE:2761098 3' similar to SW.RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;	AV731601 HTF Homo saplens cDNA clone HTFAZE05 5'	Homo saplens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mKNA, and translated products	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products	wigoart.xt NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929 ZINC FINGER PROTEIN. :	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA	Homo saplens chromosome 21 segment HS21 C080	Homo sapiens chromosome 21 segment HS21C080	nc09a09.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007608	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5	bb79a10.y1 NIH_MGC_10 Homo saplens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17. ;	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067/36 5	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5	Homo sepiens sorting nextr 3 (SNX3) mRNA	Homo saplens zinc finger protein 200 (ZNF200) mRNA, and translated products	zh76f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3	79f11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cUNA cione IMAGE:416317 3	nj42f04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995187 3	nj42f04.s1 NCI_CGAP_AA1 Homo saplens cDNA clone IMAGE:995167 3	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H J	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3	np09h03.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1115861 similar to TR:G1136406 C443eAne ผมลดนาล DECITEIN →	1130400 NIMBOLIOTEN LEINT.	nposnos, st. NCL CGAP_Frs Forme Septens CDNA Cione INVAGE. I LOSOL SILING DE L'ACTIONNO CONTRA CONTR	MR2-CT0222-211099-002-e10 CT0222 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21 CU03
I EXUIT LIODE	Top Hit Database Source	EST_HUMAN P	EST_HUMAN A			T_HUMAN		EST_HUMAN 6					EST_HUMAN 6	EST_HUMAN S	EST_HUMAN 6	EST_HUMAN 6						EST HUMAN IN		EST_HUMAN /		ESI HUMAN	EST_HUMAN C	T HUMAN	LN.
Dillo.	Top Hit Acessian No.	2.0E-40 AW303868.1	2.0E-40 AV731601.1	4506188 NT	4506188 NT	2.0E-40 AI968562.1	5453592 NT	2.0E-40 BE275932.1	5453592 NT	2.0E-40 AL163280.2	40 AL163280.2		40 BF036881.1		40 BF541030.1	1.0E-40 BF541030.1	4507142	4508012 NT		40 W92708.1	.1	40 AA573201.1	40 P26808	40 AU149345.1		40 AA614255.1	40 AA614255.1	1.0E-40 BF334112.1	41 AL163203.2
	Most Similar (Top) Hit BLAST E Value	2.0E-40	2.0E-40 /	2.0E-40	2.0E-40	2.0E-40	2.0E-40	2.0E-40	2.0E-40	2.0E-40	2.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40	1.0E-40		1.0E-40	1.0E-40	1.0E-40	8.0E-41
	Expression Signal	1.61	0.92	1.58	1.58	1.21	2.48	1.44	4.28	1.68	1.68	1.78	0.93	45.	1.18	1.18	1.27	4.52	0.75	0.75	1.77	1.77	0.69	8.34		1.89	1.89	10.09	1.62
	ORF SEQ ID NO:			27376			27630		28529		30198		28083		28185	L		29934			32727					37612	37613		33643
	Exen SEQ ID NO:	13549	L		14663					Ŀ	L		L	l		15447			18938	18938	L	L	L	上		24289	24289	1	20517
	Probe SEQ ID NO:	E	1818	1927	1027	2064	2166	2695	3123	4843	4843	883	2627	2892	2741	2741	3292	4571	6161	6161	6987	6987	7133	10834		11694	11694	12376	7822

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-		_	_	_		_	_	_	_	_		_	1	_	_	_	_	_	_		_					_	_	
Single Extributes Expressed in Diali	Top Hit Descriptor	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3803955 5'	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA	Homo saplens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA	Homo saplens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA	Human platelet activating factor acetyfhydrolase, brain isoform, 45 kDa subunit (US1) gene, exons 3 and 4	Homo saplens guanine nucleotide binding protein 10 (GNG10) mRNA	Homo septens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo sapiens DSCR5b mRNA, complete cds	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE;3682677 5'	UI-H-BW1-amp-b-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'	yc03e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79626 3'	Homo saplens target of myb1 (chicken) homolog (TOM1), mRNA	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA	QV0-HT0367-150200-114-g09 HT0367 Homo saplens cDNA	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'	ow45e06.s1 Sceres_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME CLIKE POLYPEPTIDE.; contains LTR5.b1 LTR5 repetitive element;	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sepiens cDNA clone IMAGE:1649794 3' similar to TR:000597 CVTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 resettive element:	Homo sapiens gene for activin receptor type IIB, complete cds	tm96c04.x1 NCI_CGAP_Brn25 Homo saplens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element;	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	H.saplens DNase I hypersensitive site (HSS-3) enhancer element
פום ביסוו ביס	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	FZ	NT	Į.	NT	NT	Ā	N	Į.	۲Z	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Z L	EST_HUMAN	FN	TN	L
5	Top Hit Acession No.	-41 A1934364.1	7.0E-41 Al934364.1	3E389592.1	7.0E-41 BE389592.1	11545770 NT	11419208 NT	11433010 NT	172335.1	4758445 NT	7.0E-41 AF223391.1	11417972 NT	6.0E-41 AB037163.1	7657042 NT	6.0E-41 BE567816.1	3F513783.1	5.0E-41 T62628.1	4885636 NT			4.0E-41 AU119344.1	-41 Al027117.1	4.0E.41 AI027117.1	4.0E-41 AB008681.1	4.0E-41 AI500406.1	4.0E-41 AJ229041.1	4.0E-41 AJ229041.1	(92685.1
	л ш ш ш	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41 U72335.1	7.0E-41	7.0E-41	7.0E-41	6.0E-41	6.0E-41	6.0E-41	6.0E-41	5.0E-41	5.0E-41	5.0E-41	4.0E-41	4.0E-41 /	4.0E-41	4.0E.41	4.0E-41 /	4.0E-41	4.0E-41	4.0E-41	4.0E-41 X92685.1
	Expression Signal	1.24	1.24	0.92	0.92	1.2	3.49	0.61	0.68	2.23	1.73	4.35	1.19	2.04	0.91	1.44	1.11	1.07	2.29	2.42	1.26	15.51	15.51	1.88	6.08	3.55	3.55	2.24
	ORF SEQ ID NO:		26247	29976	29977		31656	32009	30528	37366	37552		25724	27569	29797	33692	27244				26492	26810	26811	26830	27065	28302	28303	29493
	Exen SEQ ID NO:	15553	15553	17344	17344	17991	18703	19034	17971	24060	24228	25271	13081	14835	17169	20566	14535	16830	19220	13169	13834	14135	14135	14150	14378	15658	15658	16866
	Probe SEQ ID NO:	808	808	4609	4609	5183	5918	6260	6895	11411	11631	12782	274	2104	4433	7871	1795	4087	6452	382	1076	1388	1388	1403	1632	2891	2891	4124

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					ĭ:)	מסון וומעדון מופין	
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3201	L		1.05	1.0E-	41 BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4529	17264		14.08		6678468 NT	۲N	Mus musculus tubulin alpha 6 (Tuba6), mRNA
6749	17918		99'0	1.0E-41	1.0E-41 H99079.1	EST_HUMAN	yx18b03.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262061 3'
9318	21985		1.69	1.0E-41	F.	EST_HUMAN	q75c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
11111	23781	37056		1.0E-41	AW847812.1	EST_HUMAN	IL3-CT0213-190200-040-F09 CT0213 Homo sapiens cDNA
12054	24571		2.81	1.0E-41	11526291	ΙΝ	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8418	21111		1.14	9.0E-42	9.0E-42 BE179191.1	EST_HUMAN	RC0-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
9072	21761	34922	3.49	9.0E-42	11560151 NT	TN	Homo saplens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9072	21761	34923	3.49	9.0E-42	11560151 NT	LN L	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
450	13236		7.71	8.0E-42	42 AF003530.1	LN	Homo saplens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2102	14833	27567	0.92	8.0E-42	42 AB026898.1	LΝ	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12093			4.4	8.0E-42	42 AA493896.1	EST_HUMAN	nh07c02.s1 NCI_CGAP_Thr/J Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304 3678P EXPRESSED SEQUENCE TAG MRNA;
12111	25154		1.56	8.0E-42	_	EST_HUMAN	xc97a04.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2592174.3' similar to contains OFR.t2 OFR repetitive element;
911	13678		2.58	7.0E-42	42 AL163285.2	N	Homo saplens chromosome 21 segment HS21C085
9143	21874	35039	1.57	7.0E-42		EST_HUMAN	qf68g12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
11126		37071	1.3	7.0E-42	42 AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652
11126	l _		1.3	7.0E-42	42 AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652
1848	L			6.0E-42		IN	Homo sapiens phosphatidylmositol 4-kinase 230 (pi4K230) mRNA, complete cds
1848	14586			6.0E-42	42 AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
							xp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.t1 L1
2287		-	3.55	6.0E-42		EST_HUMAN	repetitive element ;
5381		30871	1.83	6.0E-42		N	Homo sapiens mRNA for KIAA1067 protein, partial cds
5630	_	30871	1.45	6.0E-42		N⊣	Homo sapiens mRNA for KIAA1087 protein, partfal cds
132				5.0E-42		NT	Homo saplens Xq pseudoautosomal region; segment 1/2
428		25859		5.0E-42	42 BE21 7913.1	EST_HUMAN	hv31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
474			2.57	5.0E-42		ΝŢ	Homo saplens SET domain and mariner transposase fusion gene (SETMAR) mRNA
475	13261		2.74	5.0E-42	5730038 NT	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETWAR) mRNA
6587	19350	32363	1.04	5.0E-42	11433063 NT	۲N	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6587	19350	32364	1.04	5.0E-42	11433063 NT	Z L	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
	ı	l					

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo saplens myotubularin related protein 3 (MTMR3), mRNA	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds	Homo sapiens reelin (RELN) mRNA	Homo saplens mRNA for KIAA1294 protein, partial cds	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA	Homo saplens MHC class 1 region	Homo saplens MHC class 1 region	Homo sapiens ribonuclease III (RN3) mRNA, complete cds	H.sapiens PROS-27 mRNA	Homo saplens SNARE protein kinase SNAK mRNA, complete cds	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA	Homo saplens zinc finger protein 177 (ZNF177) mRNA	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA	2819293.3prlme NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'	EST367438 MAGE resequences, MAGC Homo sapiens cDNA	EST367438 MAGE resequences, MAGC Homo sapiens cDNA	ow83d05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1653417.3	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5	RIBONUCLEASE K3 (RNASE K3)	RIBONUCLEASE K3 (RNASE K3)	Homo sapiens chromosome 21 segment HS21C046	Human endogenous retrovirus pHE.1 (ERV9)	UI-H-BI1-afth-e-04-0-UI.s1 NOI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:27218713'	Homo sapiens partial C9 gene for complement component C9, exon 1	Homo sapiens partial C9 gene for complement component C9, exon 1	Homo saplens NADH-ubiquinone oxidereductase AGGG subunit precursor homolog mRNA, nuclear gene	encoding mitochondrial protein, complete ods	Homo sapiens NADH-ublquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
gie Exon Proc	Top Hit Database Source	LZ	Ż	LN LN	FN	ΤN	LΝ	FZ	L	Ν	F	FN.	LN L	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	LZ	LN.	EST_HUMAN	FN	LNT		LZ LZ	NT
CIIO	Top Hit Acession No.	11417957 NT	5.0E-42 AF071569.1	4826977 NT	5.0E-42 AB037715.1	8923162 NT	4.0E-42 AF055066.1	4.0E-42 AF055066.1	4.0E-42 AF189011.1	(59417.1	4.0E-42 AF246219.1	4506496 NT	4508008 NT	4.0E-42 AW818630.1	4,0E-42 AW818630.1	4.0E-42 BF035327.1	3F376834.1	\W898344.1	W 250059.1	\W955368.1	AW955368.1	1052586.1	3E538919.1	981649	2.0E-42 P81649	L163246.2	(57147.1	1.0E-42 AW295809.1	1.0E-42 AJ251818.1	E-42 AJ251818.1		1.0E-42 AF067166.1	1.0E-42 AF067166.1
	Most Similar (Top) Hit BLAST E Value	5.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42	4.0E-42	4.0E-42 /	4.0E-42	4.0E-42 X59417.1	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42/	4.0E-42	2.0E-42	2.0E-42	2.0E-42 /	2.0E-42 /	2.0E-42 /	2.0E-42	2.0E-42	2.0E-42 F	2.0E-42 F	2.0E-42	1.0E-42 X57147.1	1.0E-42	1.0E-42	1.0E-42		1.0E-42/	1.0E-42
	Expression Signal	3.12	1.59	0.57	3.55	2.44	5,09	5.09	3.46	1.22	1.07	4.15	15.12	1.56	1.56	1.5	2.81	2.92	2.22	7.8	7.8	1.46	1.32	0.68	0.68	1.37	1.21	1.1	1.18	1.18		16.49	16.49
	ORF SEQ ID NO:	32662	32854	33489	34515	36849	26167	26168	26462	29541	29570	29589	58909	36475	36476	37297	26902		27879	31379	31380	32429	35596	35807	35808	37660	26143	26441	26495	26496		26841	26642
	Exan SEQ ID NO:	19619	19789	20375	21369	23600	13510	13510	13803	16911	16943	16964	17278	23241	23241	23995	14213	15134	15146	18465	18465	19416	22392	22603	22603	24334	13490	13779	13837	13837		15563	15563
	Probe SEQ ID NO:	6704	7101	7711	8677	10920	736	736	1044	4171	4202	4223	4543	10545	10545	11389	1466	2413	2425	5670	9299	6654	144	9955	9988	11742	717	1018	1079	1079		1220	1220

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	T	T	Т		Т	٦									Г							Г						Γ			T	T	7
Top Hit Descriptor	Homo sanians rec (1 OC51201) mRNA	The second of th	Homo sapiens major nistocompatibility complex, class II, UM alpha (TLA-UMA) mKINA	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-iike (ORCSL) mRNA, and translated	products	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens chromosome 21 segment HS21C080	RC3-ST0197-161099-012-a03 ST0197 Homo sapiens cDNA	Homo saplens proteasome inhibitor (PI31), mRNA	Homo sapiens proteasome inhibitor (Pi31), mRNA	Homo sapiens ryanodine receptor 3 (RYR3) mRNA	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA	AV736924 CB Homo sapiens cDNA clone CBLAKH08 5'	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA	Homo saptens hypothetical protein FLJ20297 (FLJ20297), mRNA	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA	yj08e11,r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'	wp69b01.x1 NQ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repelitive element;	ne72d06:s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to gb:L05095 60S	RIBOSOMAL PROTEIN L30 (HUMAN);	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'	Homo saplens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains	MER1.t3 MER1 MER1 repetitive element;	2735e06.r1 Soares_NhHMPu_S1 Homo septens cDNA clone IMAGE:665410 5' similar to TR:G529641	0.02504 1 001, 0.00m LET L. 0.00., journality element 1 11, 1 epourbe element; DKF757641 1712 1 761 (synonym: hamy?) Homo sapiens cDNA clone DKF757611 1712 5'	Home series chromesome 21 segment HS21C013	
Top Hit Database Source	TN	141	Z		N	M	NT	NT	EST_HUMAN	NT	NT	NT	NT	TN	LN	EST_HUMAN	EST_HUMAN	NT	IN	IN.	EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	Ę		EST_HUMAN	MARKET TOTAL	EST HIMAN	FIN	
Top Hit Acession No.	TIV 0503040	0170711	5174458 N		4505524 NT	7662027 NT	1.0E-42 AL163267.2	-42 AL163280,2	-42 AW813617.1	5803122 NT	5803122 NT	4506758 NT	4501912 NT	4501912 NT	4757969 NT	4V736824.1	8.0E-43 AV736824.1	8923276 NT	8923276 NT	8923276 NT	8.0E-43 H13952.1	-43 AW 246442.1	-43 A1936748.1		-43 AA491890.1	-43 AV708201.1	1 9955973 NT		-43 AW 468897.1	7 7 1 1 1 0 7 4 4	-45 AK 195154.1	E OF 43 A1 462343 2	AL 1032 13.2
Most Similar (Top) Hit BLAST E Value	7 00 73	1.05-72	1.0E-42	I	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	1.0E-42	9.0E-43	8.0E-43	8.0E-43	8.0E-43	8.0E-43	8.0E-43	8.0E-43	7.0E-43	7.0E-43		6.0E-43	6.0E-43	6.0E-43		6.0E-43	L	0.00	200.0	0.VE-10
Expression Signal	7 43	2	1.63		10.26	2.6	1.17	1.92	0.75	1.88	1.88	6.02	1.08	1.08	4.03	19.69	19.69	6.03	6.03	6.03	0.76	6.42	4.09		10.45	2.25	2.24		2.09	0,0	2.10	20.3	FV.2
ORF SEQ ID NO:			27998		28380	29088	29296	29587	29918	30062	30063	30097	30378	30379	35844			26104	26105	26106	31321	29025					31969		32492)00cs		
Exon SEQ ID NO:	14420	2	15261		15730	16449	16655	16962	17289	17431	17431	17460	17763	17763	22634	13416	13416	13459	13459	13459	18408	16385	21359		14070	15314	18993		19469		22402	40069	337
Probe SEQ ID NO:	1808	0801	2546		2964	3695	3905	4221	4554	4697	4697	4728	5044	5044	9866	637	637	884	884	884	5612	3632	8667		1321	2600	6219		8089		9/01	1000	2

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Probe SEQ ID . NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2280	15590	27746	0.96	1.0E-44	-44 AA398099.1	EST_HUMAN	zt88g11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729476 5'
							Homo saplens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domein protein, 8.4 differentiation-dependent protein, triple LIM domein protein, 8.4 differentiation-dependent protein, triple LIM domein protein, 8.4 differentiation-dependent protein, triple LIM domein protein, 8.4 differentiation-dependent protein, triple LIM domein protein, 9.4 differentiation-dependent protein, 19.4 domein protein, 19.4 d
2763	15468	28211	1.44	1.0E-44	1.0E-44 AF196779.1	LN LN	complete cds; and L-type calcium channel a>
3712	18485		3.73	1.0E-44	E-44 AA455869.1	EST HUMAN	aa01c09.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
5048		30385	1.04	1.0E-44	1.0E-44 AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5048		30386	1.04	1.0E-44	AJ130755.1	LN	Homo sapiens alpha satellite DNA, M1 monomer type
8163	20857	33988	96.0	1.0E-44	1.0E-44 AW967073.1	EST HUMAN	EST379147 MAGE resequences, MAGJ Homo saplens cDNA
8163	1			1.0E-44	-44 AW967073.1	EST_HUMAN	EST379147 MAGE resequences, MAGJ Homo sapiens cDNA
8544	21236	34380		1.0E-44	E-44 AL163209.2	١	Homo sapiens chromosome 21 segment HS21C009
8924			0.69	1.0E-44	-44 Al337183.1	EST_HUMAN	qx88g07.x1 NCI_CGAP_GC6 Hamo sapiens cDNA clone IMAGE:2009628 3'
10936	23616		4.04	1.0E-44	-44 AV714608.1	EST_HUMAN	AV714608 DCB Hamo sapiens cDNA clone DCBBYE03 5'
11518	24116	37427	3.92	1.0E-44	10092664 NT	N _T	Homo sapiens Sushi domain (SCR repeat) containing (BK65A6.2), mRNA
11583	24182	37496	3.17	1.0E-44	-44 AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo saplens cDNA
11583	Ι.	37497	3.17	1.0E-44	1.0E-44 AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4539	i i	29908	1.38	9.0E-45	8922391	TN	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4539	17274	28807	1.38	9.0E-45	8922391 NT	N	Homo saplens hypothetical protein FLJ10379 (FLJ10379), mRNA
6552	L_i	32323	1.31	9.0E-45	9.0E-45 AB023212.1	NT	Homo saplens mRNA for KIAA0995 protein, partial cds
2527	15243	27982		8.0E-45	5174718 NT	LN	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5023		30355	6.41	8.0E-45	6174718 NT	TN	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
6414	19182	32181	0.66	8.0E-45	8.0E-45 AW892763.1	EST_HUMAN	CMO-NN0005-130300-283-b09 NN0005 Homo sapiens cDNA
9008	20701	33830	0.91	8.0E-45	8.0E-45 AA377985.1	EST_HUMAN	EST90893 Synovial sarcoma Homo saplens cDNA 6' end
1545	14291		- 5	8.0E.45	8 0E 45 A 1875425 1	FST HUMAN	wb99c06.X1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.t1 L1 repetitive element
							au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to
3960	16709		4.09	6.0E-45	6.0E-45 AW157570.1	EST HUMAN	SW-R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
12555	ł		1.65	6.0E-45	11418213 NT	LZ	Homo saplens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
872	l		1.03	6.0E-45	45 AL163203.2	FZ	Homo saplens chromosome 21 segment HS21C003
1995	14731	27453	3.65	5.0E-45	-45 BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-f01 CN0044 Homo saplens cDNA
3204	15967	28621	1.79	5.0E-45	5.0E-45 AI623766.1	EST_HUMAN	to the complete of the control of th
0 7 2	1			76.77		No. H. L.	272403.s1 Soares_testis_NHT Home saplens cDNA clone IMAGE:727877.3 similar to contains element
2423	- }			30.0	-	EST TOWN	TOTAL TOTAL
2928	18713	31669	1.31	5.0E-45	5.0E-45/Y18933.1	Z	Homo sapiens MCF-1 gene and ennancer region

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Cingre Extended Expressed in Drain	Top Hit Descriptor	Homo sapiens MCP-1 gene and enhancer region	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds	Homo sapiens zinc finger protein 277 (ZNF277), mRNA	Homo sapiens zinc finger protein 277 (ZNF277), mRNA	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA	Homo saplens programmed cell death 5 (PDCD5), mRNA	Homo sapiens golgin-ilke protein (GLP), mRNA	H,saplens ART4 gene	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'	nc28e07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1	repetitive element;	yd35107.11 Sogres fetal liver spiecen TNFLS Homo sapiens cDNA clone IMAGE:110249 5	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA	AV723976 HTB Homo sepiens cDNA clone HTBAAG01 5'	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA	Homo sapiens chromosome 21 segment HS21C027	Homo sapiens chromosome 21 segment HS21 C027	H.sapiens DNA for endogenous retroviral like element	Homo sapiens chromosome 21 segment HS21C018	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	Human eosinophil Charcot-Leyden crystal (CLC) protein (Iysophospholipase) gene, promoter and exon 1	601467793F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5'	RC0-LT0001-150200-032-d11 LT0001 Homo sapiens cDNA	ts56a01.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232552 3'	MR0-HT0923-190800-201-a02 HT0923 Homo sapiens cDNA	aa87/12.r1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to	IR:G1144569 G1144509 K-SL71.	xp72a03.xt NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5
אום באחון בוסג	Top Hit Database Source	NT	TN	FZ	LN.	占	TN	. LN	LN	ΙΝ	EST_HUMAN			EST_HUMAN	님	NT	EST_HUMAN	NT	NT	NT	NT	M	LN	Ę	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST HOMAN		EST_HUMAN
31110	Top Hit Acession No.	45 Y18933.1	45 AB022318.1	45 AB022318.1	11496268 NT	11496268 NT	11418704 NT	4759223 NT	8923698 NT	45 X95828.1	45 BE265622.1		5	45 T71480.1	6753651 NT	6753651 NT	-45 AV723976.1	4758451 NT			45 X89211.1	-45 AL163218.2	45 AJ243213.1	45 L01665.1	-45 BE782184.1	45 AW834834.1	-45 AI636786.1	-45 BE934350.1		-45 AA458770.1	-45 AW 270280.1	-45 AW 270280.1	18157	-45 BE389855.1
	Most Similar (Top) Hit BLAST E Value	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	4.0E-45	4.0E-45		4.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0E-45	2.0E-45	2.0E-45	2.0E-45	2.0E-45	2.0E-45	2.0E-45	2.0E-45		2.0E-45	2.0E-45	2.0E-45	2.0E-45	1.0E-45
	Expression Signal	1.31	0.79	0.79	1.02	1.02	0.73	1.95	2.59	9.58	2.42		0.82	1.35	1.36	1.36	4.1	3.74	13.43	13.43	2.35	2.21	1.22	5.15	1.22	0.78	0.48	18.28		4.16	1.75	1.75	3.93	1.6
	ORF SEQ ID NO:	31670	31717	31718	31842	31843	34000	34773	37617	26536	27750				31890	31891		34526	36068	36069			28441	32194	33274	34145	35318	36633		37073	37400	37401		
	Exon SEQ ID NO:	18713	18756	18756	18874	18874	20868	21630	24292	13877	15014		21548	16085	18920	18920	21043	21382	22854	22854	25314	15223	15795	19197	20181	21007	22138	25130		23797	24089	24089	24987	13185
	Probe SEQ ID NO:	5929	5974	5974	9609	9609	8174	8939	11697	1121	2289		8855	4066	6142	8142	8350	0698	10206	10206	12670	2506	3029	6429	7510	8314	9485	10705		11129	11488	11488	12711	120

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	Top Hit Descriptor	601284360F1 NIH_MGC_44 Hamo saplens cDNA clone IMAGE:3806183 5'	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA	Homo saplens Langerhans cell specific c-type lectin (LANGERIN), mRNA	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds	Homo sapiens chromosome 21 open reading frame 1 (C21ort4), mRNA	Homo saplens mRNA for KIAA1591 protein, partial cds	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'	yr05b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:204363 5'	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA	Homo sapiens DNA for amyloid precursor protein, complete cds	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5	Human mRNA for KIAA0299 gene, partfal cds	Homo saplens alpha-catenin-like protein (VR22), mRNA	Homo saplens protein kinase C, alpha binding protein (PRKCABP), mRNA	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA	Mus musculus keretin complex 2, gene 6g (Krt2-6g), mRNA	Homo sapiens chromosome 21 segment HS21C009	2822449.5prime NIH_MGC_7 Homo saplens cDNA clone IMAGE;2822449 5'	t32f08.x1 NCI_CGAP_Gas4 Homo sepiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_fna2 TUBULIN BETA-1 CHAIN (HUMAN);	183708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2 TUBILLIN BETA-1 CHAIN (HUMAN):	RC5-HT0508-280200-012-C12 HT0506 Homo sapiens cDNA	Rattus novegicus espin mRNA, complete ods	601277292F1 NIH_MGC_20 Homo saplens cDNA done IMAGE:3618119 5'	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA	Homo saplens hypothetical protein FLJ10847 (FLJ10847), mRNA	601822835F1 NIH_MGC_77 Homo saplens cDNA done IMAGE:4042736 5'	wm31f08.x1 NCI_CGAP_Ut4 Homo saplens cDNA clone IMAGE:2437575 3' similar to contains MER19.t2 MER19 repetitive element ;
	Top Hit Database Source	EST_HUMAN					NT	EST_HUMAN	EST_HUMAN				EST_HUMAN	LN								EST_HUMAN	EST HUMAN	NAM II	Т	Т	HUMAN	Γ.	1	EST_HUMAN	EST_HUMAN
?	Top Hit Acession No.	45 BE389855.1	4506412 NT	7657290 NT	45 U32169.1	R659558 NT	45 AB046811.1	15 BE396633.1	45 H57443.1	11422236 NT	1422236	45 D87675.1	45 BE887843.1		7019570 NT	11418099 NT	11526291 NT	11418177 NT	11418157 NT	9910283 NT	46 AL163209.2	46 AW 246964.1	46 A1433261 1	1 13000K	46 BF 187244 1		-	46 BE084386.1	8922708 NT	46 BF105845.1	46 AI884381.1
	Most Similar (Top) Hit BLAST E Value	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	IV.	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	9.0E-46	9.0E-46	9.0E-46	8 05-46 /	97 110	9.0E	7.0E-46	7.0E-46	7.0E-46	7.0E-48	7.0E-46	6.0E-46
	Expression Signal	2.17	1.38	1.79	7.42	1.38	1.19	5.01	1.04	0.77	0.77	96.0	5.08	1.22	1.33	6.93	11.18	5.28	2.6	1.7	5.86	11.23	13.53	6	3.50	103	3.38	1 33	4.01	1.14	3.90
	ORF SEQ ID NO:		25887			28897				33752		1				31125	l		30991			36239	<u> </u>		008/7	00226	ĺ		31692		
	SEO ID	13185	13245	1	ı	16240	16315	17178	17411	20625		ı			l	L			1	ı	<u>L</u>	L		L_	10102		1				1
	Probe SEQ ID NO:	400	460	1151	3101	3483	3560	4442	4677	7930	7930	8505	9019	9422	11734	12087	12263	12269	12680	8127	8532	10378	2443		2442	2242	4541	4755	5951	6402	2759

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2759	15464	28208	3.99		6.0E-46 A1884381.1	EST_HUMAN	wm31f08.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.t2 MER19 repetitive element;
6038	18818	31779	10.94	6.0E-4	i6 A1635448.1	EST_HUMAN	ts58h10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363 SA GENE:
7118	19804	32868	0.72	7-30:9	I6 AW513244.1	EST_HUMAN	xo42e04.x1 NCI_CGAP_Ut1 Homo saplens cDNA clone IMAGE:27066543' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
11364	23175		2.04	6.0E-4	16 BE784971.1	EST_HUMAN	601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880895 5'
199	13012		8.9		5.0E-46 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3519	16275		1.07		5.0E-46 BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo saplens cDNA clone IMAGE:3279408 3'
3519	16275	28930	1.07		5.0E-46 BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
9838	19398	32413		5.0E-	BF590442.1	EST HUMAN	naa3807.x1 NCI_CGAP_KId11 Homo saplens cDNA clone IMAGE:3258757 3' similar to TR:075202 075202 HOMOLOG OF RAT KIDNEY-SPECIFIC:
6842	19542	32570	4.29	5.0E-	46 BF347229.1	EST HUMAN	602021164F1 NCI_CGAP_Brn67 Homo saplens cDNA clone IMAGE:4156670 5'
6995	19687	32736			5.0E-46 AW 582253.1	EST_HUMAN	QV4-ST0212-120100-075-f09 ST0212 Homo sapiens cDNA
9515	22168	35350	0.47		6 AA398381.1	EST_HUMAN	zf62c08.s1 Scares_testis_NHT Homo saplens cDNA clone IMAGE:726926 3'
626	13405		1.1		4.0E-46 AA601143.1	EST_HUMAN	no54e09.s1 NCI_CGAP_SS1 Homo sepiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
	,			ļ			hl86c03.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1
1698	14442	27140	6.86	4.0E-4	6 AW 770544.1	EST_HUMAN	LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element;
1699	14442	27141	6.86		4.0E-46 AW 770544.1	EST_HUMAN	hB6c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMACE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
2743	15449	28188	2.62		4.0E-46 M18048.1	±N	Human endogenous retrovirus RTVL-H2
4384	17121	29753				LNT	Homo sapiens mRNA for KIAA0622 protein, partial cds
4384	17121	29754	1.04		4.0E-46 AB014522.1	NT .	Homo sapiens mRNA for KIAA0622 protein, partial cds
5350	18153	30834			4.0E-46 M36852.1	NT	Human ig germine gamma-3 heavy-chain gene V region, partial cds
5350	18153	30835		4.0E-4	4.0E-46 M36852.1	NT	Human ig germline gamma-3 heavy-chain gene V region, partial cds
12513	24863	31014		4.0E-4	AB00205	NT	Homo sapiens DNA for Human P2XM, complete cds
2155	14885	27618			5453620 NT	NT	Homo saplens solute carrier family 35 (CMP-sialic acid transporter), member 1 (SLC35A1), mRNA
2429	15150	27884			3.0E-46 AF160212.1	N	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
4362	17100	29735	0.79	3.0E-46	4506376 NT	LN.	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA
4724	17456	30091	1.2		3.0E-46 Z73660.1	N	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; V.Lambda

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oligie caul riopes capiessed il piali	Top Hit Descriptor	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda	w/49c04.x1 NCI_CGAP_Lu19 Homo sepiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;	Human mRNA for KIAA0061 gene, partial cds	ne05a09.s1 NCI_CGAP_Co3 Homo saplens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR	2127211.s1 Soares, fetal liver splean 1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3'	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds	259e02.r1 Soares, testis, NHT Homo saplens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN.;	Mus musculus sperm tail associated protein (Stap), mRNA	601445137F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3849297 5'	yr32d01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:206977 5	xq78h03.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA	EST390625 MAGE resequences, MAGP Homo sapiens cDNA	EST48b095 WATM1 Homo sapiens cDNA clone 48b095	np78b02.s1 NC_CGAP_Pr2 Homo saplens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens MT-1I mRNA, (HUMAN);	Homo sapiens mRNA for KIAA0980 protein, partial cds	7092b01 x1 NCI_CGAP_Ov18 Homo sepiens cDNA clone IMAGE;3643705 3'	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA	Homo sapiens centaurin-eipha 2 protein (HSA272195), mRNA	7092b01 XT NCI_CGAP_OV18 Homo sepiens cDNA clone IMAGE:3643705 3'	df60e03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486861 5'	d/50e03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486861 5'	602072264F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'	602072264F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215398 57	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'	Homo sapiens Xq pseudoautosomal region; segment 1/2
אחו באחון	Top Hit Database Source	۲N	EST_HUMAN	T	I TOUR	Т		EST HUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN				EST_HUMAN	EST_HUMAN	EST HUMAN	Г	EST_HUMAN			EST_HUMAN	EST_HUMAN of	HUMAN			- HUMAN	LZ.
	Top Hit Acession No.	-46 Z73660.1	A1831462.1	3.0E-46 D31765.1		2.0E-46 AA678246.1		7.	10569	-46 BE869151.1	-46 H48391.1	-46 AW277214.1	4502694 NT	7662177 NT	7662177 NT	6.1	-46 H97330.1	-46 AA631912.1	-46 AB023197.1	-46 BF194707.1	8923762 NT	8923762 NT	-46 BF194707.1		1			1.0E-46 AV715377.1	7
	Most Similar (Top) Hit BLAST E Value	3.0E-46	3.0E-46	3.0E-48	97	2.0E-46	2.0E-48	2.0E-46	2.0E-46	2.0E-46	2.0E-46	2.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46	1.0E-46/	9.0E-47 /
	Expression Signal	1.2	7.59	2.19	791	1.55	3.43	1.2	7.67	1.48	1.5	3.38	7.67	1.23	1.23	3.44	3.06	4.55	3.17	98.9	6.14	6.14	5.27	1.53	1.53	2.28	2,28	2.37	6.18
	ORF SEQ ID NO:	30092	34483	37474	20000	20203	27070	30258				30902	26628	26999	27000	27745	27857	28654		31322	31617	31618	31322	37665	37666	31115	31116		
	Exon SEQ ID NO:	17456	21339	24163	49500	1	į.	17645		20663	25179	25170	13961	14313		15005	15120	16005	17549	18409		25080	18409	24338	24338	24564			13522
	Probe SEQ ID NO:	4724	8647	11564	2,7	1554	1637	4917	7384	7968	12257	12575	1211	1566	1566	2279	2399	3243	4818	5613	5888	5888	10770	11747	11747	12044	12044	12778	750

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4879	17606		3.02	9.0E-47	17 AW770928.1	EST_HUMAN	hI93e04 x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:075703 075703 HYPOTHETICAL 12.4 KD PROTEIN ;
6284	19057	32037	9.0	9.0E-47	11425439 NT	Ę	Homo saplens zinc finger protein ZNF286 (ZNF286), mRNA
12531	25270		2	9.0E-47	11417966 NT	TN	Homo saplens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1801		27252	6.88	8.0E-47	17 Y18536.1	ΤN	Homo sapiens HLA-C gene, exon 5, individual 19323
1801	14541	27253	6.88	8.0E-4	17 Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, İndividual 19323
2722	15429	28167	1.04	8.0E-47	5453955 NT	Ā	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
3024	15790		1.99	8.0E-47	17 AJ229043.1	F	Homo sapiens 959 kb conlig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3613	16366	59009	0.68	8.0E-4	17 AB041926.1	INT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
3613	16366		0.68	8.0E-4	17 AB041926.1	TN	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
12604	25169		1.38	7.0E-47	7.0E-47 AV683284.1	EST_HUMAN	AV683284 GKC Homo sapiens cDNA clone GKCASH11 5'
2550	15265	28000	1.66	6.0E-	17 AL163246.2	ΤN	Homo sapiens chromosome 21 segment HS21C046
8592	21284		0.49	6.0E-4	17 U77054.1	EST_HUMAN	HSU77054 Human Homo saplens cDNA clone N7
9176	21846		6.76	6.0E-4	17 AI695189.1	EST_HUMAN	tz98h02.x1 NCL_CGAP_Kid11 Homo saplens cDNA clone IWAGE:2236659 3'
9612	22265		0.68	6.0E-	7 AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
9612	22265		0.68	6.0E-	6.0E-47 AB042824.1	NT	Homo saplens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6482	19249		6.67		11423972 NT	ΤN	Homo saplens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
10896	23387		5.27	5.0E-47	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
1379	14126	26801	3.29	4.0E-47	4557556 NT		Homo saplens E1A binding protein p300 (EP300) mRNA
6733	19567	32599	1.9	4.0E-4	7 BE938896.1	EST_HUMAN	MR4-TN0108-280800-201-d04 TN0108 Homo sapiens cDNA
8379	21072		2.42	4.0E-47	7 BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo saplens cDNA clone IMAGE:3622437 5'
8379	21072		2.42	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sepiens cDNA clone IMAGE:3622437 5'
8516	21208	34351	0.61	4.0E-47	7 AW993777.1	EST_HUMAN	RC3-BN0034-220300-015-f05 BN0034 Homo sapiens cDNA
11635	24232		2.83	4.0E-47	7 AW 515509.1	EST_HUMAN	xx66b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA done IMAGE:2848597 3' similar to SW:INT6_MOUSE Q64252 VIRAL INTEGRATION SITE PROTEIN INT-8. [1];
531	13315	25950	2.05	3.0E-47	7 BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
531	13315		2.05	3.0E-4	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
799	13571		6.45	3.0E-4	N57483.1	EST_HUMAN	yy64b04.s1 Soares_multiple_sclerosis_ZNbHMSP Homo sapiens cDNA clone IMAGE:277327 3'
924	13691		10.25	3.0E-4	7 AL163284.2	NT	Homo sapiens chromosome 21 segment HS21 C084
3296	16058		0.79		4504116 NT	ΝŢ	Homo sapiens glutamate receptor, ionotropic, kalnate 1 (GRIK1) mRNA
3948				3.0E-4	3.0E-47 U93181.1	딛	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
4328		29696		3.0E-47	7 M12959.1		Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
5922	18707		5.41	3.0E-47	17 AW 408800.1	EST_HUMAN	UI-HF-BM0-adx-d-07-0-UI,r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5922	18707	31660	5.41	3.0E-47	47 AW 408800.1	EST_HUMAN	UI-HF-BM0-adx-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6469			1.76	3.0E-47	47 AI222413.1	EST HUMAN	qh04e07.x1 Soares_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1843716 3'
8732	21424	34569	0.71	3.0E-47	47 AW963796.1	EST_HUMAN	EST375869 MAGE resequences, MAGH Homo saplens cDNA
8732	L	34570	0.71	3.0E-47	47 AW963796.1	EST_HUMAN	EST375869 MAGE resequences, MAGH Homo sapiens cDNA
143	L	25600	1.61	2.0E-47	4505318/NT	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
8	L	26377	2.69	2.0E-47		L	Homo sapiens chromosome 21 segment HS21C009
947	<u> </u>		2.69	2.0E-47	2.0E-47 AL163209.2	ΤN	Homo sapiens chromosome 21 segment HS21C009
1560	<u> </u>	١		2.0E-47	AI969279.1	EST_HUMAN	wq96b02.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2479851 3'
1588	14334	27022	1.75			ΤN	Homo saplens KIAA0426 gene product (KIAA0426), mRNA
1673				2.0E	AA5245	14.1 EST HUMAN	ng43h12.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937607 3'
4313			2	2.0E	4504868	ΤN	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4351	L		1.5	2.0E	47 AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652
4351	L_		1.5	2.0E	47 AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_Pr1 Homo saplens cDNA clone IMAGE:914652
4471	17206		1.66	2.0E-47	5174648 NT	Į.	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4761	L	l		2.0E	-47 AW965166.1	EST_HUMAN	EST377239 MAGE resequences, MAGI Homo saplens cDNA
9899	İ		_	2.0E	47 AF073921.1	TN	Homo saplens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
5887	ı	31615		2.0E	-47 BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3887487 5
5887				2.0E	-47 BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo saplens cDNA clone IMAGE:3867487 5
7598	l		1.43	2.0E	-47 L09731.1	LΝ	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
7864	20559	33685	1.92	2.0E	47 D87675.1	NT	Homo saplens DNA for amytold precursor protein, complete cds
7864	L	33686		2.0E	-47 D87675.1	LN	Homo saplens DNA for amyloid precursor protein, complete cds
8618				2.0E	-47 AF071771.1	TN	Homo sapiens SPH-binding factor mRNA, partial cds
9389	L	35222	0.77	2.0E-47	11528136 NT	N	Homo sapiens BTG family, member 3 (BTG3), mRNA
11451	L	36451	1.27	2.0E-47	-47 M76125.1	LΝ	Human tyrosine kinase receptor (axt) mRNA, complete cds
	L						y/92e08.s1 Soares infant brain 1NIB Home sapiens cDNA clone IMAGE:29968 3' similar to contains OFK
12077	7 25312	30709	1.75	2.0E	-47 R42423.1	EST_HUMAN	repetitive element;
1387	L			1.0E	47 Al333429.1	EST_HUMAN	qp99h03.x1 Scares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
5017	L	L		1.0E	_	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Home saplens cDNA
	L			,	000	14 4 7 1 1 1 L	at19e06.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995 DAS DEI ATED PROTEIN RAD-AA (HLIMAN):
6944	19426	32441	6.79	Ď.	-47 AIBBUBBO.1	ESI HOMBIN	POSTALEDITEDITEDITEDITEDITEDITEDITEDITEDITEDIT
8767	21459		0.58		1.0E-47 AW 664648.1	EST_HUMAN	hi84a11.X1 Soarss_NFL_I_GBC_S1 Homo eaplens curva cione invace297.037.2 3 similar to go.iv.zo323 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1006		28112				μN	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
570	ŀ						